

937

```

201 TATGCCGCCC GAAAAACGCC GTATCTCGCT GATGTTTCAA GATTACGCGC
251 TGTTCCTCCCA TATGAGTGGC CTGGAAAATG CGGCATTTCGG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAACGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAA AACTTTCCG
401 GAGGCGAGAA GCAACGGCTG GCGTTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTTC AGTTTGGACA CGCATTTCGG
501 CGGCACGCTG CGCCGTATGA CTGCCGAACG TATCCGAAAC GGCGGCATCC
551 CTGCCGTTTT GGTAAACGCAT TCGCCCGAAG AAGCCTGTAC GACGGCAGAC
601 GAAATCGCCG TGATGCATAA AGGGAGGATT CTACAATACG GTACGCCCGA
651 AACATTGGTC AAAACACCAT CTGCGTGCA GGTCCGCCGA CTGATGGGTT
701 TGCCCAATAC CGACGATAAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCGGCACGCC GGGGCGGTAT CGGGCAAGGA TACGGTACGC
901 ATCCATATCG AAGAACGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1856; ORF 593>:

```

m593.pep ..
1 MLELNLCKR FGNKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNIIAGI
51 VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAAGFLKM
101 QKMPKAEAE LAMAALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRGTL RRMTAERIRN GGIPAVLVTH SPEEACTTAD
201 EIAVMHKGRI LQYGPETLV KTPSCVQVAR LMGLPNTDDN RHIPQHVRV
251 DQDGMCECVL SRTCLPESFS LSVLHPEHGI LWLNLMRHA GAVSGKDTVR
301 IHIEREIVR FR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m593 / g593 83.4% identity in 313 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKTVDNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
g593	MLELNLCKCFGGKTVADNICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPEKRRISLMFQDYALFPHMSALENAAGFLKMQKMPKAEAEERLAMAALAEVG					
g593	NGENITCMPEKRRISLMFQDYALFPHMSALENTAFGLKMQKMPKAEAEERLALSALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN					
g593	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTTADEIAVMHKGRI LQYGPETLVKTPSCVQVARLMGLPNTDDN					
g593	GGIPAVLVTHSPEEACTTADEIAVMHEGKILQCGTPETLIQT PAGVQVARLMGLPNTDDD					
	190	200	210	220	230	240

	250	260	270	280	290	299
m593.pep	RHIPQHAVRFDDQGM	ECRVLSRTCLPESF	SLSVLHPEHGILWL	NLDM-RHAGAVSGKDTV		
	:    :  :	:    :    :  :	:	: :  : :		
g593	RHIPQNAVCLDNHGT	ECRLSLVRLPDSLRL	SAVHPEHGELTNLNT	VTVGQHTDGISGNGTV		
	250	260	270	280	290	300
	300	310				
m593.pep	RIHIEEREIVRFRX					
	:::  :					
g593	RIRVDEGRIVRFRX					
	310					

```
a593.seq
1  ATGCTTGAAC  TGAACGGACT  CTGCAAACGC  TTCGGCGGCA  AAACGGTTGC
51  GCACGATATC  TGCCTGACTG  TCGGGCCCGG  CAAATACTC  GCCCTTTTGG
101 GCGCGTTCGG  CTGCGGCAAA  TCCACCTGCG  TGAATATGAT  TCGGGGATCG
151 GTCCGGCCGG  ACGGCGGGGA  AATATGGCTG  AATGGGGAAA  ACATTACCCG
201 TATGCCCGCC  GAAAAACGCG  GTATTTCGCT  GATGTTTCAA  GATTACGCGC
251 TGTTTCCCCA  TATGAGTGCA  CTGGAAAATG  CGGCATTCGG  TTTGAAAAATG
301 CAAAAAATGC  CGAAAGCCGA  AGCCGAAAGC  TCGCCCATGG  CGGCATCTGC
351 CGAAGTCGGA  CTGGAAAACG  AGGCGCACCG  CAAGCCTGAN  AAACCTTTCCG
401 GAGGCGAAAA  GCAACGGTTG  GCATCTGGCG  GCGCTTTGGT  TGTCCGCCCT
451 TCCCTGCTGC  TGTTTGGACG  ATCGTTTTC  AGTTTGGACA  CGCATTTGCG
501 CGACCGGCTG  CGCCGCATGA  CTGCGGAACG  TATCCGCAAG  GCGCGCATCC
551 CTGCCGTTTT  GGTACGCAT  TCGCCCGAAG  AGGCCTGCAC  GCGCGCAGAC
601 GAAATCGCGC  TCATGCACGA  GGGGAAAATC  CTTCAATGCG  GTACGCGGCG
651 AACCTTGGTT  CAAACGCCTG  CGCGCGTGCA  GGTCGCCCAT  CGTATGGGGC
701 TGCCCAATAC  CGACGATGAC  CGCCATGCA  GCGCAACATG  CGTGCGCTTC
751 GACCAAGACG  GCATGGAGTG  CCGCGTATTA  TCCCGTACCT  GTTTGCCCGA
801 ATCGTTCAGC  CTGTCCGTCC  TCCATCCGGA  ACACGGCATC  CTGTGGCTGA
851 ACCTCGATAT  GCCGCACGCC  TGTGAAATAT  CGGGAACAGA  TACGGTACGC
901 ATCCATATCG  AAGACAGGGA  AATCGTCCGC  TTCCGCTGA
```

```
a593.pep
1 MLELNLGCKR FGGKTVADDI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51 VRPDGGEIWL NGENITRMPD EKRRISLMFQ DYALFFPHMSA LENAAGFLKM
101 QKMPKAEAES LAMALAEEVG LENEAKRKPX KLSGGEQRLL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCTPPTLV QTPAVQVAH LMGLPNTDDD RHPQHAVRF
251 DDGMECRVL SRTCLPEFS LSVLHPEHGI LWNLDMPHA GEISGNDTVR
301 IHIEDREIVR FR*
```

	10	20	30	40	50	60
m593.pep	MLELNGLCKRFGNKT	VADNICLT	VGGRGKILAVL	GRSGCGKSTLL	NIAGIVR	PDGGEIWL
a593	MLELNGLCKRFGGKT	VADDICLT	VGGRGKILAVL	GRSGCGKSTLL	NMIAGIVR	PDGGEIWL
	10	20	30	40	50	60
m593.pep	70	80	90	100	110	120
	NGENITRMPPEKRRIS	LMFQDYALFPHMSA	LENAAFGLKMKMPKAE	AERLAMAALAEVG		
a593	NGENITRMPPEKRRIS	LMFQDYALFPHMSA	LENAAFGLKMKMPKAE	ESLAMAALAEVG		
	70	80	90	100	110	120
m593.pep	130	140	150	160	170	180
	LENEAHRKPEKLSGGE	KQRLALARALVVRPS	LLLLDESFS	SLDTHLRGTLRRMTA	ERIRN	
a593	LENEAHRKPKKLSGGE	KQRLALARALVVRPS	LLLLDESFS	SLDTHLRDLRRMTA	ERIRK	
	130	140	150	160	170	180
m593.pep	190	200	210	220	230	240
	GGIPAVLVTHSPEEAC	TDAEIAVMHKGRI	LQYGT	PETLVKTPSCVQ	VARLMGLPNTDD	

```

      |||||::|||::|||::|||::|||:
a593   GGIPAVLVTHSPEEACTAADEIAVMHEGKILQCGTPETLVQTPAGVQVAHLMLPNTDD
            190        200        210        220        230        240

                250        260        270        280        290        300
m593.pep RHIPQHAFVRFDQDGMCECRLSRTCLPEFSLSVLHPEHGILWLNLDMRHAGAVSGKDTVR
|||||::|||::|||::|||::|||:
a593   RHIPQHAFVRFDQDGMCECRLSRTCLPEFSLSVLHPEHGILWLNLDMPHAGEISGNDTVR
            250        260        270        280        290        300

              310
- m593.m593.pep IHIEEREIVRFRX
              |||||::|||
a593   IHIEDREIVRFRX
              310

```

g594.seq..

g594.pcp

m594.seq

m594.pep

m594 / g594 98.1% identity in 158 aa overlap

940

	10	20	30	40	50	60
m594.pep	MGADTDGDKD	VRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP				
g594	MGADTDGDKD	VRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP				
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
g594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRCQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
g594	DFLIHYSVVLIFWECRAIKHCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1863>:

```
a594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAACTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GCGCGCCTTG
251 GCTTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTCGC GAGTGTCAGG AAACGGCGGC
351 GGCCGTTGTT GATTTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGGAAATACCG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTTAAAT AAGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1864; ORF 594.a>:

```
a594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIIHYSV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*
```

m594/a594 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m594.pep	MGADTDGDKD	VRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP				
a594	MGADTDGDKD	VRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP				
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
a594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
a594	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1865>:

```
g595.seq..
1  atgagaaaat tcaatttgac cgcattgtcc gtgatgcttg ccttggttt
51  gaccgcgtgc cagccgccgg aggcggagaa agccgcgccg gccgcgtccg
101 gtgagacca atccgccaac gaaggcggtt cggtcggtat cgccgtcaac
```



151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt  
201 gttcaatatt aaaaacaaca gcggccgcaa gctcgaatgg gaaatcctga  
251 agggcgtgat ggtggtggac gaacgcgaaa atatcgcccc ggggctttcc  
301 gacaaaatga accgtaacct gctgccgggc gaatacgaat tgacctgcgg  
351 ccttttgacc aatccgcgcg gcaagctggt ggtagccgac agcggcttta  
401 aagacaccgc caacgaagcg gatttggaat aactgcccc accgctcgcc  
451 gactataaag cctacgttca aggcgaggtt aaagagctgg cggcgaaaac  
501 caaaaccttt accgaagccg tcaaagcagg cgacattgaa aaggcgaaat  
551 ccctgtttgc cgccaccgcg gtccattacg aacgcacga accgattgcc  
601 gagcttttca gcgaactcga ccccgatcgc gatgcgtgtg aagacgactt  
651 caaagacggt gcgaaagatg ccgggtttac cggcttccac cgtatcgaac  
701 acgccctttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcggcc  
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgattggc  
801 gttccctccg ggcaaagtgg tcggcggcgc gtccgaactg attgaagaag  
851 cggcgggcag taaaatcagc ggcgaagaag accgttacag ccacaccgat  
901 ttgagcgact tccaagctaa tgcggaacgga tctaaaaaaa tcgtcgattt  
951 gttccgtccg ttgattgagg ccaaaaacaa agccttggtt gaaaaaacg  
1001 ataccaactt caaacaggtc aacgaaattc tggcgaaata ccgcaccaa

942

1051 gacggttttg aaacctacga caagctgagc gaagccgacc gcaaagcatt  
 1101 acaggctcct attaacgcgc ttgccgaaga ccttgcccaa cttcgcgga  
 1151 tactcggcct gaaataa

This corresponds to the amino acid sequence <SEQ ID 1866; ORF 595.ng>:

g595.pep ..  
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIAVN  
 51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS  
 101 DKMNRNLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA  
 151 DYKAYVQGEV KELAAKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA  
 201 ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA  
 251 KLMTDVEALQ KEIDALAFPP GKVVGGADEL IEEAAGSKIS GEEDRYSHTD  
 301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK  
 351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRILGLK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1867>:

m595.seq  
 1 ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT  
 51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG  
 101 GTGAGGCGCA AACCGCCAAC GAGGCGGGTT CGGTCACTAT CGCCGTC AAC  
 151 GACAATGCCT GCGAACCAGT GGAAGTACG GTGCCGAGCG GACAGGTTGT  
 201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA  
 251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC  
 301 GATAAAATGA CCGTCACCTT GTTGCCGGGC GAATACGAAA TGACTTGCGG  
 351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA  
 401 AAGACACGCG CAACGAAGCG GATTTGAAA AACTGTCCCA ACCGCTCGCC  
 451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC  
 501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAT  
 551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC  
 601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT  
 651 CAAAGACGCG GCGAAAGATG CCGGATTAC CGGCTTTCAC CGTATCGAAT  
 701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG  
 751 AAAGTATGTA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGATTGGC  
 801 GTTCCCTCCG GCGAAGGTGG TCGGCGGCGC GTCCGAATCG ATTGAAGAAG  
 851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGCTACAG CCACACCGAT  
 901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATT  
 951 GTTCCGTCCG CTGATCGAGG CCAAAAACAA AGCCTTGTG GAAAAACCG  
 1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA  
 1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT  
 1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGCA  
 1151 TACTCGGCTT GAAATAA

This corresponds to the amino acid sequence <SEQ ID 1868; ORF 595>:

m595.pep  
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIAVN  
 51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS  
 101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA  
 151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA  
 201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA  
 251 KLMTDVEALQ KEIDALAFPP GKVVGGADEL IEEVAGSKIS GEEDRYSHTD  
 301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK  
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRILGLK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m595 / g595 95.4% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTAN	EGGSVSIAVN	DNACEPMELT
g595	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGETQSAN	EGGSVGIAVN	DNACEPMNLT
	10	20	30	40	50	60
	70	80	90	100	110	120

943

m595.pep	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
g595	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMNRNLLPGEYEMTCGLLT
	70 80 90 100 110 120
m595.pep	130 140 150 160 170 180
	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTTEAVKAGDIE
g595	NPRGKLVVADSGFKDTANEADLEKLPQPLADYKAYVQGEVKELAAKTKTFTTEAVKAGDIE
	130 140 150 160 170 180
m595.pep	190 200 210 220 230 240
	KAKSLFADTRVHYERIEPIAE L FSELD PVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK
g595	KAKSLFAATRVHYERIEPIAE L FSELD PVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK
	190 200 210 220 230 240
m595.pep	250 260 270 280 290 300
	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD
g595	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEAAGSKISGEEDRYSHTD
	250 260 270 280 290 300
m595.pep	310 320 330 340 350 360
	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTD TNFKQVNEILAKYRTKDG FET YDKLG
g595	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTD TNFKQVNEILAKYRTKDG FET YDKLS
	310 320 330 340 350 360
m595.pep	370 380 389
	EADRKALQASINALAEDLAQLRGILGLKX
g595	EADRKALQAPINALAEDLAQLRGILGLKX
	370 380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

```

a595.seq
1  ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTAGGTTT
51  GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCAGTAT CGCCGTCAAC
151 GACAATGCCT CGCAACCGAT GGAACGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAATGA CCGTCACCTT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGAAA AACTGTCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTCA AGGCGAAGTC AAAGAGCTGG TGGCGAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCGTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAACGTATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACGT ATTGAAGAAG
851 TGGCGGGCAG TAAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAAA TCGTTCGATT
951 GTTCCGTCCG TTGATCGAGA CAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CTTGCCCAA CTTGCGGCGA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

```

a595.pep
1  MRKENLTALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIQVN
51  DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVVD ERENIAPGLS

```

944

```

101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

```

m595/a595 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNL	TALSVM	LALGLT	ACQPPE	AEKAAPA	ASGEAQT
a595	MRKFNL	TALSVM	LALGLT	ACQPPE	AEKAAPA	ASGEAQT
	10	20	30	40	50	60
	70	80	90	100	110	120
m595.pep	VPSGQV	VFNKNNS	GRKLEWE	ILKGMV	VDERENI	APGLSDK
a595	VPSGQV	VFNKNNS	GRKLEWE	ILKGMV	VDERENI	APGLSDK
	70	80	90	100	110	120
	130	140	150	160	170	180
m595.pep	NPRGKL	VVTDSG	FKDTANE	ADLEKLS	QPLADY	KAYVQGE
a595	NPRGKL	VVTDSG	FKDTANE	ADLEKLS	QPLADY	KAYVQGE
	130	140	150	160	170	180
	190	200	210	220	230	240
m595.pep	KAKSLF	ADTRVH	YERIEPI	AEELFSE	LDPVIDA	REDDFKD
a595	KAKSLF	ADTRVH	YERIEPI	AEELFSE	LDPVIDA	REDDFKD
	190	200	210	220	230	240
	250	260	270	280	290	300
m595.pep	DVSGVKE	IAAKLMT	DVEALQ	KEIDALA	FPFGKV	VGGASEL
a595	DVSGVKE	IAAKLMT	DVEALQ	KEIDALA	FPFGKV	VGGASEL
	250	260	270	280	290	300
	310	320	330	340	350	360
m595.pep	LSDFQAN	VDGSKK	IVDLFR	PLIEAKN	KALLEKT	DTNFKQV
a595	LSDFQAN	VDGSKK	IVDLFR	PLIEAKN	KALLEKT	DTNFKQV
	310	320	330	340	350	360
	370	380	389			
m595.pep	EADRKAL	QASIN	ALAEDLA	QLRGIL	GLKX	
a595	EADRKAL	QASIN	ALAEDLA	QLRGIL	GLKX	
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1871>:

g596.seq. (partial).

```

1 ..atgctgctct tggacgagcc gaccaaccac ttggatgcgg aatcggtgga
51 atggctggag caattcctcg tgcgcttccc cggcacagtg gtcgcggttaa
101 cgcacgaccg ctacttcctc gacaacgccg ccgaatggat ttggaactc
151 gaccgcggac acggcattcc gtggaaaggc aattactcgt cttggctgga
201 gcagaaagaa aaacgccttg aaaacgaggc gaaatccgaa gccgcgcgcg
251 tgaaggcgat gaagcaggaa ttggaatggg tgcgccaaaa tgccaaaggc
301 cgccaagcca agcccaaagc gcgtttggcg cgttttgaag aaatgagcaa
351 ctacgaatac caaaaacgca acgaaactca ggaaatcttt atccctgttg
401 ccgagcggtt gggtaacgaa gtgattgaat ttgtgaatgt ttccaaatcg

```

945

```

451   ttcggcgata aagtgtgat tgacggtttg agcttcaaag tgcgggcggg
501   cgcgattgtc ggcacatcgc gccgaacgg cgcgggtaaa tcgacgctgt
551   tcaaaatgat tgcgggcaaa gagcagcccg attcgggcga agtgaaaatc
601   gggcaaacgg tgaaaatgag cttgattgac caaagccgcg aaggtttgca
651   aaacgacaaa accgtgttcg acaacattgc cgaaggtcgc gatattttgc
701   aggtcggaca gtttgaaatc cccgcccgcc aatatttggg acgcttcaac
751   tttaaaggca gcgaccaaag caaaatcgca aggcagcttt ccggcggcga
801   acgcgccgct ctgcacttgg caaaaacctt gttgggcggc ggcaatgtgt
851   tgctgctgga cgaaccgtcc aacgatctcg acgtggaaac cctgcgcgcg
901   ttggaagacg cattgttgga atttgccggc agcgtgatgg tgatttcgca
951   cgaccgctgg tttctcgacc gcatagccac gcatatcttg gcgtgtgaag
1001  gcgactccaa atgggtgttc ttcgacggca actatcaaga atacgaagcc
1051  gacaagaaac gccgactcgg caaagaaggc gcgaaaccga aacgcacaa
1101  atacaaaccg gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

g596.pep (partial).

```

1   ..MLLLDEPTNH LDAESVEWLE QFLVRFPGTV VAVTHDRYFL DNAAEWILEL
51  DRGHGIPWKV NYSSWLEQKE KRLNEAKSE AARVKAMKQE LEWVRQNAKG
101 ROAKPKARLA RFEEMSNYEY QKRNETQEIF IPVAERLNE VIEFVNVSKS
151 FGDKVLIDGL SFKVPAGAIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201 GQTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVGQFEI PARQYLGRFN
251 FKGSDDQSKIA RQLSGGERGR LHLAKTLGG GNVLLLEDEPS NDLDVETLRA
301 LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF FDGNYQEYEA
351 DKKRRLGKEG AKPKRIKYKP VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1   ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTG AAGATATTTC CCTTCTTTC TTCCCCGGCG
101 CGAAAATCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTGTATCCGG
251 AAAAAACCGT GCGCAGGAA GTGAAAGCG GTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAAGA AGTGTATGCC GAGTACGCCA ATCCTGATGC
351 GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGA GCGATTATTG
401 CGGCAGGTTG GTCCACGGGC GCGGTGCGG AACACGAATT GGAATCGGCC
451 GCCGACGCGC TGCGCCTGCC GGAATGGGAT GCCAAATCG ATAATTGTG
501 CGGCGGTGAA AAACGCCGCG TTGCCTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAAT TCTCGTGCGC TTCCCGGCA CAGTCGTGTC
651 GGTAAACGCAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGCCATGGT ATTCCGTGGA AAGGCAATTA CTCGTCTTGG
751 CTGGAGCAGA AAGAAAAACG CTTGGAAGAC GAGGCAAAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAATGCCA
851 AAGGCCGCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTTT TGAAGAAATG
901 AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTC
951 CGTTGCCGAG CGTTGGGTA ACGAAGTGAT TGAATTTGTA AATGTTTCCA
1001 AATCGTTCGG CGATAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTCGGCAT CATCGGCCCG AACGGCGCGG GTAAATCTAC
1101 GCTGTTCAAA ATGATTTCGG GCAAAGAGCA GCCTGATTCC GGCGAGGTGA
1151 AAATCGGACA AACCGTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GCCGCGACAT
1251 TTTGCAGGTT GGTCAAGTTG AAATCCCGC CCGCCAATAT TTGGGGCGTT
1301 TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGTCA ATTGTCTGGC
1351 GCGCAACGCG GTCGTCTGCA CTTGGCAAAA ACCTTGTGTA GCGGCGGCAA
1401 TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCTGTC
1451 GCGCGTTGGA AGACGCATTG TTGGAATTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GTTGGTTCCT CGACCGCATC GCCACGCATA TCTTGGCGTG
1551 TGAAGGCGAC TCTAAATGGG TGTCTTCGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACGC
1651 ATCAAATACA AACCGGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

946

```

1  MSQQYVYSML RVSKVVPQK TTIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAHEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILELDRGHG IPWKGNYSW
251 LEQKEKRLEN EAKSEAAVRK AMKQELWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSEFKVP
351 AGAIVGIIGP NGAGKSTLTK MISGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKIAGQLSG
451 GERGLHLAK TLLSGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYADKKRR LGEEGAKPKR
551 IKYKPVTR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m596 g596 98.4% identity in 373 aa overlap

	160	170	180	190	200	210
m596.pep	LPEWDAKIDNLSGGEKRRVALCKLLLSKPDMLLLEPTNHLDAESVEWLEQFLVRFPQTV					
g596						
				10	20	30
	220	230	240	250	260	270
m596.pep	VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLENEAKSEAAVRKAMKQE					
g596						
	40	50	60	70	80	90
	280	290	300	310	320	330
m596.pep	LEWVRQNAKGRQAKSKARLARFEEMSNYEYQKRNETQEIFIPVAERLGNIEFVNVSKS					
g596						
	100	110	120	130	140	150
	340	350	360	370	380	390
m596.pep	FGDKVLIDDLSEFKVPAGAIVGIIIGPNAGKSTLTKMISGKEQPDGSEVKIGQTVKMSLID					
g596						
	160	170	180	190	200	210
	400	410	420	430	440	450
m596.pep	QSREGLQNDKTVFDNIAEGRDILQVVGQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGR					
g596						
	220	230	240	250	260	270

947

	460	470	480	490	500	510
m596.pep	LHLAKTLLSGGNVLLLD	DEPSNDLDVETLRALED	ALLEFAGSVMVISHDRW	FLDRIATHIL		
g596	LHLAKTLLGGGNVLLLD	DEPSNDLDVETLRALED	ALLEFAGSVMVISHDRW	FLDRIATHIL		
	280	290	300	310	320	330

	520	530	540	550	559
m596.pep	ACEGDSKWVFFDGN	YQEYADKKRRLGEE	GA	PKRIKYPVTRX	
g596	ACEGDSKWVFFDGN	YQEYADKKRRLGEE	GA	PKRIKYPVTRX	
	340	350	360	370	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1875>:

```

a596.seq
1  ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTA AAGATATTTC CTTTCTTTTC TTCCCCGGCG
101 CGAAAATCGG TTTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAAGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGTATT AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGTGAGGAA GTGGAAGCG GTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAGGA AGTGTATGCC GAGTACGCCA ATCCCGATGC
351 GGATTTTGAC GCGTTGGCGG AAGAGCAGGG GCGTTTGAA GCGATTATTG
401 CGCGCGGTTT GTCCACGGGC GCGGTGCGG AACACGAATT GGAAATCGCT
451 GCGGACGGCG TGCGCTGCC GGAATGGGAT GCCAAATCG ATAATTGTC
501 CGGCGGTGAA AAACGCCGCG TCGCTTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGAGCAATT TCTCGTGC GC TCCCCGGTA CAGTCGTTGC
651 CGTAACACAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGGCACGGT ATTCCGTGGA AAGGAAATTA CTCGTCTTGG
751 TTGGAGCAGA AAGAAAAACG TTTGGAAAAC GAGGCGAAT CCGAAGCCGC
801 GCGCGTGAAA GCGATGAAGC AGGAATGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGTC AAGCAAGTCC AAAGCGCGTT TGGCGCGTTT TGAAGAAATG
901 AGCAACTATG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTCATTCC
951 CGTCGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTG AATGTTTCCA
1001 AATCGTTCGG CGACAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTGCGCAT CATCGGTCCG AACGGCGCGG GTAAATCGAC
1101 ACTGTTTAAA ATGATTGCGG GCAAAGAGCA GCCCGATTCC GGTGAAGTGA
1151 AAATCGGGCA AACCGTGAAA ATGAGCTTGA TTGACCAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GTCGCGATAT
1251 TTTACAGGTC GGGCAGTTTG AAATCCCCGC CCGCCAATAT TTGGGACGCT
1301 TCAATTTCAA AGGCAGCGAC CAAAGCAAAA TCACGGGGCA GCTTTCGGC
1351 GCGCAACGCG GACGTTTGCA CTTGGCAAAA ACCTTGTTGG GCGGTGGCAA
1401 TGTGTTGCTG CTGGACGAAC CGTCCAACGA CCTCGACGTG GAAACCCTGC
1451 GCGCGTTGGA AGACGCATTG CTGGAATTG CCGGCAGCGT GATGGTGATT
1501 TCGCAGGACC GCTGGTTCCT CGACCGTATT GCTACGCATA TCTTGGCTTG
1551 CGAAGGCGAC TCCAATGGG TGTTCTTTGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGA CTCGGCGAAG AAGGCACGAA ACCGAAACGC
1651 ATCAAATACA AACCGGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1876; ORF 596.a>:

```

a596.pep
1  MSQQYVYSML RVSKVPPQK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADFD ALAEQGRLE AIIAAGSSTG GGAHEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAEE WILELDRGHG IPWKNYSWSW
251 LEQKEKRLEN EAKSEARVK AMKQELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSEFKVP
351 AGAIVGIIGP NGAGKSTLFK MIAGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRENFKGSD QSKITGQLSG
451 GERGRHLHAK TLLGGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGN YQEYADKKRR LGEEGTPKPKR
551 IKYKPVTR*

```

m596/a596 99.3% identity in 558 aa overlap

948

m596.pep	10	20	30	40	50	60
	MSQQYVYSMLRVSKVVPQKTI IKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
a596	MSQQYVYSMLRVSKVVPQKTI IKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
	10	20	30	40	50	60
m596.pep	70	80	90	100	110	120
	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
a596	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
	70	80	90	100	110	120
m596.pep	130	140	150	160	170	180
	ALAEQGRLEAIIAAGSSTGGGAHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
a596	ALAEQGRLEAIIAAGSSTGGGAHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
	130	140	150	160	170	180
m596.pep	190	200	210	220	230	240
	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
a596	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
	190	200	210	220	230	240
m596.pep	250	260	270	280	290	300
	IPWKGNYSWLEQKEKRLNEAKSEAA RVKAMQELEWVRQNAKGRQAKSKARLARFEEM					
a596	IPWKGNYSWLEQKEKRLNEAKSEAA RVKAMQELEWVRQNAKGRQAKSKARLARFEEM					
	250	260	270	280	290	300
m596.pep	310	320	330	340	350	360
	SNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKSFGDKVLIDDL SFKVPAGAIVGII GP					
a596	SNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKSFGDKVLIDDL SFKVPAGAIVGII GP					
	310	320	330	340	350	360
m596.pep	370	380	390	400	410	420
	NGAGKSTL FKMISGKEQPD SGEVKIGQTVKMSLIDQSREGLQNDKT VFDNIAEGRDILQV					
a596	NGAGKSTL FKMISGKEQPD SGEVKIGQTVKMSLIDQSREGLQNDKT VFDNIAEGRDILQV					
	370	380	390	400	410	420
m596.pep	430	440	450	460	470	480
	GQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGRHLAKTLLSGGNVLLLDEPSNDLDV					
a596	GQFEIPARQYLGRFNFKGSDQSKITGQLSGGERGRHLAKTLLSGGNVLLLDEPSNDLDV					
	430	440	450	460	470	480
m596.pep	490	500	510	520	530	540
	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGN YQEYEADKKRR					
a596	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGN YQEYEADKKRR					
	490	500	510	520	530	540
m596.pep	550	559				
	LGEEGAKPKRIKYKPVTRX					
a596	LGEEGTPKPKRIKYKPVTRX					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1877>

g597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCTCAAA CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAA CAGCGCGAGG CTTGGGACAA ATTCCAAAA

```



949

```

151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTC CGTTTCGTAT CGGGGAAC TA AAAACAGC CGGCCGAATG
251 CGGTTGCCCT GTTCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAGG TTGTCAAGGA
351 TTTGGAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTGAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGCGCGGAA CAGACGGAAG GCCCGAGACA
501 GAATGCCAAA ATCTCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGgagaa aaAAAAagcc
601 gaacaccgCA TtcaggAtgc ggAagcaaAA agaAAATTGG CTGAagcCaa
651 actGgcggca gccgAAAAAG CCAGAAAAGA AGCGCGCAG CAGAAGGCTG
701 AAGCGCGACG TCGGGAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGgTT TCAGCCGCAT
801 GCAGGGACGT TTGAAAAAC CGGTTGACGG TGTGCCGACC GGGCTTTTCG
851 GGCAGAACCG GAGCGGcggC GATGTTTGA AAGCGGTGT CTATTCCACT
901 GCGCCTGCAA CGGTTGAAAG CATTGCGCg gAACggtaa GCTATGCGGA
951 cgaGTTGGAC GGCTACGGCA AAGTGGTCTG GATCGATCAC GGCAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCCGCCGG CAAGGGTTAT
1051 ACGGTCGCGG CAGGAAGCAA AATCGGCAG AGCGGGTCG TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCGAGGTCAG GTGTTGAACC
1151 CTTCGGGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1878; ORF 597>:

```

g597.pep
1 MLLHVSNSLK QLQEEIRQE RIRQERIRQA RGNLASVNRK QREAWDKFQK
51 LNTELNRKLT EVAATKAQIS RFVSGNYKNS RPNVAFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QOKALAVQEQ KINNELARLK KIQANVQSLN
151 KKQGVTDAAE QTESRRQNAK ISKDARKLLE QKGNEQQNLN LLSNLEKKKA
201 EHRIQDAEAK RKLAEAKLAA AEKARKEAQA QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVMKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVIDH GENYISIIYAG LSEISAGKGY
351 TVAAGSKIGT SGSLPDGEEG LYLQIRYRGQ VLNPSGWIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1879>:

```

m597.seq
1 ATGCTGCTTC ATGTCAGCAA TTCCTCATA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAGAG CGTATCCGTC AGGCGCGCGG CAACCTTGCT TCCGTCAACC
101 GCAAACAGCG CGAGGCTTGG GACAAGTTCC AAAAAGTCAA TACCGAGCTG
151 AACCGTTTGA AAACGGAAGT CGCCGCTACG AAAGCGCAGA TTTCCTGTTT
201 CGTATCGGGG AACTATAAAA ACAGCCAGCC GAATGCGGTT GCCCTGTTCC
251 TGAAAAACGC CGAACCGGGT CAGAAAAACC GCTTTTTCGG TTATACGCGT
301 TATGTAACG CCTCCAATCG GGAAGTTGTC AAGGATTGGA AAAAAACAGC
351 GAAGGCTTTG GCGGTACAAG AGCAGAAAAA CAACAATGAG CTTGCCGTT
401 TGAAGAAAAT TCAGGCAAAC GTCAATCTC TGCTGAAAAA ACAGGGTGTA
451 ACCGATGCGG CGGAACAGAC GGAAGCCCGC AGACAGAATG CCAAATCGC
501 CAAAGATGCC CGAAAACTGC TGGAAACAGAA AGGGAACGAG CAGCAGCTGA
551 ACAAGCTCTT GAGCAATTG GAGAAGAAAA AGGCCGAACA CCGCATTCAG
601 GATGCGGAAG CAAAAAGAAA ATTGGTGAA GCCAGACTGG CGGCAGCCGA
651 AAAGGCCAGA AAAGAAGCGG CGCAGCAGAA GGCTGAAGCA CGACGTGCGG
701 AAATGTCCAA CCTGACCGCC GAAGACAGGA ACATCCAAGC GCCTTCGGTT
751 ATGGGTATCG GCAGTGCCGA CGGTTTCAGC CGCATGCAAG GACGTTTGAA
801 AAAACCGGTT GACGGTGTGC CGACCGGACT TTTCCGGCAG AACCGGAGCG
851 GCGGCGATAT TTGGAAGGC GTGTTCTATT CCACTGCACC GGCAACGGTT
901 GAAAGCATTG CGCCGGGAAC GGTAAAGTAT GCGGACGAGT TGGACGGCTA
951 CGGCAAAGTG GTCGTGGTCG ATCACGGCGA GAACTACATC AGCATCTATG
1001 CCGGTTTGAG CGAAATTTCC GTCGGCAAGG GTTATATGGT CGCCGCAGGA
1051 AGCAAAATCG GTCGAGCGG GTCGCTGCCG GACGGGGAAG AGGGGCTTTA
1101 CCTGCAATAA CGTTATCAAG GTCAGGTATT GAACCTTCG AGCTGGATAC
1151 GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1880; ORF 597>:

```

m597.pep
1 MLLHVSNSLK QLQEEIRQE RIRQARGNLA SVNRRQREAW DKFQKLNTEL
51 NRLKTEVAAT KAQISRFVSG NYKNSQPNVA ALFLKNAEPG QKNRFLRYTR
101 YVNASNREVV KDLEKQOKAL AVQEQKINNE LARLKKIQAN VQSLKKQGV
151 TDAAEQTESR RQNAKIAKDA RKLLEQKQNE QQLNKLNLN EKKKAHRIQ
201 DAEAKRKLAE ARLAAAEKAR KEAAQKQKAE RRAEMSNLTA EDNRNIQAPSV
251 MGIGSADGFS RMQGRLLKPV DGVPTGLFGQ NRSGGDIWKG VFYSTAPATV
301 ESIAPGTVSY ADELGYGKV VVDHGENYI SIYAGLSEIS VGKGYMVAAG
351 SKIGSSGSLP DGEGLYLQI RYQGVNLNPS SWIR*

```

950

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 597 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. gonorrhoeae*:

m597/g597 96.1% identity in 389 aa overlap

	10	20	30	40	50	60
g597.pep	MLLHVSNSLKQLQEERIRQERIRQARGNLSVNRKQREAWDKFQKLNTELNRKLT					
m597	MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLSVNRKQREAWDKFQKLNTELNRKLT					
	10	20	30	40	50	
	70	80	90	100	110	120
g597.pep	EVAATKAQISRFVSGNYKNSRPNALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
g597.pep	QQKALAVQEOKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKISKDARKLLE					
m597	QQKALAVQEOKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
g597.pep	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEAKLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
g597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
g597.pep	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISAGKGYTVAAGSKIGT					
m597	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGRGYMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
g597.pep	SGSLPDGEEGLYLQIRYRGQVLNPSGWIRX					
m597	SGSLPDGEEGLYLQIRYQGQVLNPSWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1881>

a597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAG CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAA CAGCGCGAGG CTTGGGACAA GTTCCAAAAA
151 CTCAATACCG AGCTGAACCG TTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTCC CGTTTCGTAT CGGGGAACTA TAAAAACAGC CAGCCGAATG
251 CGGTTGCCCT GTTCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGGA AAAA CAGCAGAAG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTGAG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TGCGGCGGAA CAGACGGAAA GCCGCAGACA
501 GAATGCCAAA ATCGCCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCCTGAGCA ATTTGGAGAA GAAAAAGGCC
601 GAACACCGCA TTCAGGATGC GGAAGCAAAA AGAAAATTGG CTGAAGCCAG
651 ACTGGCGGCA GCCGAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
701 AAGCAGCAGC TGCGGAAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGTT TCAGCCGCAT
801 GCAAGGACCT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGACTTTTCG
851 GGCAGAACCG GAGCGCGGCG GATGTTTGGG AAGGCGGTGT CTATTCCACT
901 GCACCGGCAA CGGTTGAAAG CATTGCGCCG GGAACGGTAA GCTATGCGGA

```

951

```

951 CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GGTCGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCGGTCGG CAAGGGTTAT
1051 ATGCTCGCGG CAGGAAGCAA AATCGGCTCG AGCGGGTCGC TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCAAGGTCAG GTATTGAACC
1151 CTTGAGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

```

a597.pep
1  MLLHVSNSLK QLQEERIRQE RIRQERIRQA RGNLASVNRK QREAWDKFQK
51  LNTLNLRLKT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK IAKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVDH GENYISYAG LSEISVGKGY
351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQQQ VLNPSWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

m597/a597 98.5% identity in 389 aa overlap

a597.pep	10	20	30	40	50	60
	MLLHVSNSLKQLQEERIRQERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNLRLKT					
m597	MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNLRLKT					
	10	20	30	40	50	
a597.pep	70	80	90	100	110	120
	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
a597.pep	130	140	150	160	170	180
	QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
m597	QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
a597.pep	190	200	210	220	230	240
	QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
a597.pep	250	260	270	280	290	300
	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKKPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKKPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
a597.pep	310	320	330	340	350	360
	APATVESIAPGTVSYADELDGYGKVVVDHGENYISYAGLSEISVGKGYMVAAGSKIGS					
m597	APATVESIAPGTVSYADELDGYGKVVVDHGENYISYAGLSEISVGKGYMVAAGSKIGS					
	300	310	320	330	340	350
a597.pep	370	380	390			
	SGSLPDGEEGLYLQIRYQQQVLNPSWIRX					
m597	SGSLPDGEEGLYLQIRYQQQVLNPSWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1883>:

```
g601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGACGAA ATTGATGTGC CGAATATAGG
51  TCGTCTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ACGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAGGA CGACATCAAC
151 AACGATGCCG CCGCGCTGGA AAAATTTGAA ACCATCCGCG CATATGGCGC
201 GCTGAAAATG GGTTCATCA GCGACGTATC CGAAGCCGCC GCCCGCGCGC
251 GCACGCCGAA ACCCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGCGGCAAAA CCGTAAACGC CGCCGACATC GATTTGCCCG TACGCGCCCT
351 GAGCATGGGC AAATGCAACC ACGCTATGAT GGGCATCGCC TCGGTCGCCA
401 TCGCCGCCGC CGTGCTCGGT ACGCTGGTCA ACCTTGCCGC AGGCGGCGGA
451 ACGCGTAAAG AAGTGCCTT CGGGCATCCG TCAGGTACGC TCGGTGTCGG
501 TGCTGCCGCC GAATGTCAGG ACGGACAATG GACGGCCGCC aaagcggtca
551 tgaGCCGCAG CGCACgcgtg attatggaaa gttgGGTGcG cgttcccgat
601 gattGTTTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1884; ORF 601.ng>:

```
g601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE TIRAYGALKM GLISDVSEAA ARARTPKPAF VAPAADYTAS
101 SGKTVNAADI DLPVRALSMG KLHHAMMGIA SVAIAAVALG TLVNLAAGGG
151 TRKEVRFGHP SGTLRVGAAA ECQDGGWTAA KAVMSRSARV IMESWVRVPD
201 DCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1885>:

```
m601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACAGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CGGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCTCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAACGC CGCCGACATC GATTGCTGG TACGCGCCCT
351 GAGCATGGGC AAATGCAACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTA CCCGGTACGC TGGTCAACCT TGCCGCAGGC
451 GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCTTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTATGAG CCGTAGCGCA CGCGTGATGA TGAAGGTTG GGTACGGGTG
601 CCTGAGGATT GTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1886; ORF 601>:

```
m601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGLVNLAAG
151 GGTRKEVRFG HPSGTLRVGA AAECQDGGWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 601 shows 94.1% identity over a 205 aa overlap with a predicted ORF (ORF 601.ng) from *N. gonorrhoeae*:

m601/g601

```

              10      20      30      40      50      60
m601.pep      MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
              |||
g601           MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
              10      20      30      40      50      60

              70      80      90     100     110     120
m601.pep      KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG
```

953

```

|||||
g601  TIRAYGALKMGLISDVSEAAARARTPKPAFVAPAADYTASSGKTVNAADIDLVRALSMG
      70      80      90      100     110     120

      130     140     150     160     170     180
m601.ppep  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHGHPSTLRVGAAAECDGQWT
|||||
g601  KLHHAMMGTA SVAI--AAAVLGTLVNLAAGGGTRKEVRFHGHPSTLRVGAAAECDGQWT
      130     140     150     160     170

      190     200
m601.ppep  ATKAVMSRSARVMMEGWVRVPEDCFX
|||||
g601  AAKAVMSRSARVIMESWVRVPDDCFX
      180     190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1887>:

```

a601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CAGCTTTGGA AAAATTCGAG AAAATCCGCG CTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCCCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAATGC CGCCGACATC GATTGCTGG TACGCGCCCT
351 GAGCATGGGC AAATTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTG CCCGGTACGC TGGTCAACCT TGCCGCAGGC
451 GCGCGAAGCG GTAAAGAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTTATGAG CCGCAGCGCA CGCGTGATGA TGAAGGTTG GGTGAGGTTG
601 CCGGAAGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1888; ORF 601.a>:

```

a601.ppep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTRKEVRFH HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*

```

m601/a601 100.0% identity in 205 aa overlap

```

      10      20      30      40      50      60
m601.ppep  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
|||||
a601  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
      10      20      30      40      50      60

      70      80      90      100     110     120
m601.ppep  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG
|||||
a601  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG
      70      80      90      100     110     120

      130     140     150     160     170     180
m601.ppep  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHGHPSTLRVGAAAECDGQWT
|||||
a601  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHGHPSTLRVGAAAECDGQWT
      130     140     150     160     170     180

      190     200
m601.ppep  ATKAVMSRSARVMMEGWVRVPEDCFX
|||||
a601  ATKAVMSRSARVMMEGWVRVPEDCFX
      190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1889>:

```
g602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCTTCTGCT
51  CGGCGGGCAG ATAAACCGTC ATCGTCAGGC GAGCAACCGT GGATTGTGTT
101 CCTTCGGCGG TTTTCAGGGT AATCGGGAAG CGCAGGTCTT TAATGCCGAC
151 CTGATTGATC GGCAGGTTGC GCAAATCTCT GCTGGATTGC ACGTCTGCAA
201 TGGCGTTCAT GCGTTGTTG TCCTTAATAT TCAGATAATT ATTGAGATGT
251 GTGTATTGTA TGGCAGGcag atgccgtctg aAAAAacgct gtcggCCGCC
301 TGCCTGCAAA TgcgagattA TATCACTTGC TTTtgcgGC TGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1890; ORF 602.ng>:

```
g602.pep
1  MLLHQCDKAR HMRPFLGGO INRHQASNR GLCSFGGFG NREAQVFNAD
51  LIDRQVAQIS AGLHVCNGVH ALFVLNIQII IEMCVLYGRQ MPSEKTLAA
101 CLQMRDYITC FWRHL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1891>:

```
m602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCCTTCTGCT
51  CAGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAATGGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTAT GAGTTGTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC GCCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1892; ORF 602>:

```
m602.pep
1  MLLHQCDKTR HMRPLLLSRQ VNRHGQTGNG GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNIIHVI VEMCAWYGVS AGEYTVNLQM
101 RDYITRF*QL H*
```

m602/g602 65.2% identity in 115 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLLSRQVNRHGQTGNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	:     : :   ::    :  :   :    :     :					
g602	MLLHQCDKARHMRPFLGGOINRHQASNRGLCSFGGFGQGNREAQVFNADLIDRQVAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNIIHVIEMCAWYGVSAGEYTVN---LQMRDYITRF*QLH*H					
	:      :: : :    :  :  :					
g602	AGLHVCNGVHALFVLNIQIIEMCVLYGRQMPSEKTLAAACLQMRDYITCFWRHLX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1893>:

```
a602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTA CCCTTCTGCT
51  CGGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAACTGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTAT GAGTTGTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC ACCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1894; ORF 602.a>:

```
a602.pep
1  MLLHQCDKAR HMRTLLLRQ VNRHGQTGNC GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNIIHVI VEMCAWYGVS TGEYTVNLQM
101 RDYITRF*QL H*
```

m602/a602 95.5% identity in 111 aa overlap

955

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLSRQVNRHGQTGNGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
a602	MLLHQCDKARHMRITLLGRQVNRHGQTGNGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITRFQXLHX					
a602	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITRFQXLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1895>:

g603.seq

```

1  ATGGATTCCC GCCTGCGTGG GAATGACGCT AGGAAATACG GCATACGCTT
51  TGCCCAAAGA GGCGGTCTGA AACACACTCC GCCCAACGCC CATCCTTTTT
101 CAGACGGCCC CGCACCAAAA AAACAACCCAC AACTACAAG GAGAAACATC
151 ATGTCCGACC AACTCATTCT TGTCTGAAC TCGTCACTT CATCGCTCAA
201 AGGCGCCGTT ATCGACCGCA AAAGCGGCAG CGTCGTCTTA AGCTGCCTCG
251 GGGAAACGCT GACTACGCCC GAAGCCGTCA TTACCTTCAA CAAAGACGGC
301 AACAAACGCC AAGTTCCCTT GAGCGGCCGC AACTGCCACG CCGGCGCGGT
351 GGGTATGCTG TTGAACGAAC TGGAAAAACA CGGACTGCAC GACCGCATCA
401 AAGCCATCGG CCGCCGCATC GCCCAGGCG GCGAAAAATA TCACGAGTCC
451 GTCCTCATCG ACCAAGACGT CCTTGACGAA CTGAAAGCCT GCATCCCGTT
501 CGCCCCGCTG CACAACCCCG CCAACATCAG CGGCATCCTC GCCGCGCAGG
551 AACACTTTCC CGGCCTGCCC AACGTCGGCG TGATGGACAC CTCGTTCCAC
601 CAAACCATGC CGGAGCGGGC CTACACTTAT GCCGTGCGCG GCGAATGCG
651 CAAAAAATAC GCCTTCGCCC GCTACGGTTT CCACGGTACC GGTATGCGTT
701 ACGTCGCCCC TGAAGCCGCA CGCATCTTGG GCAAACCTct ggaaGACATC
751 CGCATGATTA TTGCCACTT AGGCAACGGC GCATCTATTA CCGCCGTCAA
801 AAACGGCAAA TCCGTCGATA CCGGTATGGG TTTCACGCCG ATCGAAGGTT
851 TGTAATGGG TACACGTTGC GGCGACACCG ATCCGGGCGT ATACAGCTAT
901 CCGACTTTCC ACGCAGGGAT GGATGTTGCC CAAGTTGATG AAATGCTGAA
951 CGAAAAATCA GGTTCCTCCG GTATTTCCga actTCCCAAC GACTGCCGCA
1001 CCTCGAAAT CGCCGCCGAC GAAGGCCGCG AAGGCGCGCG CCTCGCCCTc
1051 gaAGTCATGA CCTGCCGCTT CGCCAAATAC ATCGCTTCGA TGGCTGTGGC
1101 CTGCGGCAGT GTTGACGCAC TCGTGTTCAC CGGCGGTATC GGCAGAAACT
1151 CGCGTAATAT CCGTGCCAAA ACCGTTTCCT ATCTTGATTT CTGGGTCTG
1201 CACATCGACA CCAAAGCCAA TATGGAAAAA CGCTACGGCA ATTCCGGCAT
1251 TATCAGCCCG ACCGATTCTT CTCCGGCTGT TTTGGTCGTC CCGACCAATG
1301 AAGAACTGAT GATTGCCTGC GACACTGCCG AACTTGCCGG CATCTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:

g603.pep

```

1  MDSRLRGND A RYKIRFAQR GRLKHTPPNA HPFSDGPAPK KQPQTTRRNI
51  MSDQLILVLN CVSSSLKGAV IDRKSGSVVL SCLGERLTPP EAVITFNKDG
101 NKRQVPLSGR NCHAGAVGML LNELEKHLH DRIKAIGRRI AHGGEKYHES
151 VLIDQDVLDE LKACIPFAPL HNPANISGIL AAQEHFPGLP NVGVMDTSFH
201 QTMPEAYTY AVPRELRKKY AFRRYGFHGT GMRYVAPEAA RILGKPLEDI
251 RMIIAHLGNG ASITAVKNGK SVDTGMGFTP IEGLVMGTRC GDTDPGVYSY
301 PTFHAGMDVA QVDEMLNEKS GFPGISLPLN DCRTLEIAAD EGREGARLAL
351 EVMTCLAKY IASMAVACGS VDALVFTGGI GENSRNIRAK TVSYLDFLGL
401 HIDTKANMEK RYGNSGIISP TDSSPAVLV PTNEELMIAC DTABLAGIL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1897>:

m603.seq

```

1  CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACCT TGCGCTGAT GTCTGC.CTT
101 TTTCAGACGA CCCACACTA AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT CCTCGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGCGCC GTTATCGACC GAmAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG cCtGACCAG CCCGAAGCCG TCATTACGTT CAACAAAGAC

```

```

301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGAAATTGCC ACGCCGGCGC
351 GGTGGGTATG CTTTGAACG AACTGGAAAA ACACGGTCTG CACGACCGCA
401 TCAAAGCCAT CGGCCACCGC ATCGCCACG GCGGCGAAAA ATACAGCGAG
451 TCTGTTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTTGCCGCAC
551 AGGAACATT CCCCGGTCTG CCCAATGTCG GCGTGATGGA TACTTCGTTT
601 CACCAAACCA TGCCGGAGCG TGCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTC GCGCTACGG TTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCACGCATCT TGGGCAAACC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAAACGGC AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGGTACACGT TCGGCGGACA TCGATCCGGG CGTATACAGC
901 TATCTGACTT CCCACGCCGG GATGGATGTT GCCCAAGTGG ATGAAATGCT
951 GAACAAAAAA TCAGGTTTGC TCGGTATTTC CGAACTTTC AACGACTGCC
1001 GCACCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTCA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GCGGTTGACG CACTCGTGTT CACCGCGCGT ATCGCGGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 CATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTTGGTT GTCCCGACCA
1301 ATGAAGAACT GATGATTGCC TCGGACACTG CCGAACTTGC CGGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1898; ORF 603>:

```

m603.pep
1  LSSRRRGRNN DRKCGIRFAQ RGRCLKHLAPD VCXFSDDPTL KKQPQTTRRN
51  IMSDQLILVL NCGSSSLKGA VIDRXSGSVV LSCLGERLTT PEAVITFNKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHGL HDRIKAIGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHNPNANISGI LAAQEHFPLG PNVGVMDTSF
201 HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ARILGKPLED
251 IRMILAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
301 YLTSHAGMDV AQVDEMLNKK SGLLGISELS NDCRTLEIAA DEGHEGARLA
351 LEVMTYRLAK YIASMAVCGG GVDALVFTGG IGENSRNIRA KTVSYLDFLG
401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELAGIL
451 *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 603 shows 91.6% identity over a 450 aa overlap with a predicted ORF (ORF 603.ng) from *N. gonorrhoeae*:

m603/g603

```

              10      20      30      40      50      60
m603.pep      LSSRRRGRNNDRKCGIRFAQRGRCLKHLAPDVCFSDPTLKKQPQTTRRNIMSDQLILVL
              ::|| || ||: || ||||| ||||| ||: || || ||: ||||| ||||| |||||
g603           MDSRLRG-NDARKYGIRFAQRGRCLKHTPPNAHPFSDGPAPKKQPQTTRRNIMSDQLILVL
              10      20      30      40      50

              70      80      90      100     110     120
m603.pep      NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGKNKRQVPLSGRNCHAGAVGM
              || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g603           NCVSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGKNKRQVPLSGRNCHAGAVGM
              60      70      80      90      100     110

              130     140     150     160     170     180
m603.pep      LLNELEKHGLHDRIKAIGHRIAHGGEKYSESVLIDQAVMDELNACIPLAPLHNPNANISGI
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g603           LLNELEKHGLHDRIKAIGRRIAHGGEKYHESVLIDQDVLDELKACIPFAPLHNPNANISGI
              120     130     140     150     160     170

              190     200     210     220     230     240
m603.pep      LAAQEHFPLPNVGVMDSFHHQTMPERAYTYAVPRELRKKYAFRRYGFHGTSMRYVAPEA
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```



957

```

g603      LAAQEHFPGLPNVGVMDSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTGMRYVAPEA
          180      190      200      210      220      230

          250      260      270      280      290      300
m603.pep  ARILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
          |||||:|||||:|||||:|||||:|||||:|||||
g603      ARILGKPLEDIRMIIAHLGNGASITAVKNGKSVDTGMGFTPIEGLVMGTRCGDIDPGVYS
          240      250      260      270      280      290

          310      320      330      340      350      360
m603.pep  YLTSHAGMDVAQVDEMLNKKSGLLGISSELSNDCRTLEIAADEGHEGARLALLEVMTYRLAK
          |||||:|||||:|||||:|||||:|||||:|||||
g603      YPTFHAGMDVAQVDEMLNEKSGFPGISSELPNDCRTLEIAADEGREGARLALLEVMTCLRLAK
          300      310      320      330      340      350

          370      380      390      400      410      420
m603.pep  YIASMAVGC GGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          |||||:|||||:|||||:|||||:|||||:|||||
g603      YIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          360      370      380      390      400      410

          430      440      450
m603.pep  PTDSSPAVLVVPTNEELMIACDTAELAGILX
          |||||:|||||:|||||:|||||:|||||
g603      PTDSSPAVLVVPTNEELMIACDTAELAGILX
          420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1899>:

```

a603.seq
1   CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCGGTC TGAAACACAC TCCGCCAAC GCCCATCCTT
101 TTTCAGACGA CCCACACACC. AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT TCTTGTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG CCTGACCACG CCCGAAGCCG TCATTACGTT CAGCAAAGAC
301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGGAAGTCC ACGCCGGCGC
351 GGTGGGTATG CTGTTGAACG AACTGGAAAA ACACGAAGT CACGACCGCA
401 TTCAAGCCGT CGGCCACCGC ATCGCCACG GCGGCGAAAA ATACAGCGAG
451 TCTGTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTCGCCGCAC
551 AGGAACATTT CCCCGTCTG CCCAATGTCT GCGTGATGGA TACTTCGTTT
601 CACCAAACCA TGCCGAGCGG TGCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTCC GCGCTACGCG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAAACC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAAACGGC AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGGTACGCGC TGCGGCGATA TCGACCCGGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTC CGAACTCTCC AACGACTGCC
1001 GCACCTCTGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GCGGTTGACG CACTCGTGTG CACCGGCGGT ATCGGCGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 TATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTGGTT GTCCCGACCA
1301 ATGAAGAACT GATGATTGCC TGCGACACTG CCGAAGTTGT CGGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

```

a603.pep
1   LSSRRRGRNN DRKCGIRFAQ RGRLKHTPPN AHPFSDPTX KKQPQTTRRN
51  IMSDQLILVL NCGSSSLKGA VIDRKSGSVV LSCLGERLTT PEAVITFSKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHEL HDRIQAVGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHNPANISGI LAAQEHFPGL PNVGVMDSF

```

958

201 HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ACILGKPLED  
 251 IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS  
 301 YLTSHAGLDV AQVDEMLNKK SGLLGISELS NDCRTLEIAA DEGHEGARLA  
 351 LEVMTYRLAK YIASMAVGCG GVDALVFTGG IGENS RNIRA KTVSYLDFLG  
 401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELVGIL  
 451 \*

m603/a603 96.7% identity in 450 aa overlap

	10	20	30	40	50	60
m603.pep	LSSRRRGRNDRKCGIRFAQRGLKHLAPDVCXFSDDPTLKKQPQTTRRNIMSDQLILVL					
a603	LSSRRRGRNDRKCGIRFAQRGLKHTPPNAHPFSDDPTXKKQPQTTRRNIMSDQLILVL					
	10	20	30	40	50	60
m603.pep	70	80	90	100	110	120
	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDG NKQVPLSGRNCHAGAVGM					
a603	NCGSSSLKGAVIDRKSGSVVLSCLGERLTTPEAVITFSKDG NKQVPLSGRNCHAGAVGM					
	70	80	90	100	110	120
m603.pep	130	140	150	160	170	180
	LLNELEKHGLHDRIKAIGHRIAHGGEKYESV LIDQAVMDELNACIPLAPLHNPNANISGI					
a603	LLNELEKHELHDRIQAVGHRIAHGGEKYESV LIDQAVMDELNACIPLAPLHNPNANISGI					
	130	140	150	160	170	180
m603.pep	190	200	210	220	230	240
	LAAQEHFPGLPNVGVMDSF HQTMPERAYTYAVPRELRKKYAFRRYGFHG TSMRYVAPEA					
a603	LAAQEHFPGLPNVGVMDSF HQTMPERAYTYAVPRELRKKYAFRRYGFHG TSMRYVAPEA					
	190	200	210	220	230	240
m603.pep	250	260	270	280	290	300
	ARILGKPLEDIRMIIAHLGN GASITAIKNG KSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
a603	ACILGKPLEDIRMIIAHLGN GASITAIKNG KSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
	250	260	270	280	290	300
m603.pep	310	320	330	340	350	360
	YLTSHAGMDVAQVDEMLNKKSGLLGISELSNDCRTLEIAA DEGHEGARLA LEVMTYRLAK					
a603	YLTSHAGLDVAQVDEMLNKKSGLLGISELSNDCRTLEIAA DEGHEGARLA LEVMTYRLAK					
	310	320	330	340	350	360
m603.pep	370	380	390	400	410	420
	YIASMAVGCGGVDALVFTGGIGENS RNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
a603	YIASMAVGCGGVDALVFTGGIGENS RNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
	370	380	390	400	410	420
m603.pep	430	440	450			
	PTDSSPAVLVVPTNEELMIACDTAELAGILX					
a603	PTDSSPAVLVVPTNEELMIACDTAELVGILX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1901>:  
 g604.seq

1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCTGCG GCAAGGTTGA  
 51 CCAGCGTACC GAGCACGGCG GCGGCGATGG CGACCGAGGC GATGCCCATC  
 101 ATAGCGTGGT CGAGTTTGCC CATGCTCAGG GCGCGTACCG GCAAATCGAT  
 151 GTCGGCGGCG TTTACGGTTT TGCCGCTGGA GGCGGTGTAA TCGGCGGCGG  
 201 GCGCGACGAA GGCGGGTTTC GCGTGC GCGG CGCGGCGGC GGCTTCGGAT

g604 . pep

```

1  MPEAHFFTRS AACGKVDQRT EHGGGDGDRG DAHHSVVQFA HAQGAYRQID
51  VGGVYGAAG GGVIGGRDE GGFRRARAGG GFGYVADQTH FORAICADGF
101 KFFQGGIVV DVVLQLFARV AOVGGVQENG RNARVDERGF QTTYIRHINF
151 VDOIAGWEHT AFAVGWI*

```

m604.seq

1	ATGCCCGAAG	CGCACTTCTT	TACGCGTTCC	GCCGCTGCG	GCAAGGTTGA
51	CCAGCGTACC	GGGTACGGCG	GCGCGGTCG	CAATGGCAAC	AGAGGCGGTA
101	CCCATCATCG	CGTGGTGCAG	TTTGCCCATG	CTCAGGGGCG	GTACCAGCAA
151	ATCGATGTCG	GCGGCGTTCA	CGGTTTGGCC	ACTGGAGGCG	GTGTAATCGG
201	CGGCGGGCGC	GACGAAGGCG	ACTTTTCGGG	TGTGCGCGCG	AGCGGCAGCT
251	TCGGATACGT	CGCTGATCAG	ACCCATTTC	AGCGCACCGT	AAGCGCGGAT
301	TTTCTCGAAT	TTTTCCAAAG	CCGCGGCATC	GTTGTTGATG	TCGTCTTGCA
351	ACTCTTTGCC	TGTGTAGCCC	AAGTCGGCGG	CATTCAAGAA	AACGGTCGGA
401	ATGCCCGCGT	TGATGAGCGT	GGCTTTCAAA	CGGCCTATAT	TCGGCACATC
451	AATTTTCATC	ACCAAATTGC	CGGTTGGGAA	CATACTGCCT	TCGCCGTCGG
501	CTGGATC				

m604.pep

```

1  MPEAHFFTRS AACGKVDQRT GYGGGGRNGN RGGTHHRVQ FAHAQGAYQQ
51 IDVGGVHGFA TGGGVIGGGR DEGDFRRVRA SGSFGYVADQ THFORTVSAD
101 FLEFFQSRGI VVDVVLQLFA CVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDOIAGWE HTAFAVGWI

```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 604 shows 83.4% identity over a 169 aa overlap with a predicted ORF (ORF 604.ng) from *N. gonorrhoeae*:

m604/g604

```

      10          20          30          40          50          60
m604.pep MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVQFAHAQGAYQQIDVGGVHGFA
|||||:||||:|:||:|||||||:|||||:||||
g604 MPEAHFFTRSAACGKVDQRTEHGGG--DGDGRDAHHSVVQFAHAQGAYRQIDVGGVYGF
      10          20          30          40          50

      70          80          90         100         110         120
m604.pep TGGGVIGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFLEFFQSRGI VVDVVLQLFA
:|||||:||||:|:||:|||||||:| ||:| | ||| ||| ||| |||
g604 AGGGVIGGRDEGGFRRARAGGGFGYVADQTHFQRAICADGFKFFQRGGI VVDVVLQLFA
      60          70          80          90         100         110

      130        140        150        160        169
m604.pep CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWI
|||||:|||||:|||||:|||||:|||||
g604 RVAQVGGVQENGRNARVDERGFQTTYIRHINFVDQIAGWEHTAFAVGWIX
      120        130        140        150        160

```

a604.seq

1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCTGCG GCAAGGTTGA  
51 CCAGCGTACC GGGCACGGCG GCGCGGTCG CAATGGCAAC AGAGGCGGTA  
101 CCCATCATCG CGTGGTGCAA TTTGCCCATG CTCAGGGCGC GTACCAGCAA  
151 ATCGATGTCG GCGGCATTCA CGGTTTGGCC ACTGAGGGCG GTGTAATCGG

960

```

201  CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG GGCGGCAGCT
251  TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301  TTTCTCGAAT TTTTCCAAAG CTGCGGCATC GTTGTGTATG TCGTCTTGCA
351  ACTCTTTGCC CGTGTAGCCC AAGTCGGCGG CATTCAGGAA AACGGTCGGA
401  ATGCCCCGCGT TGATGAGCGT GGCTTTCAAA CGGCCTATAT TCGGCACATC
451  AATTTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501  CTGGATCAAG AAATTCGATT TGTACTTCGG CTGCCGGGAA CGTTACGCCG
551  TCGAGCTCAA AATCGCCTGT TTCCAAACT GCGCCGTTTT GCATCGGTAC
601  ATGGGCAATA ATGGTTTTGC CGATGTTTTT CTGCCAGATT TTGACTGTGC
651  AGATGCCGTC TGA

```

-- This corresponds to the amino acid sequence <SEQ ID 1906; ORF 604.a>:

```

a604.pep
1  MPEAHFFTRS AACGKVDQRT GHGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51  IDVGGIHFQA TGGGVIGGGR DEGDFRRVRA GGSFGYVADQ THFQRTVSAD
101 FLEFFQSCGI VVDVVLQLFA RVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFAVGWIK KFDLYFGCRE RYAVELKIAC FQNCVHLHRY
201 MGNNGFADVF LPDFDCADAV *

```

m604/a604 97.0% identity in 169 aa overlap

	10	20	30	40	50	60
m604.pep	MPEAHFFTRSAAACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGF					
	:     :     :     :     :					
a604	MPEAHFFTRSAAACGKVDQRTGHGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGIHFQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m604.pep	TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFFLEFFQSRGIVVDVVLQLFA					
	:     :     :     :     :					
a604	TGGGVIGGGRDEGDFRRVRAGGSFGYVADQTHFQRTVSADFFLEFFQSCGIVVDVVLQLFA					
	70	80	90	100	110	120
	130	140	150	160	169	
m604.pep	CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVAGWI					
	:     :     :     :					
a604	RVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVAGWIKFDLYFGCRE					
	130	140	150	160	170	180
a604	RYAVELKIACFQNCVHLHRYMGNNGFADVFLPDFDCADAVX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1907>:

```

g605.seq
1  ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51  AATCGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCGAC
151 TATATGCAGG CCGGCGACAG CAGCATTGAT TACGCCGCTa tGCCGGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATgc cgtcaaagtc aaAGGCTATT
251 TCATctacCc cgGCCAGCTT TTTTgcaata ttgccgcca agcCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGaa atCTTTACCG CGATTGAAAG
351 CTCGCCTCC GGCTAaccgT CCGAACAAAG CATCAAAGGC TTGTTTGACG
401 ACTTCgACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAAAAC
451 AAACGCCTTG CCGCGTCCTT TAAAGGCGTG GCGGAACTCG ATTCGGCAA
501 TTTTGAAGAC CACCGCATCG ACCTTTTCGG TGATGCCTAC GAATACCTGA
551 TTTCCTAATA CGCcgCAAC GCAGGCAAA CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TCTCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA
651 GAAAGTCAAC AAAATCTACG ACCCGCCTG CGGCTCGGGC AGCCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAACACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACACAC CACCTACAAC CTCGCCGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAAATCCA CATCGAATTG GCGGACACGC
851 TGACCAACCC CAAACTCAA GACAGCAAA CCTTTGATGC CGTCGTCTCC
901 AATCCGCCCT ATTCCATCGA CTGGATAGGC AGCGACGACC CCACCTtgaT

```

961

```

951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCTA TCGTCTCATT CCCCAGCATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATC CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCCG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTG AAGCCGAAGA CACCCGCGAG GTCATCGACA
1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CCgtcgCcaa AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CCTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

g605.pep

```

1 MMTEMQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNTKLKE IFTAIESSAS GYPSEQGIKG LFDDDFDTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGNFED HRIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLOAKKQF DEHIEEGFF
251 GQEIHNHTYIN LARMNMFLHN VNYNKFHIEL GDTLTNPCLK DSKPFDVVS
301 NPPYSIDWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTCLAVNI
401 LVLCHKHNDT DIQFIDASGF FKKETNNNV L TEEHIAEIVK LPADKADVPH
451 IAQNAAQQT V KONGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

m605.seq

```

1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTGGA
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTTGC CGACAAGAAC
451 AAACGCCTTG CCGCCGTCCT CAAAGGCGTG GCGGAACGCG ATTTCCGGCA
501 TTTTGAAAAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAACCTA CGCTGCCAAC GCAGGCAAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGTCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GCGGACACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
901 AATCCGCCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTTGCCCCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCCAGCATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCCG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

m605.pep

```

1 MMTEMQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

```

101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN  
 151 KRLAAVLKGV AELDFGNFEN HHIDLFGDAY EYLISNYAAN AGKSGGEFFT  
 201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLQAKKQF DEHIEEGFF  
 251 GQEIINHHTYN LARMNMFLHN VVYNQFHIEL GDTLTNPKLK DSKPFDIVS  
 301 NPPYSINWIG SDDPTLINDD RFAPAGVLAP KSKADFAPIL HALNYLSGRG  
 351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI  
 401 LVLSKHKDNT DIQFIDASGF FKKETNNNVL IEEHIAEIVK LFADKADVPH  
 451 IAQNAAQQT V KONGYNLAVS SYVEAEDTRE IIDIKQLNAE IGETVAKIER  
 501 LRREIDEVIA EIEA\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 605 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 605.ng) from *N. gonorrhoeae*:

m605/g605

m605.pep	MMTEMQRAQLHRQIWKIAD	EV	RG	AV	DG	WDFKQYVLGTLFYRFISENFTDYM	QAGDSSID
g605	MMTEMQRAQLHRQIWKIAD	EV	RG	AV	DG	WDFKQYVLGTLFYRFISENFTDYM	QAGDSSID
m605.pep	YAAMPDSIITPEIKDDAVKVG	YFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
g605	YAAMPDSIITPEIKDDAVKVG	YFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
m605.pep	GYPSEQDIKGLFDDFDTTSSRLG	STVADKNKRLAAVLKGV	AELDFGNFENHHIDLFGDAY				
g605	GYPSEQGIKGLFDDFDTTSSRLG	STVADKNKRLAAVLKGV	AELDFGNFEDHRIDLFGDAY				
m605.pep	EYLISNYAANAGKSGGEFFT	PQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLQAKKQF					
g605	EYLISNYAANAGKSGGEFFT	PQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLQAKKQF					
m605.pep	DEHIEEGFFGQEIINHHTYNLARM	NMFLHN	VVYNQFHIELGDTLTNPKLKDSKPFDIVS				
g605	DEHIEEGFFGQEIINHHTYNLARM	NMFLHN	VVYNQFHIELGDTLTNPKLKDSKPFDAVVS				
m605.pep	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAPILHALNYLSGRGRAAIVSFPGI						
g605	NPPYSIDWIGSDDPTLINDDRFAPAGVLAPKSKADFAPILHALNYLSGRGRAAIVSFPGI						
m605.pep	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF						
g605	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF						
m605.pep	FKKETNNNVLIEEHIAEIVKLFADKADVPHIAQNAAQQT	V KONGYNLAVSSYVEAEDTRE					
g605	FKKETNNNVLIEEHIAEIVKLFADKADVPHIAQNAAQQT	V KONGYNLAVSSYVEAEDTRE					

963

	430	440	450	460	470	480
	490	500	510			
m605.pep	IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX					
	:   :     :					
g605	VIDIRQLNAEISETVAKIERLRREIDEVIAEIEAX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1911>:

```

a605.seq
1 ATGATGACCG AATACAACA ACGCGCCCAA CTGCACCGGC AAATTTGGAA
51 AATTGCCGAG GAAGTACCGG GCGCGGTGGA TGGCTGGGAC TTCAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGGAAAA CTTCACCGAC CTTTACCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCGGCTA TGCCGAGACG
201 CATCATCAGC CCCGAAATCA AAGACGATGC CGTCAAAGTC AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCGCCGCA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GTCTGAAAGAA ATTTTTCGCG CATTGGAAG
351 CTCGCCCTCC GGCTATCCGT CCGAACAAGA CATTAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAAGCAG CGGCTCGGCA GCACCGTTGC CGACAAGAAC
451 AAACGCCCTG CCGCCGTCCT AAAAGGCGTG GCGGAACCTG ATTTCCGCGA
501 TTTTGAAGAC CACACATCG ACCTTTTCGG CATGACCTATC GAATACCTGA
551 TTTCCAACCTA CGCTGCCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGGAGGC
651 GAAAGTAAAC AAAATCTACT ACCCAGCTTG CGGCTCGGGC AGCCTGCTCT
701 TACAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCACA TGAATATGTT
801 TCTGCACACA GTCAATTACA ACAAAATCCA CATCGAATTG GGGCAGACAC
851 TGACCAATCC CAAACTCAA GACAGCAAA CCTTTGATGC CGTCGTTTTC
901 AATCGCCCTT ATTCATCAA CTGGATAGGC AGCGGCGACC CCACCTTAAT
951 CAACGACGAC CGCTTGCCC CTGCAGGCGT ACTCGCCCCG AAATCCAAAG
1001 CCGATTTTGC CTTCATTCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCGCCCA TCGCTTCATT CCCCAGCATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTCA
1151 TCGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATA
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCTCGACGAC
1251 AGGCGGCTTC TTTAAAAGAG AAACCAACAA CCAAGCTCTT AACGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCGG ATAAAGCCGA TGTGCGCGAT
1351 ATCGCCCAAA ACGCGGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTGAGC AGCTATGTTT AACCCGAAAG CACCCGCGAA ATTATCGACA
1451 TCAAAACAGT TAACGCGGAA ATCAGCGAAA CGGTTGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA CAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1912; ORF 605.a>:

```

a605.pep
  1  MMTEIQQRAQ  LHRQIWKIAD  EVRGAVDGDW  FKQYVLGTLF  YRFISENFTD
51  YMQAGDSSID  YAAMPDSIIT  PEIKDDAVKV  KGFIYIPGQL  FCNIAAEAHQ
101 NEELNTKLKE  IFTAESSAS  GYPSEQDIKG  LFDDFDPTSS  RLGSTVADKN
151 KRLAAVLKGV  AELDFGSFED  HHIDLFGDAY  EYLISNYANA  AGKSGGFEFT
201 PQSVSKLIAR  LAVHGEQKVN  KIYDPACGSG  SLLLQAKKQF  DEHIIEEGFF
251 GQEINHTTYN  LARMNMFLNH  VFYNKFHIEL  GDTLTNPCLK  DSKPFDVAVS
301 NPPYSINWIG  SGDPFLINDD  RFAPAGVLAP  KSKADFAPIL  HALNYLSGRG
351 RAAIVSFPGI  FYRGGAEQKI  RQYLVEGNYV  ETVIALAPNL  FYGTGIAVNI
401 LVLSKHKDNT  KDQNTDAGGF  FKKETNNNVL  TEEHIAEIVK  LFADKADVPH
451 IAQNAAQQTQ  KONGYNLAVS  SYVEPEDTRE  IDIKQLNAE  ISETVAKIER
501 LRREIDEVIA  EIEA*

```

m605/a605 98.1% identity in 514 aa overlap

	10	20	30	40	50	60
m605.pep	MMTEMQQR	QLHRQIWKI	ADVEVRG	AVDGVDFK	QYVLGTLF	YRFISENFTDYM
	QAGDSS	IIIIIIIIII	IIIIIIIIII	IIIIIIIIII	IIIIIIIIII	IIIIIIIIII
a605	MMTEIQQR	QLHRQIWKI	ADVEVRG	AVDGVDFK	QYVLGTLF	YRFISENFTDYM
	QAGDSS	IIIIIIIIII	IIIIIIIIII	IIIIIIIIII	IIIIIIIIII	IIIIIIIIII
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDS	IIITFEIK	DDAVKVK	GYFIYPG	QLFCNIA	AEAHQNEELN
	TKLKEI	FTAIESS	SSSSSSSS	SSSSSSSS	SSSSSSSS	SSSSSSSS

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1913>:

1	ATGTCCAAAT	TTATCGCCAA	ACAATCGGTC	GGTGC GGAAG	TCATCGACAC
51	GCCGcgCACC	GAAGAAGAAG	CCTGGCTTCT	GAACACTGTC	GAAGCCCCAag
101	cgcGGCgAATG	GAATCTGAAA	ACGCCAGAGA	TGCGCATCTA	CCACTCcccc
151	GAACCCAATG	CCCTTTGCCAC	GGCGCGCATCG	AGAAACAGCT	CCCTGATCGC
201	CGTCACGacc	gggttctctcg	acctatgaC	GCGCGACgaa	gtggaagccg
251	tgTTGGCGCA	CGAAATGGCG	CACGTGCGCA	ACGGCGCATG	GATTACGCTG
301	ACGCTGatTC	AAGCGGTGGT	CAATACCTTT	GTCTGTTC	TGTCGCGCAT
351	TATTGCCAAC	CTGATTGCCC	GAAAACAACGA	CGCGACGCCA	TCCCAGGGAA
401	CTTATTCTCT	AGTCAGCATC	GTAATCCAAA	TCCTGTTCCG	CTTCCTTGCC
451	AGCCTGATTG	TCATGTGGTT	CAGCGCCCAA	CCGGAATACC	GCGCCGAcgc
501	gggCGcggCA	AAACTGGTCG	GCGCACCGAA	AATGATTTC	GCCCTGCAAA
551	GGCTTAAAGG	CAACCCGGTC	GATTTCGCCG	AAGAAATGAA	CGCAATGGGC
601	ATCCGCGGAG	ATACGCGCGA	CTCCCTGCTC	AGCACCACC	CTTCGCTGGA
651	CAACCGGAATC	GCCCCGCTCA	AATCGCTTTA	A	

This corresponds to the amino acid sequence <SEQ ID 1914; ORF606.ng>:



g606.pep

```

1  MSKFIQKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIIVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq

```

1  ATGTCCAAAT TTATCGCCAA ACAATCGGTC GGCGCGGAAG TTATCGACAC
51  GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTTGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCTT GGTGAGCATG GTATTCCAAA TCCTGTTCCG CTTCTTGGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGATGC
501 GGGCGCGGCA AAACCTGGTC GCGCGCCGAA AATGATTTCC GCCCTGCAAA
551 GGCTCAAAGG CAACCCGGTC GATTGCCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGAGG ATACGCGCGA CTCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGTATC GCCCGCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep

```

1  MSKFIQKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIIVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng) from *N. gonorrhoeae*:

m606/g606

m606.pep	10	20	30	40	50	60
	MSKFIQKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
g606	MSKFIQKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS					
	10	20	30	40	50	60
m606.pep	70	80	90	100	110	120
	RNSSLIIVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
g606	RNSSLIIVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
m606.pep	130	140	150	160	170	180
	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	190	200	210	220		
	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
g606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq

966

```

1  ATGTCCAAAT TCATCGCCAA ACAATCGGTC GCGCGGAAG TTATCGACAC
51  GCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTCGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCCT GGTCAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGACGC
501 GGGCGCGGCA AAACCTGGTCG GCGCGCCGAA AATGATTTC GCGCTGCAA
551 GGCTTAAAGG CAACCCGGTC GATTGCCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGAG ATACGCGCGA CTCCTGCTC AGCACCACC CTTGCTGGA
651 CAACCGAATC GCCCGCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1918; ORF 606.a>:

```

a606.pep
1  MSKFIKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRE VEAVALHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTFFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

m606/a606 100.0% identity in 226 aa overlap

m606.pep	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS
a606	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS
m606.pep	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVNGDMVTLTLIQGVVNTFVVFLSRIIAN
a606	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVNGDMVTLTLIQGVVNTFVVFLSRIIAN
m606.pep	LIARNNDGSQSQGTFFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS
a606	LIARNNDGSQSQGTFFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX
a606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1919>:

```

g607.seq
1  ATGCTGCTCG accTgaCCG CTTTTCTTt tccGTCTTCC TGAAAGAAAT
51  CCGCCTGCTG ACCGCCCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTCGTC GATACCGTGA TGGCGGGCGG TCGCGGCAAG
151 GAAGATTGGC CGGCGGTGGC TTTGGGCAGC AGCGCGTTT CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCAGC
251 TTTACGGCGC GGGTAAAACC GgtgAAGCAG GCGAAACGGG GCGGAGGGG
301 ATTTGGTTTC GGCTGATTTT GGGGATTTTC GGCATGATTT TGATGTGGGC
351 GCGGATTACG CCGTTCGCA ACTGGCTGAC TTTGAGCGAT TATGTGGAAG
401 gcacAAtggc gcAGTATATG CTGTTACCA GCTTGGCGAT GCCGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCT TCCAGCCTGA ACCGCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTT GGTGGCGCA

```

```

601 GGTTCGCGCG TGGCGACAAT GCGGGTGT TT TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAAATTCTT CCGCCCGTTC GGA CTGACAG
701 CGAAATTCGg caaACCGGat tGGgcGGTGT TCAAACAGAT TtGGAAAATC
751 gGcgcgCCCA TCGGGCTGTC TTATTTTGTG GAAgccaGcg cGTTTTTCGTT
801 TATCGTGT TTGATTGCGC CTtccggCGA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCAG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GCGCGGAATT
951 TTCGCGGGCG CGTTATATTT CAGGAGTGTC GCTGGTGTG GGTGGGTGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCGGTTC GCCGCTGGCA
1051 AGCATGTACA ACGATGaTCC GGCAGTTT TA AGCATCGCCT CCACCGTCCT
1101 GCTGTTTCGCC GGCCTGTtcc aACCGGCAGA CTTACCCCAA TGATCGCGT
1151 CCTATGCCCT GCGCGGCTAC AAAGTCACCA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCTT TCTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC AGCCGTCGCC TTGGTGTGGT GCTTGAAAA ATACAGTATG
1351 GAGTTGGTCA AATCACACAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

g607.pep

```

1 MLLDLDRFSF SVFLKEIRLL TALALPMLLA QVAQVGIGFV DTVMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT GEAGETGRQG
101 IWFGLILGIF GMILMWAAIT PFRNWLTLSD YVEGTMAYM LFTSLAMPAA
151 MVHRAHAYA SSLNRPRLLM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGVATMAVF WFSALALWIY IAKEKFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSEFIV LIAPFGEDYV AAQVQGISLS GILYMIPOSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWVLAVITVL SLVLFERSPLA
351 SMYNDPAVL SIASVTLLFA GLFQPADFTQ CIASYALRGY KVTKVPMPFIH
401 AAAPFWGGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAVA LVWCLEKYSM
451 ELVKSHKAV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

m607.seq

```

1 ATGCTGCTCG ACCTCAACCG CTTTTCCTTT CCCGCTCTTC TGAAAGAAGT
51 CCGCCTGCTG ACCACTCTTG CCCTGCCCAT GCTGTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTGTG GATACTGTGA TGGCGGGCGG TCGGGCAAG
151 GAAGACTTGG CCGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCAGC
251 TTTACGGCGC GGGTAAACC GACGAAGTGG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCA ACTGGCTGAC CTTGAGCGAT TATGTGAAG
401 GCACGATGGC GCAGTATATG TTGTTACCA GCTTGGCGAT GCCGGCGCA
451 ATGGTACACC GCGCGCTGCA CGCCTACACT TCCAGCCTGA ACCGCCGCG
501 CCTGATTATG TTGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GCGGTGT TT TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAATTTCTT CCGCCCATTC GGA CTGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGAAAATC
751 GCGCACCCA TCGGGCTGTC TTATTTTGTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGT TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GCGCGGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTTA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCGGTTC GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTT TA AGCATCGCCG CCACCGTCTT
1101 ACTGTTTCGCC GGCTTGTTC AACCGGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCCCT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCTT TTTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCAAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

m607.pep

```

1 MLLDLNRFSF PVFLKEVRL TLLALPMLLA QVAQVGIGFV DTVMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG

```

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N.gonorrhoeae*

ORF 607 shows 94.8% identity over a 459 aa overlap with a predicted ORF (ORF 607.ng) from *N. gonorrhoeae*:

m607/q607

m607.pep	MLLDLNRFSFPVFLKEVRLTLTALPMLLAQVAQVGIGFVDITVMAGGAGKEDLA	10	20	30	40	50	60
g607	MLLDLDRFSFSVFLKEIRLLTALPMLLAQVAQVGIGFVDITVMAGGAGKEDLA	10	20	30	40	50	60
m607.pep	SAFATVYITFMGIMAALNPIMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVL	70	80	90	100	110	120
g607	SAFATVYITFMGIMAALNPIMIAQLYGAGKTGEAGETGRQGIWFGFLILGIFGMIL	70	80	90	100	110	120
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRALHAYTSSLNRPRLIMLV	130	140	150	160	170	180
g607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRALHAYASSLNRPRLIMLV	130	140	150	160	170	180
m607.pep	VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGL	190	200	210	220	230	240
g607	VPLNYIFVYGKFGMPALGGAGCGVATMAVFWFSALALWIYIAKEKFFRPFGL	190	200	210	220	230	240
m607.pep	WAVFKQIWKIGAPIGLSYFLEASAFSFIIVFLIAPFGEDYVAAQQVGISLS	250	260	270	280	290	300
g607	WAVFKQIWKIGAPIGLSYFLEASAFSFIIVFLIAPFGEDYVAAQQVGISLS	250	260	270	280	290	300
m607.pep	GSAGTVRIGFSLGRREFSRARYISGVSVLVGWLAVITVLSVLVFRSPLVSM	310	320	330	340	350	360
g607	GSAGTVRIGFSLGRREFSRARYISGVSVLVSGWLAVITVLSVLVFRSPLASM	310	320	330	340	350	360
m607.pep	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLP	370	380	390	400	410	420
g607	SIASVTVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLP	370	380	390	400	410	420
m607.pep	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSKHAVX	430	440	450	460		
g607	MGIYGFWTALIASLTIAAVALVWCLEKYSMELVKSHKAVX	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1923>:

```
a607.seq
1  ATGCTGCTCG ACCTCAACCG CTTTTCCTTT TCCGTCTTCC TGAAAGAAGT
51  CCGCCTGCTG ACCGCTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTGCGCG
101 AGGTGGGCAT CGGTTTTGTC GATACCGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GACGAAGTGG GCGAAACGGG ACGGCAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
401 GCACAATGGC GCAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCC TCCAGCCTGA ACCGCCCGCG
501 CCGTATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GGCGGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTAT ATCGCCAAGG AAAATTCTT CCGCCCATTC GGACTGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAAAATC
751 GGCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTGCGCAT CAGTTTGTCT GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGGC CATCGGCTTT TCGCTTGGGC GCGCGCAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTCA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTT GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTTTA AGCATCGCGG CCACCGTCTT
1101 ACTGTTTCGCC GGCTTGTTC AACCGGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TTTGGGGCTG CGGTCTGCTG CCGGGCTACC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGATAA GGCTGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

```
a607.pep
1  MLLDLNRFSF SVFLKEVRLT TALALPMLLA QVAQVGIGFV DTMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG
101 IWFGLEFLGV GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRLAHAYA SSLNRPRILM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 CGGLATMAVF WESALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWMLAVITVL SLVLFERSPLV
351 SMYNNDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPFHIH
401 AAAFWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAIA LVWCLELCRS
451 EMVRSHKAV*
```

m607/a607 98.9% identity in 459 aa overlap

```
m607.pep      10      20      30      40      50      60
MLLDLNRFSF  PVFLKEVRLT TALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS
|||||
a607          10      20      30      40      50      60
MLLDLNRFSF  PVFLKEVRLT TALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS

m607.pep      70      80      90      100     110     120
SAFATVYITF  MGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGLEFLGVFGMVLMWAAIT
|||||
a607          70      80      90      100     110     120
SAFATVYITF  MGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGLEFLGVFGMVLMWAAIT

m607.pep      130     140     150     160     170     180
PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRLAHAYTSSLNRPRILMLVSFAAFVLN
|||||
a607          130     140     150     160     170     180
PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRLAHAYTSSLNRPRILMLVSFAAFVLN

190      200      210      220      230      240
```

970

```

m607.pep      VPLNYIFVYKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
a607          VPLNYIFVYKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
              190      200      210      220      230      240

              250      260      270      280      290      300
m607.pep      WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMPQSV
a607          WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMPQSV
              250      260      270      280      290      300

              310      320      330      340      350      360
m607.pep      GSAGTVRIGFSLGRREFSRARYISGVSLVGLWMLAVITVLSLVLFRSPLVSMYNNPFAVL
a607          GSAGTVRIGFSLGRREFSRARYISGVSLVGLWMLAVITVLSLVLFRSPLVSMYNNPFAVL
              310      320      330      340      350      360

              370      380      390      400      410      420
m607.pep      SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPMFIAAAFWGCGLLPGYLLAYRFN
a607          SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPMFIAAAFWGCGLLPGYLLAYRFD
              370      380      390      400      410      420

              430      440      450      460
m607.pep      MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSRKAVX
a607          MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSRKAVX
              430      440      450      460

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1925>:

```

g608.seq
1   ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTACCT CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CAGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATT ACCTTCCGCA ACAGCGCGAT
201 ACGGAAAATC CTCCAAGGCG GCGAACC CGCTGGCGAC ATCAGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCTCGC CATCGGacgA ATTGGCACGG ATTTTCGGCA CGCAGGCAGg
351 catcggcagc CGTGCCACCG ACATCGGACA CGGCaTCaaa CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAACC CGAGTCcgCa
451 aacaccggca acgaagccct tgccgactgc ctCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACAGG CTCGAACGCG
551 ACATTTGGAT AGACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1926; ORF 608.ng>:

```

g608.pep
1   MSALLPIINR LILQSPDSRS ELTSFAGKTL TLNIAGLKLA GRITEDGLLS
51  AGNGFADTEI TFRNSAIRKI LQGGEPGAGD IRLEGLDILG IAVLSLLGSL
101 RSRASDELAR IFGTQAGIGS RATDIGHGIK QIGRNIAEQI GGFSREPESA
151 NTGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1927>:

```

m608.seq
1   ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTGC CGTTCGAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATT ACCTTCCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGAG GCGAACC CGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCTCGC CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCGG ACATCGGACA CGGCATCAAA CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAATC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT

```

971

501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG  
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS  
51 AGNGFADTEI TFRNSAVQKI LQGGEFGAGD IGLEGLILG IAVLSLLGSL  
101 RSRASDELAR IFGTQADIGS RAADIGHGK QIGRNIAEQI GGFSRESESA  
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng) from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	::					
g608	MSALLPIINRLILQSPDSRSELTSFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGGEFGAGDIGLEGLILGIAVLSLLGSLRSRASDELARIFGTQADIGS					
	::					
g608	TFRNSAIRKILQGGEFGAGDIRLEGLILGIAVLSLLGSLRSRASDELARIFGTQAGIGS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m608.pep	RAADIGHGKIQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR					
	::					
g608	RATDIGHGKIQIGRNIAEQIGGFSREPESANTGNEALADCLDEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
	189					
m608.pep	LERDIWIDX					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq

1 ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA  
51 CAGCCGCTCG GAACTTGCCG CCTTCGAGG CAAAACACTG ACCCTGAACA  
101 TTGCCGGGTT GAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG  
151 GCGGGAACG GCTTTGCAGA CACCGAAATC ACCTTCGCA ACAGCGCGGT  
201 ACAGAAAATC CTCCAAGGCG GCGAACCCGG GCGGGGCGAC ATCGGGCTCG  
251 AAGGCGACCT CATCTCGGC ATCGCGGTAC TGTCCTGCT CGGCAGCCTG  
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA  
351 CATCGGCAGC CGTGCCGCCG ACATCGGACA CGGCATCAA CAAATCGGCA  
401 GGAACATCGC CGAACAAATC GGCAGATTT CCCGCGAACC CGAGTCCGCA  
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT  
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG  
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS  
51 AGNGFADTEI TFRNSAVQKI LQGGEFGAGD IGLEGLILG IAVLSLLGSL  
101 RSRASDELAR IFGTQADIGS RAADIGHGK QIGRNIAEQI GRFSREPESA  
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID\*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

972

```

m608.pep  MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
a608      MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
           10      20      30      40      50      60

           70      80      90      100     110     120
m608.pep  TFRNSAVQKILQGGEPGAGDIGLEGLLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
a608      TFRNSAVQKILQGGEPGAGDIGLEGLLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
           70      80      90      100     110     120

           130     140     150     160     170     180
m608.pep  RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR
a608      RAADIGHGIKQIGRNIAEQIGRFSREPESANIGNEALADCLDEISRLRDGVERLNERLDR
           130     140     150     160     170     180

           189
m608.pep  LERDIWIDX
a608      LERDIWIDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1931>:

```

g609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTTTGA
51  TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGTT TCCACATAAT
201 CGATAACTTC CTCGATACCG ACTTCGGCAT CGGAAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGATTATG CGCGCCATAT TGGGAAATT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTG TGGCCGTATG
351 CCCCGTCTTT CATTCACCC GTGAGGCTGA CATCATAATC CAGtaa

```

This corresponds to the amino acid sequence <SEQ ID 1932; ORF 609.ng>:

```

g609.pep
1  MVVDRLEILA LDETLDAFV GNQRSSDIAH HIFHEFRV FVGLFGNVFFIG
51  AFEQAVELAA RLRPHIIDNF LDTDFGIGSQ ADGNVRTLM RAILGNFFGT
101 RAKRGYGNHD LHTVAVCPVF HFTREADIII Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1933>:

```

m609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTTTGA
51  TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGTTGTG CGCGCCGTAT TGGGAAATT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTG TGGCCGTATG
351 CCCCGTCTTT GATTCGCCC GTGAGACAGA CATCATAATC CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1934; ORF 609>:

```

m609.pep
1  MVVDRLEILA LDETLDAFV GNQRSSDIAH HIFHEFRV FVGLFGNVFFIG
51  AFEQAVELAA RLRPHIIDNF LDTDFGIGSQ ADGNVRTLVV RAVLGNFFGT
101 RAKRGYGNHD LHTVAVCPVF DFARETDIII Q*

```

m609/g609 93.1% identity in 131 aa overlap

```

           10      20      30      40      50      60
m609.pep  MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRV FVGLFGNVFFIGAFEQAVELAA
           10      20      30      40      50      60
g609      MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRV FVGLFGNVFFIGAFEQAVELAA
           10      20      30      40      50      60

           70      80      90      100     110     120
m609.pep  RLRPHIIDNFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF
           70      80      90      100     110     120

```



973

```

g609      RLRFHIIIDNFDLDFGIGSQADGNVRTLIMRAILGNFFGTRAKRGYGNHDLHTVAVCPVF
           70      80      90      100     110     120

           130
m609.pep  DFARETDIIIQX
           |:|:|:|:|:|
g609      HFTREADIIIQX
           130

```

-- The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1935>:

```

a609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AACTCTTGA
51  TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTCG GGTTTTCGTA GGCTTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTGTG CGGCCATAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCATACTG TGGCCGTATG
351 CACCGTCTTT CATTCGCCC GTGAGGCTGA CATCATAATC CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1936; ORF 609.a>:

```

a609.pep
1  MVVDRLEILA LDEETLDAFV GNQRSSDIAH HIFHEFRV FV GFFGNVFFIG
51  AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAILGNFFGT
101 RAKRGYGNHD LHTVAVCTVF HFAREADIII Q*

m609/a609 96.9% identity in 131 aa overlap

           10      20      30      40      50      60
m609.pep  MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRV FVGFFGNVFFIGAFEQAVELAA
           |||
a609      MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRV FVGFFGNVFFIGAFEQAVELAA
           10      20      30      40      50      60

           70      80      90      100     110     120
m609.pep  RLRRLHIIDDFLDLDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF
           |||
a609      RLRRLHIIDDFLDLDFGIGSQADGNVRTLVVRAILGNFFGTRAKRGYGNHDLHTVAVCTVF
           70      80      90      100     110     120

           130
m609.pep  DFARETDIIIQX
           |||
a609      HFAREADIIIQX
           130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1937>:

```

g610.seq
1  ATGATTGGAG GGCTTATGCA ATTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ATGATTTTTC ACGCCGCCCTG ATGCGCGAGC
101 ATATGCTGAC CGCCGATGAT TTGATTTATC CGGTGTTCTG ATTGGAGGGG
151 GCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGTGAAG CTCGGTATTC
251 CGATGTTGGC ACTCTTTCCC GTGGTTACGG CAAACAAAC CGGGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG tccgagccTT
351 GCGCGAGAGG TtccCgaac tggggattat gacggatgtc gcgctcgAtc
401 cttatacggT gcacGGTCAG GACGGACTGA CGGACgaaaa cggttaCGTG
451 ATGAatgATg aaacCGTAGA AGTCTTGGTG AAACAGGCTT TATGTCATGC
501 AGAGGCGGGC ACGCAGGTCG TTGCTCCTTC CGATATGATG GACGGGCGTA
551 TCGGCGCCAT CCGCGAGGCT TTGGAGGATG CCGGACATAT CCATACGCGG
601 ATTATGGCAT ATTCCGCCAA ATATGCTTCT GCATTCTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTGGGG AAAGGCAGAT AAAAAGACCT
701 ATCAGATGGA TCCTGCAAAT ACCGATGAGG CGCTGCATGA AGTGGCGCTC
751 GATATTCAGG AAGGTGCGGA TATGGTGATG GTGAAGCCCG GTTGGCCGTA

```

974

```
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTA CCGACTTATG
851 CCTATCAGGT TTCGGGCGAA TATCGCATGT TGCAGGCGGC GGTGCGCAAC
901 GGTGCGCTGG ACGGCGGCAA AGTGGTTTGT GAAAGCCTGC TGGCATTCAA
951 ACGTGGCGGT GCGGACGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1938; ORF 610.ng>:

m610.pep

```
1 MIGGLMQFPY RNVPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
51 AAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTGRA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG TQVVAPSDMM DGRIGAIRES LEDAGHIHTR
201 IMAYSASYAS AFYGPFRDAV GSSGNLKGAD KPTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFV PTYAYQVSGE YAMLOAAVAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYAI EAAKMLKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1939>:

m610.seq

```
1 ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CCGCTTCGCG
51 TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCGTG ATGCGCGAAC
101 ACACGCTGAC CGCCGATGAT TTGATTATAT CCGGTGTTCT ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGTGTGA AGCGTCAAAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGGC
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT TCACGGTCAG GACGGGCTGA CGGACGAAAA CGGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTTGGT AAGCAGGCTT TGTGCCACGC
501 TGAAGCGGGC GCGCAGGTGG TTGCCCTTC CGATATGAT GACGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGCGGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTGGG CAAGGCAGAT AAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTGAGG AAGGTGCGGA TATGGTAATG GTCAAGCCCG GTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TAAAGACGA GTTCGGTGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGT TGCAGGCGAG GATTGCCAAC
901 GGTGCGCTGG ACGGCGGCAA AGTGGTTTGT GAAAGCCTGC TGGCATTCAA
951 ACGTGGCGGT GCGGACGGGA TTTTGACCTA TTACGCTATT GAGGCGGCAA
1001 AGATGTTGAA GCGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1940; ORF 610>:

m610.pep

```
1 MIGGLMQFPY RNVPASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51 SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIRES LEDAGHIHTR
201 IMAYSASYAS AFYGPFRDAV GSSGNLKGAD KPTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFV PTYAYQVSGE YAMLOAAIAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYAI EAAKMLKR*
```

m610/g610 98.5% identity in 338 aa overlap

	10	20	30	40	50	60
m610.pep	MIGGLMQFPYRNV	PASRMRRMRDD	FSRRLMREHTLT	ADDLIYPVFVLE	GSAREEDVPSM	
g610	MIGGLMQFPYRNV	PASRMRRMRDD	FSRRLMREHMLT	ADDLIYPVFVLE	GAAREEDVPSM	
	70	80	90	100	110	120
m610.pep	PGVKRQSLDRLL	FTAEEAVKLGIP	MLALFPVVTANK	TERAQEAYNPE	GLVPSTVRALR	
g610	PGVKRQSLDRLL	FTAEEAVKLGIP	MLALFPVVTANK	TGRAQEAYNPE	GLVPSTVRALR	
	130	140	150	160	170	180
m610.pep	FPELGIMTDVAL	DPYTVHGQDGL	TDENGYVMNDET	VEVLVKQALCH	AEAGQVVAPSD	
g610	FPELGIMTDVAL	DPYTVHGQDGL	TDENGYVMNDET	VEVLVKQALCH	AEAGTQVVAPSD	
	190	200	210	220	230	240
m610.pep	DGRIGAIRESLE	DAGHIHTRIMAY	SASYASAFYGP	FRDAVGSSGNL	KGADKPTYQMD	

975

```

g610      DGRIGAIREALDAGHIHTRIMAYSAKYASAFYGFPRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAIAN
           250      260      270      280      290      300
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300
m610.pep  GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330      339
g610      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```

a610.seq
1  ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCTG ATGCGCGAGC
101 ATACGCTGAC TGCCGATGAT TTGATTATC CGGTGTTCGT ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCGGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT GCACGGTCAG GACGGGCTGA CCGACGAAA CCGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTGGTC AAGCAGGCTT TGTGTCATGC
501 AGAGGCAGGC GCACAGGTCG TTGCTCCTTC CGATATGATG GATGGCGGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTGGG CAAGGCAGAT AAAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAGG AAGGTCCGGA TATGGTGATG GTCAAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGC TGCAGGCGGC GGTGCGCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGATGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```

a610.pep
1  MIGGLMQFPY RNVSASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGFPRDAV GSSGNLGKAD KPTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLQAAVAN
301 GWLDGGKVV L ESLLAFKRAG ADGILTYAI EAAKMLKR*

```

m610/a610 99.4% identity in 338 aa overlap

```

           10      20      30      40      50      60
m610.pep  MIGGLMQFPYRNVPASRMRRMRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60
a610      MIGGLMQFPYRNVSASRMRRMRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60
           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120
           130     140     150     160     170     180

```

976

```

m610.pep  FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
a610      FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
           130      140      150      160      170      180

           190      200      210      220      230      240
m610.pep  DGRIGAIREALDAGHIHTRIMAYSAKYASAFYGFPRDAVGSSGNLGKADKKTYQMDPAN
a610      DGRIGAIREALDAGHIHTRIMAYSAKYASAFYGFPRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240

           250      260      270      280      290      300
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAIAN
a610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300

           310      320      330      339
m610.pep  GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
a610      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1943>:

```

g611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGGCG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCCCGGA CTCTGTCGAG
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TTTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT Ctcgcgcagg ttgtGGCtgt
201 taticctTGGG CGGGCTGggt tgtttgcccg ccataaTTtc cagtacctga
251 TcgcgGTcta tggtttccCa ttCcatcagg gctttgcaca TCGTTTCCAT
301 cttgTCCGGG TTTTcatcga ggaTTTGTa ggcaacCTGA TACTgctcgt
351 ccaaaAtccg Gcggatttcc gcgtcgAtgt cctgctgggt TTTCTCGGAA
401 ATGTTTTGCG AACGGgttac gctGCGCCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGtc gCTCAtgcG TAGCGCGTTA
501 CCATTTCCGC TGCCATTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1944; ORF 611.ng>:

```

g611.pep
1  MPSENGMGRK QLAGCRLFGK LSLVFRLLPG LCRGGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVILG RAGLFARHNF QYLIAYVGFP FHQGFARHNF
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AAPQEDFAFV
151 FRINHHAHFV AHAVARYHFA CHLGCAFKVV *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1945>:

```

m611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGGCG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTCGCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCTGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTGTGCGCGG TTTTCATCGA GGATTTGTa GGCAACCTGA TATTGCTCGT
351 CCAAAATCCG GCGGATTTCG GCGTCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTGCG AACGGGTtAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTc GCTCATGCCG TAGCGCGTTA
501 CCATTTCCGC CGCCATTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1946; ORF 611>:

```

m611.pep
1  MPSENGMGRK QLAGCRLFGK LSLVFRLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGFH FHQGFARHNF
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/g611 96.1% identity in 180 aa overlap

10 20 30 40 50 60

977

```

m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
g611          MPSENGMGKRQLAGCRLFGKLSLVFRLLPGLCRGGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPPFHQGFARHFLVAVFIEDFVGNLILLVQNP
g611          LAQVVAVILGRAGLFARHNFQYLIADVGFPPFHQGFARHFLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
g611          ADFRVDVLLGFLGNVLRGTGYAAPQEDFAFVFRINHHAHFVAHAVARYHFACHLGCAFKVV
              130     140     150     160     170     180

m611.pep      X
               |
g611          X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1   ATGCCGCTCTG AAAACAGGAT GGGAAAACGG CAGCTTCCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTGCCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCTGA TGGTTTCCCA TTCCATCAGG GCTTGCACA TCGTTTCCAT
301 CTTGTCCGCG TTTTCATCGA GGATTTTGTA GGCAACCTGA TACTGCTCGT
351 CCAAAATCCG GCGGATTTCC GCATCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTCG AACGGGTTAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTGTC GTCATGCCG TAGCGCGTTA
501 CCATTTCCGC CGCCATTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1   MPSENRMGKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGF PPFHQGFARH
101 LVAVFIEDFV GNILLVQNP ADFRIDVLLG FLGNVLRGTY AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/a611 98.9% identity in 180 aa overlap

```

              10      20      30      40      50      60
m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60
a611          MPSENRMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPPFHQGFARHFLVAVFIEDFVGNLILLVQNP
a611          LAQVVAVIFGRAGLFARHDFQYLIADVGFPPFHQGFARHFLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
a611          ADFRIDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
              130     140     150     160     170     180

m611.pep      X

```

978

a611           |  
                  X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1949>:

```
g612.seq
1  ATGGgcttcg gcggaatat tgcAAAAAAG CTGGCcgGg taGATGAAAT
51  AGCCTttgac tttgacggca TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCataG CGGCGTAATC AATGCTGCTG TCGCCGGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCGATTTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA TAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTtttac GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1950; ORF 612.ng>:

```
g612.pep
1  MGFGGNIAKK LAGVDEIAFD FDGIVDFDGR DDAVRHSGVI NAAVAGLHIV
51  GEVFADKAVE KCAENVLFKV PAIHRAAYFV GDFPNLAVQL GALLHFGHHR
101 NPYIKLNKSK SPDIFRFFY GHSN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1951>:

```
m612.seq
1  ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51  AGCCTTTAAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA .AAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTtttac GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1952; ORF 612>:

```
m612.pep
1  MGFGGNIAKK LAGVDEIAFN FDGIVDFDGR DDAVRHSGVI NTAVACLHIV
51  GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR
101 NPYXKLNKSK SPDIFRFFY GHSN*
```

m612/g612 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m612.pep	MGFGGNIAKKLAGVDEIAFNFDGIVDFDGRDDAVRHSGVINTAVACLHIVGEVFADKAVE					
g612	MGFGGNIAKKLAGVDEIAFDGIVDFDGRDDAVRHSGVINAAGVAGLHIVGEVFADKAVE					
	10	20	30	40	50	60
m612.pep	KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRFFY					
g612	KCAENVLFKVP AIHRAAYFVGDFPNLAVQLGALLHFGHHRNPYIKLNKSKSPDIFRFFY					
	70	80	90	100	110	120
m612.pep	GHSNX					
g612	GHSNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1953>:

```
a612.seq
1  ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51  AGCCTTTGAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTAAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTGAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGTATTTCGG TCATCATCGA
301 AATCCATAT .AAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTttt .AC GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
  1  MGFGGNIAKK LAGVDEIAFD FDGIVDFGR DDAVRHSGVI NTAVACLHIV
 51  GKVFDKAVE KCAENVLFEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
101  NPYXKLNKSK SPDIFRRFFX GHSN*

m612/a612    96.0% identity in 124 aa overlap

              10      20      30      40      50      60
m612.pep      MGFGGNIAKKLAGVDEIAFNFDGIVDFGRDDAVRHSGVINTAVACLHIVGEVFADKAVE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a612           MGFGGNIAKKLAGVDEIAFDGIVDFGRDDAVRHSGVINTAVACLHIVGKVFADKAVE
              10      20      30      40      50      60

              70      80      90     100     110     120
m612.pep      KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFY
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a612           KCAENVLFEPV AIHRAAYFVGNFPNLAVQLGALLYFGHHRNPYXKLNKSKSPDIFRRFFX
              70      80      90     100     110     120

m612.pep      GHSNX
              ||||
a612           GHSNX
  
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
  1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCGT CGaggcagtc ggcaagggct tcgttgccgg
101  tgtttGcgGA CTCGGGTTTCG CGGGAAAATC CGCCGATTG TTCGGCGATG
151  TTCCTGCCGA TTTgtttGat GCCGTGTCCG ATGTCGGTGG CACGgctgcc
201  gatgcCTGCC TGCCTGCCGA AAATCCGTGC CAATTcgtCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTCCG
301  CCTTCGAGCC TGATGTCGCC AGCCCCGGGT TCGCCGCTT GGAGGATTTT
351  CCGTATCGCG CTGTTGCGGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATTGGGGC GGAGAATGCC TGTGTGTGCT GTTGCCGCTT
601  ATTTACAGG CTTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
  1  MSRSSLSRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSAM
 51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101  PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFPAESKPS SVMRPASFSP
151  AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLLPL
201  ILQA*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

m613.seq
  1  ATGTCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101  TGTTTGCgGA CTCGATTTCG CGGGAAAATC CGCCGATTG TTCGGCGATG
151  TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201  GATGTCTGCC TGCCTGCCGA AAATCCGTGC CAATTCTGCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCCG
301  CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT
351  CTGTACCGCG CTGTTGCGGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGCGGCAA GTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTGTGCT GTTGCCGCTT
  
```

980

601 ATTTTACAGG CTAA

This corresponds to the amino acid sequence <SEQ ID 1958; ORF 613>:

m613.pep

```

1  MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLPMFADSDS RENPPICSA
51  FLPICLMPCP MSAARLPMSA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101 PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KPFPAESKPS SVMRPASFSP
151 AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLPL
201 ILQA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m613/g613 94.6% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSA					
g613	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPVFADSGSRENPPICSA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRIFCTA					
	:					
g613	MSVARLPMPACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSLMSPAPGSPPWRIFRIA					
	70	80	90	100	110	120



981

	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFS	PAMFRVSVLP	AKAASSERLS	SGLCRIRRLMMG		
g613	LLRKVISVSAKPFPAESKPSSVMRPASFS	PAMFRVSVLP	AKAVSSERLS	SGLCRIRRLMMG		
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
g613	RRADIFSDWGGECLLLLLPLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```

a613.seq
1  ATGTCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
51  GCGCAGTCTG CTTATTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101 TGTTCGCGGA CTCGGGTTTCG CGGGAAAATC TGCCGATTTC TTCGGCGATG
151 TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201 GATGTCGTCC TGCCTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
251 AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCG
301 CCTTCGAGCC CGATGTCGCC CGCCCGGGT TCGCCGCCTT GGAGGATTTT
351 CTGTACCGCG CTGTTGCGGA AGGTGATTTC GGTGTCTGCA AAGCCGTTTC
401 CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAACCCG
451 GCAATGTTCA GGGTCAGTGT TTTGCCTGCG AAGGCGGCAA GTTCCGAGCG
501 GCTGTCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551 ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTTGCT GTTGACGCTT
601 ATTTTACAGG CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

```

a613.pep
1  MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLPMFADSGS RENLPICSAM
51  FLPICLMPCE MSAARLMSA CVPKIRANSS DARERRLPSR DSTAMPRMR
101 PSSPMSAPG SPPWRIFCTA LLRKVISVSA KPFAESKPS SVMRPASFP
151 AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLTL
201 ILQA*

```

m613/a613 98.0% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSL	LISSRQSARASLPMFADSDS	RENPPICSAMFLPICLMPCP			
a613	MSRSSRSRRSLRRSTPSRSL	LISSRQSARASLPMFADSGS	RENLPICSAMFLPICLMPCP			
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLMSACVVKIRANSS	DARERRLPSRDSTAMPRMR	SPSSPMSAPGSPWRIFCTA			
a613	MSAARLMSACVVKIRANSS	DARERRLPSRDSTAMPRMR	SPSSPMSAPGSPWRIFCTA			
	70	80	90	100	110	120
	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFS	PAMFRVSVLP	AKAASSERLS	SGLCRIRRLMMG		
a613	LLRKVISVSAKPFPAESKPSSVMRPASFS	PAMFRVSVLP	AKAASSERLS	SGLCRIRRLMMG		
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
a613	RRADIFSDRGGECLLLLLTLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:

982

g614.seq  
 1 AtggcTgcgt tcAacgcttt ggacggcaaa aaagaagaca acggggcaaat  
 51 cgaaTATtCT CAGTTCATCC GACAGGTCAA CAACGGCGAA GTATCCGGCG  
 101 TCAACATCGA AGGATCCGTC GTCAGCGGTT ACCTGATTAA AGGCGAGCGC  
 151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCCTTGGATG ACAACCTGAT  
 201 TCAAACCTTT TTGAACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA  
 251 AACCGAGCGC GCTGACTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG  
 301 CTGATTGGCG CATGGTTCTA CTTTATGCGT ATGCAGGCGG GCGGCGGCGG  
 351 AAAAGGCGGC GCATTCTCCT TCGGCAAAAG CCGCGCCCGC CTGCTGGACA  
 401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC  
 451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCAC CGAACCGCTa  
 501 tcaAAGcctc ggcgggcctg ttcCGGCGCG CATCctgCtg gcgGgcagcc  
 551 CGGGAaccgg taaAACACTC TTGGCGAAAG CCATTGCAGG CGAGGCCGGC  
 601 GTGCCGTTCT TCAGCATTTC CGGTTCGAT TTTGTGCGAA TGTTCGTCGG  
 651 TTGCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCA AAGAAAAACG  
 701 CCCCATGCAT TATCTTTATC GACGAGATTG ACGCGGTAGG CCGCCAACGC  
 751 GGCGCAGgTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA  
 801 ATTATTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA  
 851 TTGCGGCAAC CAACGCCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC  
 901 GGCCGCTTCG ACCGCCAAGT CGTCGTCCCC CTGCCGACA TCCGGGGCGG  
 951 CGAACAGatn ttGAACGTCC ATTCTaaAAA AGTGCcttTG gacgaATCTg  
 1001 tggaTTTATT GTCCCTCGCG CGCGGCACGC ccggttttTC cggcgcgat  
 1051 tTggcgaaac tggTcaacga agccccctg tttgccggcc gccgcaacaa  
 1101 agtgaagtc gatcaaagcg attTGAAGAC GCCAAAGACA AAATCTATAT  
 1151 GGGTCCGGA CGCCGAGTA TGGTGA

This corresponds to the amino acid sequence <SEQ ID 1962; ORF 614.ng>:

g614.pep  
 1 MAAFNALDGK KEDNGQIEYS QFIRQVNNGE VSGVNIIEGSV VSGYLIKGER  
 51 TDKSTFFTNA PLDDNLIQTL LNKNVVRVKT PEEKPSALTA LFYSLLPVLL  
 101 LIGAWFYFMR MQAGGGGKGG AFSFGKSRAR LLDKDKANKVT FADVAGCDEA  
 151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAGEAG  
 201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR  
 251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP  
 301 GRFDRQVVVP LPDIRGREQX LNVHSHKKVPL DESVDLLSLA RGTPGFSGAD  
 351 LAKLVNEAPL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1963>:

m614.seq  
 1 ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT  
 51 CGAATACTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG  
 101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC  
 151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTTGGAGC ACAACCTAAT  
 201 TAAACACTG CTCGACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA  
 251 AACCAGAGCG GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG  
 301 CTGATTGGCG CATGGTTCTA CTTATGCGT ATGCAGACGG GCGGCGGCGG  
 351 AAAAGGCGGC GCATTCTCAT TCGGTAAAAG CCGCGCCCGC CTGCTGGACA  
 401 AAGATGCCAA CAAAGTGACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC  
 451 AAAGAAGAAG TACAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA  
 501 TCAAAGCCTG GCGGGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC  
 551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC  
 601 GTGCCGTTCT TCAGCATTTC AGGTTCGAC TTTGTGCGAA TGTTCGTCGG  
 651 TGTCGGTGCG AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG  
 701 CCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC  
 751 GGCGCAGGTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA  
 801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA  
 851 TTGCGGCAAC CAACGCCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC  
 901 GGCCGTTTCG ACCGCCAAGT GGTGTCCCC CTGCCGACA TCCGAGGGCG  
 951 CGAACAGATT TTGAACGTCC ATTCTAAAA AGTGCCTTTG GACGAATCTG  
 1001 TGGATTATTT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT  
 1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA  
 1101 AGTCAAAGTC GATCAGAGCG ATTGAAGAC GCCAAAGACA AAATCTATAT  
 1151 GGGTCCGGA CGCCGAGTA TGGTGA

This corresponds to the amino acid sequence <SEQ ID 1964; ORF 614>:

983

```

m614.pep
1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIIEGSV VSGYLIKGER
51  TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAAGEAG
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGNDE REQTLNQLLV EMDGFESNOT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQI LNVHSHKVPL DESVDLLSLA RGTGPGFSGAD
351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m614/g614 98.0% identity in 391 aa overlap

	10	20	30	40	50	60
m614.pep	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFTNA					
g614	MAAFNALDGKKEDNGQIEYSQFIRQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFTNA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m614.pep	PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGGKGG					
g614	PLDDNLIQTLLNKNVRVKVT PEEKPSALTALFYSLLPVLL LIGAWFYFMR MQAGGGGKGG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m614.pep	AFSFGKSRARLLDKDANKVT FADVAGCDEAKEEVQEIVDY LKAPNRYQSL GGRVPRGILL					
g614	AFSFGKSRARLLDKDANKVT FADVAGCDEAKEEVQEIVDY LKAPNRYQSL GGRVPRGILL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m614.pep	AGSPGTGKTL LAKAIAAGEAGVPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI					
g614	AGSPGTGKTL LAKAIAAGEAGVPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m614.pep	DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNOT VIVIAATNRP DVLDPALQRP					
g614	DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNOT VIVIAATNRP DVLDPALQRP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m614.pep	GRFDRQVVVPLPDIRGREQILNVHSHKVPLDESVDLLSLARGTGPFGSGADLANLVNEAAL					
g614	GRFDRQVVVPLPDIRGREQXNVHSHKVPLDESVDLLSLARGTGPFGSGADLAKLVNEAAL					
	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
g614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1965>:

```

a614.seq
1  ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
51  CGAATATTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTTGGACG ACAACCTGAT
201 TAAACACTG CTGACAAAA ACGTCCGTGT AAAAGTAACG CCGGAAGAAA
251 AACCGAGCGC GCTGGCTGCC CTGTTTACAC GCCTGCTGCC CGTCTGCTG

```

984

```

301 CTGATTGGCG CGTGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGCAAAAG CCGCGCCCGC CTACTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
501 TCAAAGCCTG GCGGGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCGTTCCT TCAGCATTTC AGGTTCCGAC TTTGTCGAAA TGTTCTGTCG
651 TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GCGCGAGGTT TGGGCGGCGG TAATGATGAG CGCGAGCAAA CATTAAACCA
801 ATTGTTGGTT GAAATGGACG GTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGGCGTTTCG ACCGCCAAGT GGTGTGCCCG CTGCCGAGCA TCCGGGGGCG
951 CGAACAGATT TTGAACGTCC ACTCTAAAAA AGTGCCTTTG GACAAATCTG
1001 TGGATTATTT GTCCTCGCG CGCGGCAGCG CGGGTTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGA CGCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1966; ORF 614.a>:

a614.pep

```

1 MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIIEGSV VSGYLIKGER
51 TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGGKGG AFSFGKSRR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAEAG
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGND EQLTNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQI LNVHKKVPL DKSVDLLSLA RGTGPGFSGAD
351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

m614/a614 99.7% identity in 391 aa overlap

m614.pep	10	20	30	40	50	60
a614	10	20	30	40	50	60
m614.pep	70	80	90	100	110	120
a614	70	80	90	100	110	120
m614.pep	130	140	150	160	170	180
a614	130	140	150	160	170	180
m614.pep	190	200	210	220	230	240
a614	190	200	210	220	230	240
m614.pep	250	260	270	280	290	300
a614	250	260	270	280	290	300
m614.pep	310	320	330	340	350	360
a614	310	320	330	340	350	360

985

	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

```

g615.seq
1  ATGTGGAAC  GCGCGCGCG  CGGTGtcggC  AGCTTtgaag  agcagcGaAt
51  agatgCCGCC  GGCAAACCAC  AATGCGGAa  gcaggCtgaa  gcGGTTgcgC
101  GGCagcTTca  tGCCGCCTCC  TcGTCCaGCC  ACGtttGgca  gattttggac
151  aggcgcAGGa  ATTTGcgcCc  gcgtgcggCA  agtatgtcgc  gcCAttgtgc
201  cacttcttcg  gcggacggTG  cttcgtcgaT  gctgCATTcG  TACagcagga
251  aatcgagggt  ttcttcgatg  acggGgatgg  AttcggTTTG  GataAgCTgc
301  ttgagttcgt  tcatgactGt  TCgGATAcgg  aaatcgggaa  aatgccgtct
351  gAaagggtt  CAGACGGCat  tggATTATTT  GCTGTGCAGG  AAgcgcgttg
401  cctcttccca  ttgCGGAA  AtgATGTCGg  gtacggcctg  cAGGGATttg
451  gCGACGGcat  cgtcgatttg  ccgGcggtgc  ttCcgcgctc  ggtttGTTca
501  agacgtagcc  gaCGACGagg  ttgcggtcGC  CGGGTggtcC  GATGCCGAGG
551  CGCAGCGCGT  aatagtctgc  CGTCCCGAGT  TTTGCctgAA  TGCTTTTCAA
601  GCCGTTGTGT  CgcCGttgc  cgcCGCCGAG  TTTGAATTTg  ATCCGTCCCG
651  AAGGGATGTC  GAGTTCGTCG  TGGACGACGA  GGATTTCTTC  GGGTTTGATT
701  TTGTAGAACT  GTGCAAGCGC  GGCAACCGCC  TGTCCGGAAC  GGTTCATGAA
751  CGTGGCCGGT  TTGAGCAGCC  AAACATCGCC  GTCGGGCAGG  GCGGCGCGGG
801  CAACTTCGCC  GAAGAATTTT  TTTTCTTCTT  TAAACGAAGC  CTTCATTTC
851  CACGCCAGTT  CGTCGAGGAA  CCAAAAGCCC  GCATTGTGGC  GGTCTGTTC
901  GTATTCTTTG  CCCGGGTGTC  CCAAGCCGAC  AACCATTTTG  ATTGTGttcg
951  acatgataTT  TtccgtgTTT  CTgTCGaag  cggTctgaAG  GCTTCAGacg
1001  gcatggTtat  TCTTCTTgat  TTtgaACgct  tgtgcggCGC  GCTTCTTTGG
1051  GTTCGATCAA  CAGCGGCGG  TACACTTCGA  TCGGTCGCC  GTCGCGCAGC
1101  GCGGTGTCGT  CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```

g615.pep
1  MWKRRRRGVG  SFEEQRIDAA  GKPQCGKQAE  AVARQLHAAS  SSSHVWQILD
51  RRRNLPPRAA  SMSRHCAATSS  ADGASSMLHS  YSRKSRVSSM  TGMDSVWISC
101  LSSFMTVRI  KSGKRLKGL  QTALDYLLCR  KRVASSHLPE  MMSGTACRDL
151  ATASSICRRC  FRARFVQDVA  DDEVAVAGVA  DAEAQAVIVC  RAEFCLNVFQ
201  AVVSAVA  AAE  FEFDP  SARDV  EFVVD  DEDFF  GFDFELCKR  GNRLSGTVHE
251  RGRFEQPNIA  VGQGGAGNFA  EEEFF  FFKRS  LPFPRQFVEE  PKARIVAGLF
301  VFFARVAQAD  NHFDCVRHDI  FRVSE  CGLK  ASDGMVILLD  FERVCALLW
351  GRSTAGGTLR  CGRRRAAACR  L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

```

m615.seq Length: 1116
1  ATGCGGAAAA  GCGGGTGGCG  CGGTTTCGGC  AGCTTTGAAA  AGCAGTGAGT
51  AAATGCTGCC  TGCAAACCAC  AATGCCGAGA  GCAGGATAAA  GCGGTTGCGT
101  GGCAGATTCA  TGCTTGTTCC  TCTTCAAGCC  ATGTCTGGCA  TAGTTTGAT
151  AGGCGCAGGA  ATTTCCGCC  GCGTGGCGCC  AGCATATCGC  GCCAAACGGC
201  AATTTCTTCG  GCGGAGGGGG  CATCGTCTAT  GCTGCATTcG  TAGAGCAGGA
251  AATCGAGGGT  TTCTTCGATG  ACGGGGATGG  ATTCGGTTTG  GATAAGCTGC
301  TTGAGTTCGG  TCATGACTGT  TCGGATATGG  AAATCGGGAA  CATGCCGTCT
351  GAAAGGGCTT  CAGACGGCAT  CGGGTCATT  GCTGTGCAGG  AAGCGGGTTG
401  CTTCTTCCCA  TTTGCCGGCA  AGGATGTCGG  GTATGGCTTG  CAGGATTTG
451  GCGACGGCAT  CGTCAATCTG  TCGGCGGTGT  .TCCGTACTG  GGTTTGTTCA
501  GGACATAGCC  GACGACGAGG  TTGCGGTGCG  CCGGGTGGCC  GATGCCGAGG
551  CGCAGCGGGT  AATAGTCTGC  CGTGCCGAGT  TTTGCCTGAA  TGTCTTTCAA
601  GCCGTTGTGT  CCGCCGTTGC  CGCCGCGGAG  TTTGAATTTG  ATCCGTCCGC
651  AGGAATGTC  GAGTTCGTCG  TGGACGACGA  GGATTTCTTC  GGGTTTGATT
701  TTGTAGAACT  GTGCAAGCGC  GGCAACTGCC  TGTCCGGAAC  GGTTCATGAA
751  CGTGGCAGGT  TTGAGCAGCC  AAACGTCGCC  GTCGGGCAGG  GCGGCACGGG

```

986

```

801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTC
851 CACGCCAGTT CGTCGAGGAA CAAAAAAGCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGTGCAATG CTGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTGCGGCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGGCGG TACACTTCGA TGCGGTGCGC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1970; ORF 615>:

m615.pep Length: 372

```

1 MRKRRWRGFG SFEKQXVNAA CKPQCREQDK AVAWQIHACS SSSHVWHS LD
51 RRRNFPPRAA SISRQTAISS AEGASSMLHS XSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRC XRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSAAAAAE FEFDPASAGNV EFWVDEDEFF GFDFVELCKR GNCLSGTVHE
251 RGRFEQPNVA VGQGGTGDFE EFFFFFFKXS LPFPQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCVXHDI FRVSVECLLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m615/g615 86.8% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRGFGSFEKQXVNAA	CKPQCREQDKAVAWQIHACS	SSSHVWHS	LD	RRRNFP	PRAA
g615	MRKRRWRGFGSFEKQXVNAA	CKPQCREQDKAVAWQIHACS	SSSHVWHS	LD	RRRNFP	PRAA
	10	20	30	40	50	60
m615.pep	SISRQTAISSAEGASSMLHS	XSRKSRVSSMTGMDSVWIS	CLSSVMTVRIWKSGTCRLKGL			
g615	SISRQTAISSAEGASSMLHS	XSRKSRVSSMTGMDSVWIS	CLSSVMTVRIWKSGTCRLKGL			
	70	80	90	100	110	120
m615.pep	QTASGHLLCRKRVASSHLPA	RMSGMACRDLATASSICRRC	XRTGFVQDIA	DDEVAVARVA		
g615	QTASGHLLCRKRVASSHLPA	RMSGMACRDLATASSICRRC	XRTGFVQDIA	DDEVAVARVA		
	130	140	150	160	170	180
m615.pep	DAEAQAVIVCRAEFCLNVFQ	AVVSAAAAAEFEFDPASAGNV	EFWVDEDEFFGFDFVELCKR			
g615	DAEAQAVIVCRAEFCLNVFQ	AVVSAAAAAEFEFDPASAGNV	EFWVDEDEFFGFDFVELCKR			
	190	200	210	220	230	240
m615.pep	GNCLSGTVHERGRFEQPNVA	VGQGGTGDFE	EFFFFFFKXS	LPFPQFVEE	PKTRIVACLF	
g615	GNCLSGTVHERGRFEQPNVA	VGQGGTGDFE	EFFFFFFKXS	LPFPQFVEE	PKTRIVACLF	
	250	260	270	280	290	300
m615.pep	VFFARVAQADNHFDCVXHDI	FRVSVECLLKASDGMVILLD	FERVCGALLW	GRSTAGGTLR		
g615	VFFARVAQADNHFDCVXHDI	FRVSVECLLKASDGMVILLD	FERVCGALLW	GRSTAGGTLR		
	310	320	330	340	350	360
m615.pep	CGRRRAAACRLX					
g615	CGRRRAAACRLX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1   ATGCGGAAAC GCGCGCGGCG CGGTGTCGGC AGCTTTGAAG AGCAGCGAAT
51  AGATGCCGCC GGCAAACCAC AATGCGGAAA GCAGGCTGAA GCGGTTGCGC
101 GGCAGCTTCA TGCCGCCTCC TCGTCCAGCC ACGTTTGGCA GATTTTGGAC
151 AGGCGCAGGA ATTTGCCGCC GCGTGCGGCA AGTATGTCGC GCCATTGTGC
201 CACTTCTTCG GCGGATGGTG CGTCGTCGAT GCTGCATTCG TACAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCGGTTTG GATAAGCTGC
301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGGTCATTT GCTGTGCAGG AAGCGGGTTG
401 CCTCTTCACA TTTGCCGGCA AGGATGTCGG GTATGGCTTG CAGGGATTTG
451 GCGACGGCAT CGTCAATCTG TCGGCGGTG. TTCCGTA CTG GGTTTGTTC
501 GGACATAGCC GACGACGAGG TTGCGGTGCG CCGGGTGGCC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCTGAA TGTCTTCAA
601 GCCGTTGTGT CCACCGTTGC CGCGCGGAG TTTGAATTTG ATCCGTCGCG
651 AGGGAATGTC GAGTTCGTCG TGGACGACGA GGATTTCTTC GGGTTTGATT
701 TTATAAACT GCGCAAGGGC GGCAACTGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGTCGGC TTGAGCAGCC AGACATCGCC GTCGGGCGAG GTAGCACGGG
801 CGACTTCGCC GAAGAATTTT TTTCTTCTT TAAATGAAGC CTTCCATTTC
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGCCGAATG CCGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTCCGATCAA CAGCGGGCGG TACACTCGA TCGCGTCGCC GTCGCGCAGC
1101 GGCGTGTCTG CTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1   MRKRRRRGVG SFEEQRIDAA GKPQCGKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMSRHCA TSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLP A RMSGMACRDL
151 ATASSICRRX FRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSTVAAAE FEFDP SAGNV EFVVDDEDF GFD FIKLRKG GNCLSGTVHE
251 RGRLEQPDIA VGQGSTG DFA EEEEEFFK* S LFFPRQFVEE BKTRIVACLF
301 VFFARVAQAD NHFDCV* HDI FRVSAECRLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAACR L*

m615/a615 90.3% identity in 371 aa overlap

10      20      30      40      50      60
m615.pep MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSHVWHS LDRRNFP PRAA
||||| || ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
a615      MRKRRRRGVGSFEEQRIDAAGKPCGKQAEAVARQLHAASSSSHVWQILD RRRNLPPRAA
10      20      30      40      50      60

70      80      90      100     110     120
m615.pep SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL
|:|:| | |||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a615      SMSRHCA TSSADGASSMLHSYSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL
70      80      90      100     110     120

130     140     150     160     170     180
m615.pep QTASGHLLCRKRVASSHLP ARMSGMACRDLATASSICRRXRTGFVQDIADDEVAVARVA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a615      QTASGHLLCRKRVASSHLP ARMSGMACRDLATASSICRRXRTGFVQDIADDEVAVARVA
130     140     150     160     170     180

190     200     210     220     230     240
m615.pep DAEAQAVIVCRAEFCLNVFQAVVSAAAEFEFDP SAGNV EFVVDDEDF GFD FVELCKR
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a615      DAEAQAVIVCRAEFCLNVFQAVVSTVAAAEFEFDP SAGNV EFVVDDEDF GFD FIKLRKG
190     200     210     220     230     240

250     260     270     280     290     300
```

988

```

m615.pep  GNCLSGTVHERGRFEQPNVAVGQGGTGDFAEFFFKXSLFPFPRQFVEEPKTRIVACLF
          |||||||||||:||||:|||||||||||||||||||||||||||||||||
a615       GNCLSGTVHERGRLEQPDIAVGQGGTGDFAEFFFKXSLFPFPRQFVEEPKTRIVACLF
          250      260      270      280      290      300

          310      320      330      340      350      360
m615.pep  VFFARVAQADNHFDCVXHDFRVSVECCLKASDGMVILLDFERVCGALLWGRSTAGGTLR
          |||||||||||:||||:|||||||||||||||||||||||||||||||||
a615       VFFARVAQADNHFDCVXHDFRVSACRLKASDGMVILLDFERVCGALLWGRSTAGGTLR
          310      320      330      340      350      360

          370
m615.pep  CGRRRAAACRLX
          |||||||||||
a615       CGRRRAAACRLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1973>:

```

g616.seq
1  atgtcgaaCA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACCCGCCACA ATGCGGGCTT TTGGTTCCTC GACGAACCTGG
101 CGTGGAAATG GAAGGCTTCG TTTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTTGCCCGCG CCGCCCTGCC CGACGGCGAT GTTTGGCTGC TCAAACCGGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGGT TGCCGCGCTT GCACAGTTCT
251 ACAAATCAAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATC
301 CCTTGGCGAC GGATCAAAAT CAAACTCGGC GcgggcaacG gcgGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGcagac tattaCCGCC
401 TGCGCCTCGG CATCGgccaC CCCGGCgacc gcaacctCGT CGtcggctac
451 gtcttgAACa aaccgagcgc gGaagcaccg Ccggcaaatc gacgatGCCG
501 TCGCCaaATC CCTGcaggcc gtaccCGACA TcaTTTCCGg caaatgggaa
551 gaggcaacgc gCTTCTGCA CAGCAATAA TccaatGCCG TCTGaagccc
601 ttTcagacgc cattttcccg atttccgTAT CcGAaCagtc atgaacgaac
651 tcaagcAGcT tatCCAAAcg gaaTccatcC ccgtcatcga agaaacctc
701 gatttctcgc tGTACGAATG cagcAtcgac gaagCACcgt ccgccgaaga
751 agtggcacia TGcgcgacac tactTGcgcg acgcgGcgGC AAATtCTGc
801 gcctgtccaa aatctgcCaa aCGTGGctGG ACgAGGAGGC GGCatgAAgc
851 tGGCGcgcaa CCgcttcaGc ctgctTTCCG CATTGTGGT TGCCGGCGCG
901 atctATtCgc tgctcttcaA AGCTGccgaC ACCGCGCCGC CGCCGTTTCC
951 ACATTtccaC AAAGCAGCAC ACCTTGCCCT GTTTTCGCA CaaatCTTgt
1001 tTtGGCCAA AGCATTCAAA ACCGGAaAAC TTCCCATCCC CTACCGCAGC
1051 CTGATTGCGT TCGCCTTCTG TTTTGCCGTC GGCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGCGAA CCGGCAGTTT GGCAGATGTC CTTGCCgACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTGC CGCGTTCGTC CTGCGCcccg
1201 gactaa

```

This corresponds to the amino acid sequence <SEQ ID 1974; ORF 616.ng>:

```

g616.pep
1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51  VARAALPDGD VWLLKPATFM NRSQQAVAL AQFYKIKPEE ILVHDELDI
101 PCGRIKFKLG GNGGGHNLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSAEAP PANRRCRRQI PAGRTRHHFR QMGRGNALPA QQIIQCRLKP
201 FQTAFSREPY PNSHRTQAA YPNGIHPRHR RNPRFPAVRM QHRRSTVRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRGG GMKLPNRNFS LLSALWFAGG
301 IYSLLFKAAD TAPPPFPFHD KAAHLALFFA QILFLAKAFK TGKLPYPYRS
351 LIAFAFCFAV GSECAQAWFT ATRTGSIGDV LADLTGAALA LFAARSACRP
401 D*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1975>:

```

m616.seq
1  ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAACCTGG
101 CGTGGAAATG GAAGGCTTCA TTTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTCGCCCGTG CCGCCCTGCC CGACGGCGAC GTTTGGCTGC TCAAACCTGC
201 CACGTTTCATG AACCGTTCCG GACAGGCACT TGCCGCGCTT GCACAGTTCT
251 ACAAATCAAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCTTGGCGAC GGATCAAAAT CAAACTCGGC GCGGCAACG GCGGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAACA.CCG CCGACAGATT GACGATGCCG
501 TCGCAAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGGGAA

```



989

```

551 GAAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCCTC
701 GATTTCCTGC TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
751 AATTGCCGTT TGGCGCGATA TGCTGGCCGC ACGCGCGGGA AAATTCCTGC
801 GCCTATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGGTT TGCAGGCAGC
901 ATTTACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCGCCAC CGCCTTTTCC
951 GCATTTTGAC AAAGTGGCGC ACCTCGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTCTGACCAA AGCATTGAGA ACCGACAACC GCCCATCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTC CTTGCCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTACCG CGCGAGCTGC CTGCCGCCCG
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

m616.pep

```

1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51 VARAALPDGD VWLLKPATFM NRSQQAVAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTD YVRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTDXRRCRRI PASHTRHPCR QMGRSNPLPA QQMTRCRLK
201 FQTACSRFPY PSHDRTOAA YPNRIHPRHR RNPRFPALRM QHRCPLRRR
251 NCRLARYAGR TRRKIPAPIQ TMPDMAXRGT SMNLPRNRFI LLSALWFAGS
301 IYSLLFKAAE TAPPPFPFHD KVAHLALFFA QIWLTKAFR TDNRPIPYRS
351 LMVFALCFAL FSECAQAWFT ATRTGLGDV LADLTGAALA LFTARAACRP
401 D*

```

m616/g616 86.0% identity in 401 aa overlap

m616.pep	10	20	30	40	50	60
	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
g616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
	10	20	30	40	50	60
m616.pep	70	80	90	100	110	120
	VWLLKPATFMNRSQQAVALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGHGLK					
g616	VWLLKPATFMNRSQQAVALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGHGLK					
	70	80	90	100	110	120
m616.pep	130	140	150	160	170	180
	DIQAKLGTDYYRLRLGIGHPGDRNLVVGYNLKPSTEXPPTDXRCRRIQIPASHTRHPCR					
g616	DIQAKLGTDYYRLRLGIGHPGDRNLVVGYNLKPSTEXPPTDXRCRRIQIPAGRTRHHFR					
	130	140	150	160	170	180
m616.pep	190	200	210	220	230	240
	QMGRSNPLPAQQMTRCRLKPFQTACSRFPYPSHRTQAAYPNRIHPRHRNPRFPALRM					
g616	QMGRSNPLPAQQIQCRLKPFQTAFSRFPYPSHRTQAAYPNRIHPRHRNPRFPALRM					
	190	200	210	220	230	240
m616.pep	250	260	270	280	290	300
	QHRCPLRRRNCRRLARYAGRTRRKIPAPIQTMPDMAXRGTSMNLPRNRFILLSALWFAGS					
g616	QHRCPLRRRNCRRLARYAGRTRRKIPAPIQTMPDMAXRGTSMNLPRNRFILLSALWFAGS					
	250	260	270	280	290	300
m616.pep	310	320	330	340	350	360
	IYSLLFKAAETAPPPFPFHDKVAHLALFFAQIWLTKAFRTDNRPIPYRSIMVFALCFAL					
g616	IYSLLFKAAETAPPPFPFHDKVAHLALFFAQIWLTKAFRTDNRPIPYRSIMVFALCFAL					
	310	320	330	340	350	360
m616.pep	370	380	390	400		
	FSECAQAWFTATRTGLGDVLADLTGAALALFTARAACRPDX					
g616	FSECAQAWFTATRTGLGDVLADLTGAALALFAARSACRPDX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:

990

a616.seq

```

1 ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51 ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAACGGG
101 CGTGGAAATG GAAGGCTTCA TTAAAGAAG AAAAAAATTT CTTCGGCGAA
151 GTCGCCCCGTG CTACCTGCCG CGACGGCGAT GTCTGGCTGC TCAAGCCGAC
201 CACGTTTCATG AACCGTTCGG GACAGGCAGT TGCCGCCCTT GCGCAGTTTT
251 ATAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCCTGCGGAC GGATCAAAAT CAAACTCGGC GCGGCAACG GTGGACACAA
351 CGGCTTGAAA GACATTGAGG CAAAACTCGG CACGGCAGAC TATTACCGCC
401 TCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAA.CACCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGTGAA
551 GAGGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCTC
701 GATTTCCTGC TGTACGAATG CAGCATCGAC GACGCACCAT CCGCGAAGA
751 AGTGGCACAA TGGCGCGACA TACTTGCCGC ACGCGCGGC AAATTCCTGC
801 GCCTGTCCAA AATCTGCCAA ACGTGGCTGG ACGAGGAGGC GGCATGAAGC
851 TGCCGCGCAA CCGCTTCAGC CTGCTTTCGG CATTGTGGTT TGCCGGCGGC
901 ATCTATTGCG TGCTCTTCAA AGCTGCCGAC ACCGCGCCGC CGCCGTTTCC
951 GCATTTTCGAC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTTTGACCAA AGCATTCAA ACCGAAAAC TTCCCATCCC CTACCGCAGC
1051 CTGATGTGCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGATTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTT CTTGCCGATA
1151 TGGCAGGTAC GGTTCCTGCA CTCTTTGCCG CCCGCGCCGC CGACCGCCCG
1201 GACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1978; ORF 616.a>:

a616.pep

```

1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKKAS FKEEKKFFGE
51 VARATLPDGD VWLLKPTTFM NRSGQAAVAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTA DYYRLRGIGH PGDRNLVVG
151 VLNKPSTEXP PTD*RCRRQI PASHTRHPCR QM*RGNPLPA QQMTNCRCLKP
201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPREFAVRM QHRRRTIRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRG GMKLPNRFSL LLSALWFAGG
301 IYSLLFKAAD TAPPPFPFHD KAAHLALFFA QIWLTKAFK TGKLPFIPYRS
351 LMVFALCFAL FSECAQA*FT ATRTGS LGDV LADMAGTVLA LFAARAADRP
401 D*

```

m616/a616 90.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKKASFKEEKKFFGEVARAALPDGD					
a616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKKASFKEEKKFFGEVARATLPDGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m616.pep	VWLLKPATFMNRSGQAAVALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNGLK					
a616	VWLLKPTTFMNRSGQAAVALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNGLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m616.pep	DIQAKLGTADYYRLRGIGHPGDRNLVVGIVLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
a616	DIQAKLGTADYYRLRGIGHPGDRNLVVGIVLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m616.pep	QMGRSNPLPAQQMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRRNPREFALRM					
a616	QMXRGNPLPAQQMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRRNPREFAVRM					
	190	200	210	220	230	240
	250	260	270	280	290	300

```
g619.seq
1      ATGCCGCTCTG  AAAAAAATAT  CGGTTTTATG  GCAGGAAGCA  GCCGTCGGTT
51     GCGGGTCGCC   TTTGCGCTGT  TCGTGGTTTC  CTGCATCCTG  TTTATGACGC
101    TCAACGCTCAA   AGGAGATTGG  GACTTTGTCT  TGCACCTGCG  CCTGACCAAC
151    CTTGCCCGCG   TGCTGATGGT  CGCCTATGCG  GTGCGCGGTG  CCACATCAAC
201    CTTCCAAACG   CTGACAACAA  ACCGATTCT  GACCCCTTCG  ATTTTGGGTT
251    TCGATTTCGCT  GTATGTGTTT  TTGCAGACTT  TGCTGgtGTT  TACGTTcgGC
301    GGGCTGGGGCT  ATGaccctct  gcggttacct  gGCAAAATCG  GCTTTGAACAT
351    GGTGTGTATG   ATGatcgcct  CGCTGCTGCT  GTTTTACACG  CTTACCTCGTC
401    AGGGCGGGCG   CGATTTTGCC  CACATGATT  TAATCGGCGT  GATTTTCGGG
451    ATTTTGTTC    GCAGCCTTTC  CTCGTGCTTT  TCGCGCATTC  TAGACCCTCGA
501    AGAATTTTACC  GCGCGCGACG  CGAATATGTT  TGCCGGATTG  AATACCGTCG
551    GCAGCGAGCT   TTTAGGCATA  GGCGCGCTGG  TCCTGCTCGT  CAGCGCGGCG
601    TCGGTTTGGC   ACGAAACGTA  CCGCTCGGAG  GTACACCTTT  TGGGGCGGCA
651    CCAAGCCGTC   AATTGGGCTA  TCAGCTACAC  GCGCAACACC  TTTATGGATG
701    TGCTTTGGAT   TGCGCGATTG  GTGGCGACCG  CGACCGCCCT  TGTGCGCCCG
751    GTGAGCTTTT   TCGGGCTTCT  CGCCGCTCTG  CTTGCCAACG  ACTTTTCCCG
801    gtgcgctgcgc  CATTCTGCTC  GCTCTGCgat  gacggtttgc  gtcgGggyCG
851    TCCCTTTGgt   cggCggaaca  ACCGATTTCG  AACACTTCTT  GGGCATGAag
901    gCggTATTAA   GCGTGGTGgt  cgAAATTTGG  ggcggyactcG  TTTTCTCTTA
951    TCTCGTTTTA   AAACACAAAA  AATGA
```

**g619.pap**

1	MPSEKNIGFM	AGSSRPLRVA	FALLLVSCIL	FMTLVNKGDW	DFVLHLRLTK
51	LAALLMVAYA	VGVSTQLFQT	LTNNPILTPS	ILGFDSLHYV	LQTLVLVFFG
101	GVGYTSLPLT	GKGFELVLMV	MGGSLLLFYT	LIRQGGRDLE	HMILIGVIEG
151	ILFRSSLSLL	SRMIDPEEFT	AAQANMEAFG	NTVRSLELGI	KALLVLLVSA
201	VVWHERYRSD	VHLLGRDQAV	NLGISYTRNT	LWILLWIAAL	VATATAVVPG
251	VSFSGLLAAS	LANHFSPSVR	HSVRLPMTVC	VGGILLVGGQ	TVFEHFLGMK
301	AVLSVLLVEA	GGLVFLYLVL	KHKK*		

```
m619.seq
1      ATGCCGCTCTG  AAAAAAATAT  CGGTTTTATG  GCAGGAAGCA  GCCGCCCGTT
51     GTGGGTGCGCC  TTTGCGCTGT  TGCTGGTTTC  CTGCGTCCTG  TTTATGACGC
101    TCAACGTCAA   AGGCGATTGG  GATTTTGTTT  TGCAACTGCG  GCTGACCAAA
151    CTTGCGCCGCG  TGCTGATGGT  CGCCTATGCG  GTGCGCGCTG  CCACGCAACT
201    CTTCCAAACG  CTGACCAATA  ATCCGATTCT  GACCCCTTCA  ATTTTGGATT
251    TCGATTCCGCT  GTA TGTTT  TTGCAGACCT  TGCTGGTGTT  TACGTTCCGC
301    GGCCTGGGCT  ATGCTTCCCT  GCGGTGACG  GGCAAATTCC  GCTTTGAART
351    GGTGCTCATG  ATGGGCGGCT  CGCTGCTGCT  GTTCTACACG  CTTATCAAAC
401    AGGGCGGACG  CGATTGTGCT  CGCATGATT  TAATCGCGCT  GATTTTCCGG
451    ATTTTGTTC   CGACGCTGTC  GTGCGTGCTT  TCGCGCATGA  TCGATCCCCA
501    AGAATTTACC  CCCGCGCAGG  CGAATATGTT  TGCCGGATT  AATACCGTCC
551    ACAAGCGAGT  TTTGGGCATA  GCGCGCGTGA  TTTCTGCTGT  CAGCGCGCGC
601    GTCGCTTTGG  CGCAACGCTA  CCGCTTGGAC  GTTTACCTTT  TGGGCGTGTA
651    CCAAGCCGCT  AATTTGGGCA  TGAGCTACAC  CGCGAACACC  TTTGGGATAC
701    TGCPTTGGAT  TGCCGCATTG  CTGCGACCG  CGACCGCGGT  GTATGCGCCC
751    GTAAGCTTTT  TCGGGCTTCT  CGCCGCGCTG  CTTGCCAACC  ACTTTTCCCC
801    GTCGGTCAAA  CATTCCGTCC  GCGCTGGCGAT  GACGGTTTGT  ATCGCGGCAG
851    TCCTTGTGGT  CCGCGGACAG  ACCGTGTTCG  AACACCTGCT  CGGTATGCAG
```

992

901 GCAGTGTGA GCGTAGTAGT AGAATTTGCC GCGGACTCG TTTCTCTA  
 951 TCTCGTTTA AACACAAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1982; ORF 619>:

m619.pep  
 1 MPSEKNIGFM AGSSRPLWVA FALLLVSCVL FMTLNVKGDW DFVLQLRLTK  
 51 LAALMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLYVF LQTLVFTFG  
 101 GVGYASLPLT GKFGFELVVM MGGSLLLFYT LIKQGGRLS RMILIGVIFG  
 151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA  
 201 VVWRERYRLD VYLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG  
 251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC IGGILLVGGQ TVFEHLLGMQ  
 301 AVLSVVVEFA GGLVFLYLVL KHKK\*

m619/g619 95.1% identity in 324 aa overlap

m619.pep	10	20	30	40	50	60
	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQLRLTKLAALLMVAYA					
g619	MPSEKNIGFMAGSSRPLRVAFALLLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA					
m619.pep	70	80	90	100	110	120
	VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLVFTFGGVGYASLPLTGKFGFELVVM					
g619	VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLVFTFGGVGYTSLPLTGKFGFELVVM					
m619.pep	130	140	150	160	170	180
	MGGSLLLFYTLIKQGGRLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
g619	MGGSLLLFYTLIRQGGRLPHMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
m619.pep	190	200	210	220	230	240
	NTVHSELLGIGALILLVSAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
g619	NTVRSELLGIGALVLLVSAVVWHERYRSDVHLLGRDQAVNLGISYTRNTLWILLWIAAL					
m619.pep	250	260	270	280	290	300
	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
g619	VATATAVVGVPVSFFGLLAASLANHFSPSVRHVRLPMTVCVGGILLVGGQTVFEHFLGMK					
m619.pep	310	320				
	AVLSVVVEFAGGLVFLYLVLKHKKK					
g619	AVLSVVVEFAGGLVFLYLVLKHKKK					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1983>:

a619.seq  
 1 ATGCCGCTG AAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCCGTT  
 51 GTGGGTTGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC  
 101 TCAACGTCAA AGGCGATTGG GATTTTGTTT TGCACCTGCG CCGACCAAG  
 151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTTT CGACCCAGCT  
 201 TTTTCAAACG CTGACCAACA ATCCGATTCT GACCCCTTCG ATTTGGGTT  
 251 TCGATTCGCT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTCCGGC  
 301 GCGGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAACT  
 351 GGTCTTATG ATGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCAAAC  
 401 AGGGCGGGCG CGATTGCCG CGTATGATT TAATCGGCGT GATTTTCGGG  
 451 ATTTTGTTC GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGACCCGA  
 501 AGAATTACG GCGGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC  
 551 ACAGCGAGCT TTTAGGCATA GCGCGCTGA TTCTGCTCGT CAGCGCGGCG  
 601 GTCGTTTGGC GCGAACGCTA CCGCTTGAC GTACACCTT TGGGCGCGA  
 651 CCAAGCCATA AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC  
 701 TGCTTTGGAT TGCCGCGCTG GTGGCGACGG CGACCGCGT TGTCGGCCCG

993

```

751 GTAAGCTTTT TCGGGCTTCT CGCCGCCTCG CTGCCAACC ACTTTTCCCC
801 GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
851 TCCTCTTGGT CGGCGGACAG ACCGTATTCG AACACTTCTT GGGCATGAAG
901 GCGGTATTAA GCGTGGTGGT CGAATTTGCG GGCGGACTCG TTTTCCTCTA
951 TCTCGTTTTA AGACACAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

```

a619.pep
1  MPSEKNIGFM AGSSRPLWVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLYVF LQTLLEVTFG
101 GVGYASLPLT GKFGFELVVM MGSLLLFYT LIKQGGDLPL RMILIGVIFG
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
201 VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVLSVVVEFA GGLVFLYLVL RHKK*

m619/a619 97.2% identity in 324 aa overlap

      10      20      30      40      50      60
m619.pep MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLTKLAALLMVAYA
a619      MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLHLRLTKLAALLMVAYA
      10      20      30      40      50      60

      70      80      90     100     110     120
m619.pep VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLLEVTFGGVGYSPLTKFGFELVVM
a619      VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLLEVTFGGVGYSPLTKFGFELVVM
      70      80      90     100     110     120

      130     140     150     160     170     180
m619.pep MGSLLLFYTLIKQGGDLRMLIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
a619      MGSLLLFYTLIKQGGDLRMLIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
      130     140     150     160     170     180

      190     200     210     220     230     240
m619.pep NTVHSELLGIGALILLVSAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL
a619      NTVHSELLGIGALILLVSAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL
      190     200     210     220     230     240

      250     260     270     280     290     300
m619.pep VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ
a619      VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK
      250     260     270     280     290     300

      310     320
m619.pep AVLSVVVEFAGGLVFLYLVLKHKXX
a619      AVLSVVVEFAGGLVFLYLVLRHKKX
      310     320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

```

g620.seq
1  ATGAAGAAAA CCCTGTTGGc AATTGTTGCC gTTTCGCCT TAAGTGCCTG
51  CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTTG CAAAGGATAA AGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1986; ORF 620.ng>:

```
g620.pep
1  MKKTLLAIVA VFALSACRQA EEAPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1987>:

```
m620.seq
1  ATGAAAAAAA CCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTGGTTCTC
201 CACCATCAAG CAGATGTTG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTGTCTCGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1988; ORF 620>:

```
m620.pep
1  MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

m620/g620 97.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g620	MKKTLLAIVAVFALSACRQAEEAPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDGMNVTDWTDNPNADTEWMDAKKAFYVIDS					
g620	DQPVWFSTVKQMFGYTKLPEEPKGIRVIYVTDGMNVTDWTDNPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDTYIFKX					
g620	GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1989>:

```
a620.seq
1  ATGAAAAAAA CCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTGGTTCTC
201 CACCATCAAG CAGATGTTG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTGTCTCGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1990; ORF 620.a>:

```
a620.pep
1  MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

995

m620/a620 100.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTL	LAIVAV	SALSAC	RQAEEG	PPPLPR	QISDRSV
a620	MKKTL	LAIVAV	SALSAC	RQAEEG	PPPLPR	QISDRSV
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWF	STIKQM	FGYTKL	PEEPKG	IRVIYV	TDMGNV
a620	DQPVWF	STIKQM	FGYTKL	PEEPKG	IRVIYV	TDMGNV
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGM	GAEDAL	PFGNKE	QAEKFA	KDKGGK	VVGFDD
a620	GFIGGM	GAEDAL	PFGNKE	QAEKFA	KDKGGK	VVGFDD
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

g622.seq

```

1  ATGCAactta cgcgtgtcgg ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAag ctggCGTTTG CCGCCGCCGC CCTGCCAGAA gccgTccgCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGCGAT TCGGAAGaaa TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACACGCTGGA TATGCAGGAA ACCGTGCGCC ACGCCCTCCG CGTTGCCTGC
301 GGCTTGATT CGATGGTTT GGGCGAGCCG CAGATTTTGG GGCAGATTAA
351 AGATGCGGTG CGTGCGGCTC AAGAACAGGA AAGTATGGGG GCAAAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCCGTTG CTAAAGAAGT CCGTACCGAT
451 ACCGCTGTCG GCGAAAATTC GGTTCGATG GCTTCCGCGT CCGTCAAGTT
501 GCGGGAACAG ATTTTCCCG ACATCGGCGA TTGAACGTA TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAAT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTTA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTGGTGG TTTCTTCAAC GGCAGGCCAG
751 CTTCCGATAG TCGGCAAAGG CATGGTCGAA CGCGCATTGA AACAGCGTCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGC GATATTGAAG
851 CGGAAGTCGG CGATTTGAAC GATGCGTATC TTTATACGGT GGACGATATG
901 GTCACATCGC TCCAAAGCGG caaggaggca aggcagaaa cgcgcgcCgc
951 cgcgcgaacg ctggTGTCGG AAAAGGTTGC CGAATTGTGC AGGCAGCAGC
1001 AGGGCAGGCA GagcgttcCG CTGATTAAAG CCTTGCGGGA CGAGGGCGAG
1051 AAAGCGCGCA AGCAGGTGTT GAAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGcaacGGCG GAAGaggttt TGgaacggct gtccgctCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCAAT CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGatttGG TTCATGCCgt cGCGCAGATt tatcatttGG ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>:

g622.pep

```

1  MQLTAVGLNH QTAPLSIREK LAFAAAALPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYTLDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RAAQEQUESM AKLNALFQRT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKN
201 PRIMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHDY DVVVSSTASQ
251 LPIVVGKMEV RALKQRQSMP LFMLDLAVPR DIEAEVGLN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSV LKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

m622.seq

```

1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCCGCCGC CCTGCCATAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGTGAT TCGGAAGAAA TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACGCGCTGGA TATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC

```

996

```

301 GGGCTGGATT CGATGGTGT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCGGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACTC GGTTTCCATG GCTTCCGCTT CCGTCAAATT
501 GCGCGAACAG ATTTTCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCC GGCTGA TGACGGTTC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTAGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTT TCGGCAAAAG CATGGTGGAG CGTGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTCATG TTGATTGGC AGTGCCCGCT GACATTGAAG
851 CGGAAGTCGG CGATTGAAT GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCGCCGCG
951 CGCCGAAACG CTGGTGTCCG AGAAAGTTGC CGAATTGTG AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCG TTGATTAAGG CGTTGCGGGA CGAGGGCGAG
1051 AAAGCGCGCA AACAGGTGTT GGAAATGCC ATGAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGAACGGCT GTCCGTCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTGG TTCATGCCGT CGCGCAGATT TATCATTGG ACAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1994; ORF 622>:

m622.pep

```

1  MQLTAVGLNH QTAPLSIREK LAFAAAAALPK AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYALDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMPL FMLDLAVPR DIEAEVGDNL DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVPL IKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAQAQI YHLDK*

```

m622/g622 98.8% identity in 415 aa overlap

m622.pep	10	20	30	40	50	60
	MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
g622	MQLTAVGLNHQTAPLSIREKLAFAAAAALPEAVRNLARSNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
m622.pep	70	80	90	100	110	120
	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
g622	SEEIIRWLADYHSLPIEEIRPYLYTLDQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
m622.pep	130	140	150	160	170	180
	RVAQEQESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
g622	RAAQEQESMGAKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
	130	140	150	160	170	180
m622.pep	190	200	210	220	230	240
	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
g622	LFIGAGEMIELVATYFAAKNPRMLTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
	190	200	210	220	230	240
m622.pep	250	260	270	280	290	300
	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMDLAVPRDIEAEVGDNLDAYLYTVDDM					
g622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMDLAVPRDIEAEVGDNLDAYLYTVDDM					
	250	260	270	280	290	300
m622.pep	310	320	330	340	350	360
	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
g622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
	310	320	330	340	350	360
m622.pep	370	380	390	400	410	
	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAQAQIYHLDKX					
g622	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAQAQIYHLDKX					



997

370 380 390 400 410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

```
a622.seq
1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCGGCCTG CCTGCCCGAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTTG
201 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCCTACCTTT
251 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC
301 GGCTTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
401 ATGCCCTGTT CAAAAAACC TTTTCTGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAACTC GGTTCCTCATG GCTTCCGCTT CCGTCAAGTT
501 GGCAGAGCAG ATTTTCCCGG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTC ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTG TCGGCAAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGA GACATTGAGG
851 CGGAAGTCGG AGATTTGAAC GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCCG
951 CGCCGAAACG CTGGTGTCG AGAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGGAGAG
1051 AAAGCGCGCA AACAGGTCTT GGAAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTGTT TTCACGCCGT CGCGCAGATT TATCATTGTT ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

```
a622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAACLPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SLPAILHEY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGD LN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQGGRQSVF LIRALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSIQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*
```

m622/a622 98.1% identity in 415 aa overlap

```

10      20      30      40      50      60
m622.pep MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD
|||||
a622     MQLTAVGLNHQTAPLSIREKLAFAAACLPEAVRNLARSNAATEAVILSTCNRTELYCVGD
10      20      30      40      50      60

70      80      90      100     110     120
m622.pep SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
|||||
a622     SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
70      80      90      100     110     120

130     140     150     160     170     180
m622.pep RVAQEQESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
|||||
a622     RVAQEQESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
130     140     150     160     170     180
```

998

	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
a622	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHEY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDLDNDAYLYTVDDM					
a622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDLDNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
a622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIRALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSIQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1997>:

g624.seq  
 1 ATGATCCGTT ATCTTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG  
 51 GATAATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTAATAC  
 101 TCTCCGCCGC CTGCTGGGCA AAGGCATccc cgcgcTTTCa ccgCTGGCTG  
 151 CACcgcGacc gCTATTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG  
 201 CGCAGTGC CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaaccgcAt  
 251 cctgcctcat gatcctTTtg CatTTTCccc aacnctgggtg ggtcGGGGCG  
 301 GTTTCATCGG TTTTGTGTT CTTGTGcac ATacggatgt gGcacAGacC  
 351 cgaatCTTGA

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>:

g624.pep  
 1 MIRYLLIACG GISLLGLIIG IFPLPLPTTP FVLLSAACWA KASPRFHRWL  
 51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIFW HFPQXWWVGA  
 101 VSSVFCSLVT IRMWRPES\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1999>:

m624.seq  
 1 ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTCTCC TACTGTTGGG  
 51 TATCATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTAATGC  
 101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG  
 151 CACCGGCACC GCTATTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG  
 201 CGCAGTGC CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT  
 251 CCTGCCTGAT AATGTTTGG CAGTTTCCC AACGCTGGTG GGTGCGGGCG  
 301 GTTTCATCGG TTTTGTGTT CTTGTGCGCC ATATGGATGT GGCGCAGGCC  
 351 CGAATCTTGA

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>:

m624.pep  
 1 MIRYLLIACG CISLLGLIIG IFPLPLPTTP FVLLSAACWA KASPRFYRWL  
 51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMEW QFPQRWWVGA  
 101 VSSVFCSLVA IWMWRPES\*

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACG CISLLGLIIG IFPLPLPTTP FVLLSAACWAKASPRFYRWLHRHRYFGPMV					
g624	MIRYLLIACGGISLLGLIIG IFPLPLPTTP FVLLSAACWAKASPRFHRWLHRHRYFGPMV					
	10	20	30	40	50	60

999

```

              70      80      90      100      110      120
m624.pep      HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g624          HNWEQNGAVPRKAKIFAISMITASCLMIFWHFPQXWWVGAVSSVFCSLVTIRMWHRPESX
              70      80      90      100      110      120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2001>:

```

a624.seq
1  ATGATACGTT ATCTTTTAAAT TGCCTGCGGC TGCATTTCCTG TGTGTTGGG
51 TATCATCGGC ATTTTTTTGCG CGCTGTTGCC GACCACGCCG TCGTACTGCG
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTCA CCGCTGGCTG
151 CACCGGCACC GCTATTTCGG TCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTTCG CATCAGTATG ATGACCGCAT
251 CCTGCCGTGAT AATGTTTTGG CAGTTTCCCC AACGCTGGTG GGTCGGGGCG
301 GTTTCATCGG TTTTTGTTC CCTTGTGCGC ATATGGATGT GGCGCAGGCC
351 CGAATCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```

a624.pep
1  MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*

```

m624/a624 99.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
m624.pep      MIRYLLIACGCISLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a624          MIRYLLIACGCISLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV
              10      20      30      40      50      60

              70      80      90      100      110      120
m624.pep      HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a624          HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              70      80      90      100      110      120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2003>:

```

a625.seq
1  ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGTTTGGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCTGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2004>:

```

g625.seq
1  atGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGtTTGGG TTGGCTTTCA GCAGCGGACG AATCATCAGC AttgCCGCGC
101 CGGtcgttCc CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAGGGG ATATATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TGATTTTGCC
351 gTAA

```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>:

```

g625.pep
1  MFATRKMKKM TMCTRRVRSW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA

```

1000

51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT  
101 KLNGMRKSNV QKAVILP\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2006>:

m625.seq  
1 ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT  
51 ACGGTTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC  
101 CCGTCGTGCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG  
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC  
201 TGAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT  
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC  
301 AAACGAAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC  
351 GTAA

This corresponds to the amino acid sequence <SEQ ID 2007; ORF 625>:

m625.pep  
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA  
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT  
101 KLNGMRKSNV QKAVILP\*

m625/g625 98.3% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
g625	MFATRKMKKMTMCTRRVRSWLAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
g625	PQTMPPEMVYRASSSRMKG IYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

This corresponds to the amino acid sequence <SEQ ID 2008; ORF 625.a>:

a625.pep  
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA  
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT  
101 KLNGMRKSNV QKAVILP\*

m625/a625 100.0% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
a625	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
a625	PQTMPPEMVYRASSSRMKG MYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2009>:

g627.seq  
1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG  
51 CCGTTACGCC CTGCAAAACC TTGTCCGCGA TGTATCCTG ATTACATTGA  
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA  
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAATCTTCC TCGGCATCTT  
201 CATCACCATC TTCCCCGTCC TGAGCATTC TGAAGCAGGC GAGGCAGGCG  
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT  
301 AATACGATGT ATTTCTGGAT GAGCGGCATA TTGTCCGCGT TCTTGGATAA  
351 CGCGCCCACT TATCTCGTGT TTTTCAATAT GGCGGGCGGC GATGCCCAAG  
401 CCTTAATGAC GGGTCCCCTG TTTCATTcgc TGCTGGCGGT TTCTAtgggT  
451 tCGGTATTCA TGGGCGCACT GaccTACATc gGCAAcgcac cgaactTCAT

1001

```

501  GGTCaaggcc aTTGCCGaaC agcgcgGCgt accgaTGCcg actTTCTTcc
551  ggtaTAtgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CatcgTACAT
601  ACCCTcgtCT TTTTCgTTtt cAAACTACTg taa

```

This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

```

g627.pep
  1  MSGLWKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE
 51  FNFEPIAEVG KFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101  NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSLLAVSMG
151  SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH
201  TLVFFVFKLL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

```

m627.seq
  1  ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
 51  CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
101  CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151  TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT
201  CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251  CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301  AATGTGATGT ATTTTGGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
351  CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401  CCTTGATGAC GGGTACCCTG TTTCATTTCG TGCTGGCGGT TTCTATGGGT
451  TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501  GGTCAAGGCC ATTGCCGAAC AGCGGGCGGT ACCGATGCCG ACTTCTTCG
551  GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601  ACCCTTATCT TTTTCGTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2012; ORF 627>:

```

m627.pep
  1  MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
 51  FNFEPIAEVG KFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101  NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGTL FHSLLAVSMG
151  SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201  TLIFFVFKLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

```

          10          20          30          40          50          60
m627.pep  MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG
          |||
g627       MSGLWKPEHPGFEILGSRYALQNLVRDVILITLTAVSMAITPKQVRAGNEFNFEPIAEVG
          10          20          30          40          50          60

```

1002

	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVL	SILKAGEAGALGGV	SLVHDTAGHPINVMY	FWMSGILSAFLDNAPT		
g627	KLFLGIFITIFPVL	SILKAGEAGALGGV	SLVHDTAGHPINTMY	FWMSGILSAFLDNAPT		
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGT	LFHSL LAVSMG SVFMGALTY	IGNAPNFMVKAIAEQ	RGVVPMP		
g627	YLVFFNMAGGDAQALMTGT	LFHSL LAVSMG SVFMGALTY	IGNAPNFMVKAIAEQ	RGVVPMP		
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTL	IFFVFKLLX				
g627	TFFRYMMWSVAFLTPVFIVHTL	LVFFVFKLLX				
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2013>:

```

a627.seq
1  ATGTCCGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51  CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTATCCTG ATTGCATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAATCTTCC TCGGCATCTT
201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTTCCCTG TTTTATTTCG TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTTT CAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2014; ORF 627.a>:

```

a627.pep
1  MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
51  FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGSL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201 TLIFFVFKLL *

```

m627/a627 99.5% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVIL	IALTAVSMAITPKQVRAGNEFNFEPIAEVG				
a627	MSGLWKPEHPGFEILGSRYALQNLVRDVIL	IALTAVSMAITPKQVRAGNEFNFEPIAEVG				
	10	20	30	40	50	60
	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVL	SILKAGEAGALGGV	SLVHDTAGHPINVMY	FWMSGILSAFLDNAPT		
a627	KLFLGIFITIFPVL	SILKAGEAGALGGV	SLVHDTAGHPINVMY	FWMSGILSAFLDNAPT		
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGT	LFHSL LAVSMG SVFMGALTY	IGNAPNFMVKAIAEQ	RGVVPMP		
a627	YLVFFNMAGGDAQALMTGT	LFHSL LAVSMG SVFMGALTY	IGNAPNFMVKAIAEQ	RGVVPMP		
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTL	IFFVFKLLX				

1003

a627                    TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX  
                               190                200                210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2015>:

g628.seq  
 1    ATGTGCGTGC   CACTCAAGCC   GGCAGGATGC   GGGCCGCCAA   ATTCATGTGT  
 51   TTCGATATTG   GCAGCATTTT   CAGACGGCAC   GTCTGCGCCT   GCTGCTTAC  
 101   ACACATGGAT   TTTACGTTTC   GTCAGGCGGC   TCAATACCAA   CAGGCCGCGT  
 151   TTGAAGTCTT   CGGCGGCTTC   TTTGATGATG   ACCGTAGGGT   CGGCAGCCAG  
 201   CGGATTGGTG   TCCATCGCAT   TGACGAAGAT   GGCGAACGGC   TCGGCATCTA  
 251   CGGCAGGGAT   TTTGCTGAAC   GGACGGGTGC   GAAGCGCAGT   CCATAAGCCT  
 301   GATTGAATCA   GGTTCGGCGC   CACTTTTTCG   CTGCTCAATT   TTGCCAGCGC  
 351   TTCAGGTacg   TAG

This corresponds to the amino acid sequence <SEQ ID 2016; ORF 628.ng>:

g628.pep  
 1    MCVPLKPAGC   GPPNSCVSIL   AAFSDGTSAP   AALHTWILRS   VRLNLTNRPR  
 51   LKSSAASLMM   TVGSAASGLV   SIALTKMANG   SASTAGILLN   GRVRSVHKP  
 101   D\*IRLRRTFS   LLNFASASGT   \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2017>:

m628.seq  
 1    ATGTGCGTGC   CACTCAAACC   GGCAGGATGC   GGGCCGCCGA   ATTCATGTGT  
 51   TTCGATGTTG   GCAGCATTTT   CAGACGGCAC   GTCTGCGCCA   GCTGCCTTAC  
 101   AAACATGGAT   TTTGCGTTTC   GTCAAACGGC   TCAATACCAA   CAGGCCGCGT  
 151   TTGAAATCCT   CGGCGGCTTC   TTTGATAATG   ACCGTAGGGT   CGGCAGCCAG  
 201   CGGATTGGTG   TCCATCGCAT   TGACGAAGAT   GGCGAACGGC   TCGGCATCGA  
 251   CGGCAGGAAT   TTTGCTGAAC   GGACGGGTGC   GCAGCGCAGT   CCACAAACCG  
 301   GATTGGATCA   GGTTCGGCGC   CACTTCTTCG   CCGCTTAAGT   TTGCCAGCGC  
 351   TTCAGGTGCG   TAG

This corresponds to the amino acid sequence <SEQ ID 2018; ORF 628>:

m628.pep  
 1    MCVPLKPAGC   GPPNSCVSML   AAFSDGTSAP   AALQTWILRS   VKRLNLTNRPR  
 51   LKSSAASLIM   TVGSAASGLV   SIALTKMANG   SASTAGILLN   GRVRSVHKP  
 101   DWIRLRRTSS   PLKFASASGA   \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m628/g628 93.3% identity in 119 aa overlap

		10	20	30	40	50	60
m628.pep		MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAA	LQTWILRSVKRLNLTNRPR	LKSSAASLIM		
g628		MCVPLKPAGCGPPNSCVSILA	AFSDGTSAPAA	LHTWILRSVRLNLTNRPR	LKSSAASLMM		
		10	20	30	40	50	60
		70	80	90	100	110	120
m628.pep		TVGSAASGLVSIALTKMANGS	ASTAGILLN	GRVRSVHKPDWIRLRRTSS	PLKFASASGA		
g628		TVGSAASGLVSIALTKMANGS	ASTAGILLN	GRVRSVHKPD	XIRLRRTFS	LLNFASASGT	
		70	80	90	100	110	120
m628.pep	X						
g628	X						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2019>:

1004

```

a628.seq
1  ATGTGCGTGC  CACTCAAACC  GGCCGGATGC  GGGCCGCCGA  ATTCATGTGT
51  TTCGATGTTG  GCAGCATTTT  CAGACGGCAC  GTCTGCGCCA  GCTGCCTTAC
101 ACACATGGAT  TTTACGCTCG  GTCAAACGGC  TCAATACCAG  CAAACCTCGT
151 CTGAAATCCT  CGGCGGCTTC  TTTGATCACA  ACCACAGGGT  CTGCCGCCAG
201 CGGATTGGTG  TCCATCGCAT  TGACGAAGAT  GGCGAACGGC  TCGGCATCGA
251 CGGCAGGGAT  TTTGCTGAAC  GGACGGGTAC  GCAGCGCAGT  CCACAAACCG
301 GATTGGATCA  GATTGCGGCG  CACTTCTTCG  CCGCTTAAGT  TTGCCAACGC
351 TTCGGGCGCG  TAG

```

This corresponds to the amino acid sequence <SEQ ID 2020; ORF 628.a>:

```

a628.pep
1  MCVPLKPAGC  GPPNSCVSML  AAFSDGTSAP  AALHTWILRS  VKRLNTSKPR
51  LKSSAASLIT  TTGSAASGLV  SIALTKMANG  SASTAGILLN  GRVRSVHKP
101 DWIRLRRTSS  PLKFANASGA  *

```

m628/a628 95.0% identity in 120 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAAFSDGTSAPAALQTWILRSVKRLNTNRRLKSSAASLIM					
a628	MCVPLKPAGCGPPNSCVSMLAAAFSDGTSAPAALHTWILRSVKRLNTSKPRLKSSAASLIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSIALTKMANGSASTAGILLNGRVRSVHKPDWIRLRRTSSPLKFASASGA					
a628	TTGSAASGLVSIALTKMANGSASTAGILLNGRVRSVHKPDWIRLRRTSSPLKFANASGA					
	70	80	90	100	110	120

```

m628.pep  X
           |
a628      X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2021>:

```

g629.seq
1  ATGACTGCca  aacCTTTTTC  CCTCAACCTG  GCcaaCCTCC  TGCTGCCggc
51  ggatatGTtT  GCCGTCAGcc  tGtcggTCGG  cattgcggaT  TTCCGCTGGT
101 CGGATGTGTT  TTCGCTGTCC  GACAGCCAGC  AAGTGATGTT  CATCAGCCGC
151 CTGCCGCGCa  CGTTTGcgaT  TGTGTTGACG  GGCgcgtcga  tagcgGtggc
201 gGGGAtgatt  atgcagATTC  TGATGCGCAA  CcgtTTTGTC  GAGCCTtcta
251 tggcgGGTGC  GGGCCAAAGt  gcgGCTTTGG  GTttgcttct  gAtgtccctg
301 ctgctgcctg  CgcGccgct  gccggtcaAA  ATGTCGGtag  Cgcgccgttg
351 CGCGCTGATC  GGGATGTTGG  tctTtatgct  gctaataccgC  Cgcctgccac
401 cgacggcgca  gctgatgGTg  ccgCTGGTGG  Gg.ttATTTT  CGGCGGCGTG
451 GttgaGGCGG  TGGCAGCAGT  TGTCGCGTAT  GAGTTTGAGA  TGCTGCAAAAT
501 GTTGGGCGTG  TGGCAGCAGG  GCGACTTTTC  AAGCGTGCTG  CTGGGGCGGT
551 ACGAGCTGCT  TTGGATTACG  GGCGGTTTGG  CGGTGTTTGC  CTACCTGATT
601 GCCGACCGGC  TGACGATTTT  GGGGCTGGGC  GAGACGCTGA  GCGTGAATTT
651 GGGTTTGAAC  CGGACGGCGG  TGTGTTGGTC  GGGTTTGATT  ATTGTGGCAC
701 TGATTACATC  GCTGGTCATT  GTAACGCTCG  GCAATATTCC  GTTTATCGGG
751 CTGGTCGTGC  CGAATATCGT  CAGCCGCTCG  ATGGGCGACA  GGCTGCGCCA
801 AAGCCTGCCT  GCGGTCGCCC  TCTTGGGCGC  GTCTTTGGTT  TTATTGTGCG
851 ACATTATCGG  ACGCATGATT  GTGTTCCGT  TTGAAATTCC  GGTCTCCACG
901 GTTTTGGTG  TGTTGGGTAC  GGCTTTGTTT  TTGTGGCTTT  TGTTGAGGAA
951 ACCCGCTAT  GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2022; ORF 629.ng>:

```

g629.pep
1  MTAKPFSLNL  ANLLPAVLF  AVLSVGIAD  FRWSDVFSLS  DSQQVMFISR
51  LPTFAIVLT  GASIAVAGMI  MQILMRNRFV  EPSMAGAGQS  AALGLLMSL
101 LLPAAPLPVK  MSVAAVAALI  GMLVFMLLIR  RLPPTAQLMV  PLVGXIFGGV

```



1005

151 VEAVATFVAY EFEMLQMLGV WQQGDFSSVL LGRYELLWIT GGLAVFAYLI  
 201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG  
 251 LVPVNIIVSRL MGDRLRQSLP AVALLGASLV LLCDIIGRMI VFPFEIPVST  
 301 VEGVLTALF LWLLLRKPAY AV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2023>:

m629.seq  
 1 ATGACTGCCA AACCTTTTTC CCTCAACCTG ACCAACCTGC TGCTGCTGGC  
 51 GGTGTTGTTT GCCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT  
 101 CTGATGTGTT TTTACTGTCC GACAGCCAGC AGGTCATGTT CATCAGCCGC  
 151 CTGCCGCGCA CGTTTTCGAT TGTGCTGACG GCGCGCTCGA TGGCGGTGGC  
 201 CGGCATGATT ATGCAGATT TGTGCGCAA CCGTTTGTGTC GAACCGTCGA  
 251 TGGTGGGCGC AAGCCAAAGC GCGGCTTAG GTTGTCTGCT GATGACCTG  
 301 CTGCTGCCCG CCGCGCCGCT GCCGCGGAAA ATGTCGGTTG CCGCCGTTGC  
 351 CCGCTGATC GGGATGTTGG TCTTTATGCT GCTGATCCGC CGCCTGCCGC  
 401 CGACCGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGGCGGTGTG  
 451 ATTGAGGCGG TAGCCACCTT TATCGCGTAT GAAAACGAAA TGTCGCAAT  
 501 GCTCGGCGTG TGGCAGCAGG GCGATTTTTC GAGCGTGCTG CTGGGGCGGT  
 551 ACGAGCTGCT TTGGATTACG GCGGTTTGG CCGTGTGTC CTATCTGATT  
 601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAAACGGTAA CCGTGAATTT  
 651 GGGTTTGAAC CGGACGGCGG TGTGTGGTC GGGTTTGATT ATTGTGGCTT  
 701 TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG  
 751 CTGGTCGTGC CGAACATCAT CAGCCGCCTG ATGGGCGACA GGTTCGCCCA  
 801 AAGCCTGCCT GCGGTGGCCT TGCTGGGCGC ATCTTTGGTG TTGCTGTGCG  
 851 ACATTATCGG ACGCGTGATT GTGTTCCGT TTGAAATTCC GGTCTCTACG  
 901 GTTTTTGGTG TATTGGGTAC GGCTTTGTTT TTGTGGCTTT TGTTGAGGAA  
 951 ACCCGCTAT GCCGCTGA

This corresponds to the amino acid sequence <SEQ ID 2024; ORF 629>:

m629.pep  
 1 MTAKPFSNLN TNNLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR  
 51 LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMV GASQS AALGLLMTL  
 101 LLPAAPLPAK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGIIFGGV  
 151 IEAVATFIAY ENEMLQMLGV WQQGDFSSVL LGRYELLWIT GGLAVFAYLI  
 201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG  
 251 LVPVNIIVSRL MGDRLRQSLP AVALLGASLV LLCDIIGRVI VFPFEIPVST  
 301 VEGVLTALF LWLLLRKPAY AV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m629/g629 95.7% identity in 322 aa overlap

	10	20	30	40	50	60
m629.pep	MTAKPFSNLNLTNNLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISR					
	:     :     :     :     :     :     :     :     :					
g629	MTAKPFSNLNLTNNLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m629.pep	GASMAVAGMIMQILMRNRFVPSMV GASQS AALGLLMTLLPAAPLPAKMSVAAVAALI					
	:     :     :     :     :     :     :     :					
g629	GASIAVAGMIMQILMRNRFVPSMAGAGQSAALGLLMSLLPAAPLPVKMSVAAVAALI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m629.pep	GMLVFMLLIRRLPPTAQLMVPLVGIIFGGVIEAVATFIAYENEMLQMLGVWQQGDFSSVL					
	:     :     :     :     :     :     :     :					
g629	GMLVFMLLIRRLPPTAQLMVPLVGXIFGGVVEAVATFVAYEFEMLQMLGVWQQGDFSSVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m629.pep	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					
	:     :     :     :     :     :     :     :					

1006

```

g629      LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g629      VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRMIVFPFEIPVST
           250      260      270      280      290      300

           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g629      VFGVLGTALFLWLLLRKPAYAVX
           310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2025>:

```

a629.seq
1  ATGACTGCCA AACCTTTTTC CCTCAACCTG ACTAACCTCC TGCTGCTGGC
51 GGTGTTGTTT GCGGTCAGCC TGTGCGTGGG CGTTGCCGAT TTCCGCTGGT
101 CGGATGTGTT TTCGCTGTCG GACAGCCAGC AGGTTATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGGCAT TGTGTTGACG GGCGCGTCGA TGGCGGTGGC
201 GGGGATGATT ATGCAGATTG TGATGCGTAA CCGTTTGTGC GAGCCTTCTA
251 TGGCGGGCGC GGGTCAGAGT GCGGCTTTGG GTTGTCTTCT GATGTCCCTG
301 CTGCTGCCTG CCGCGCCGCT GCCGGTCAAA ATGTCGGTTG CCGCCGTTGC
351 CGCGTTAATC GGGATGTTGG TGTTTATGAT GCTTATCCGC CGCCTGCCGC
401 CGACGGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGCGCGCGTG
451 GTTGAGGCGG TGGCCACCTT TATTGCGTAT GAAAACGAAA TGCTGCAAAAT
501 GCTGGGCGTG TGGCAACAGG GCGATTTTTC CGGCGTGTG CTCGGACGGT
551 ATGAACGTGT GTGGGCAACG GGGATTTTGG CTTTGTGTGC CTATTTGATT
601 GCCGACCAGC TGACGATTTT GGGTTTGGGC GAAACGGTAA GCGTGAACCT
651 GGGGCTGAAC CGGACGGCGA TTCTGTGGTC GGGGCTGATT ATTGTGGCTT
701 TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCTG ATAGGCGACA GGCTGCGCCA
801 AAGCCTGCCT GCGGTGGCTT TGCTGGGTGC GTCTTTGGTT TTATTGTGCG
851 ACATTATCGG ACGAGTGATT GTGTTCCGT TTGAAATTCC GGTATCGACC
901 GTCTTCGGCG TATTGGGTAC GCGTTGTTT TTATGGCTTT TGTTAAGGAA
951 ACCTGCTCAT GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2026; ORF 629.a>:

```

a629.pep
1  MTAKPFSLNL TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
51 LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLMLS
101 LLPAAPLPVK MSVAAVAALI GMLVFMLLR RLPPTAQLMV PLVGIIFGGV
151 VEAVATFIAY ENEMQLMGV WQQGDFSGVL LGRYELLWAT GILALFAYLI
201 ADQLTILGLG ETVSVNLGLN RTAILWSGLI IVALITSLVI VTVGNIPFIG
251 LVVPNIISRL IGDRLRQSLP AVALLGASLV LLCDIIGRVI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAH AV*

```

m629/a629 95.7% identity in 322 aa overlap

```

           10      20      30      40      50      60
m629.pep  MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a629      MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISR
           10      20      30      40      50      60

           70      80      90      100     110     120
m629.pep  GASMAVAGMIMQILMRNRFVEPSMVGASQSAALGLLMTLLLPAAPLPKMSVAAVAALI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a629      GASMAVAGMIMQILMRNRFVEPSMAGAGQSAALGLLMSLLLPAAPLPVKMSVAAVAALI
           70      80      90      100     110     120

           130     140     150     160     170     180
m629.pep  GMLVFMLLRRLPPTAQLMVPLVGIIFGGVIEAVATFIAYENEMQLMGVWQQGDFSSVL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

1007

```

a 629      GMLVFMMILIRRLPPTAQLMVPLVGIIIFGGVVEAVATFIAYENEMLQMLGVWQQGDFSGVL
              130      140      150      160      170      180

              190      200      210      220      230      240
m629.pep    LGRYELLWITGGIAYFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
              ||||| || ||:|||||:|||||:|||||:|||||:|||||:|||||
a 629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
              190      200      210      220      230      240

              250      260      270      280      290      300
m629.pep    VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFPEIPVST
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a 629      VTVGNIPFIGLVVPNIISRLIGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFPEIPVST
              250      260      270      280      290      300

              310      320
m629.pep    VFGVLGTALFLWLLLRKPAYAVX
              |||||:|||||:|||||:|||||
a 629      VFGVLGTALFLWLLLRKPAHAVX
              310      320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```

g630.seq (partial)
1  aTgatGATT  TGGTGTGGCT  ggctttgttt  ccccccattg  tttacggcat
51  gtacaacgtc  GGCGCACAGG  CATTGCGTGC  CTTAACGCCC  GAtttgtctc
101 aacaaagcat  cgcccacgac  ggcaattacg  ccctcgccaa  cgctttgggc
151 atcaatatgt  cccccgaaGc  gggcgtgtTg  ggcaaaatgc  tgttcgGCGC
201 GATttacttc  ctgccgattt  acgcgaccgt  aTTTATTGTG  GGcggcttct
251 ggGaaqtCTT  GTTCGCATCc  gtACGCAAAc  ACGAAATCAa  CGAAGGTTTC
301 TTCGTTACTT  CGATTCTGTT  TGCCTTAATC  GTTCGCCCAc  CGCTGCCGCT
351 GTGGCAGGCG  GCTTTGGGTA  TTTCTTTCGG  CGTTGTGGTT  GCGAAAGAAG
401 TATTCGGCGG  TACAGGTAAa  AACTTCATGa  ACCCTGCGCT  GGCAGGCCGC
451 GCCTTCCTGT  TCTTCGCCTa  CCCCGCCAAc  TTGAGCGGCG  ATGCGGTTTG
501 GACGGCGGTT  GACGGCTATT  CCGGCGCAAc  CGCGCTGGCG  CAATGGGCGG
551 CACACGGTGC  AGACGGCCTG  AAAAACGCCG  TAACCGGTCA  AACCATCACT
601 TGGATGGACG  CGTTTATCGG  CAAACTGCCc  GGCTCCATCG  GCGAAGTCTC
651 CACTTTGGCA  CTCTTAATCG  GCGGCGCGTT  TATCGTGTtT  GCCCGCATCG
701 CttcttgCGG  CATTATTGCC  ggCGTGATGa  TCGGTatGat  tGcgatgTCT
751 tcgctgatta  acttcatCGg  ttctgacacc  aaagctatgt  ttgctatgca
801 cttggtacat  ggcacttggT  GGAaagatGa  ttAtcactca  ctgtacatta
851 aa.....

```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```

g630.pep
1  MMILVWLALF  PPMFYGMYNV  GAQAFGALTP  DLLQQSIAHD  GNYALANALG
51  INMSPEAGVL  GKMLFGAIYF  LPIYATVFIV  GGFWEVLFAc  VRKHEINEGF
101 FVTSILFALI  VPPTLPLWQA  ALGISFGVVV  AKEVFGGTGK  NFMNPALAGR
151 AFLFFAYPAN  LSGDAVWTAV  DGYSGATALA  QWAAHGADGL  KNAVtGQTIT
201 WMDAFIGKLP  GSIGEVSTLa  LLIGGAFIVF  ARIASWRIIA  GVMIGMIAMS
251 SLINFIGSDT  KAMFAMHLVH  GTWWKDDYHS  LYIK....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```

m630.seq
1  ATGATGATT  TGGTGTGGCT  GGCTTTGTTC  CCTGCCATGT  TCTACGGTAT
51  GTACAACGTC  GCGCGCAGG  CATTGCGTGC  GTTAACGCCT  GATTGCTGc
101 AACAAAACAT  CGCCAACGAC  TGGCATTACG  CCTTGCCAAc  CGCTTGGGc
151 ATCAATATGT  CGTCTGAAGC  GGGCGTGTCG  GACAAAATGc  TGTTTGGCGc
201 GATTTACTTC  CTGCCGATT  ACGCCACTGT  ATTTGTTGTG  GGCGGTTTCT
251 GGGAAAGTTT  GTTCGCCACC  GTGCGCAAAc  ACGAAATCAa  CGAAGGTTTC
301 TTCGTTACTT  CGATTCTGTT  TGCCTTAATC  GTTCGCCCAc  CGCTGCCGCT
351 GTGGCAGGCG  GCTTTGGGTA  TTTCTTTCGG  CGTTGTGGTT  GCGAAAGAAG
401 TATTCGGCGG  TACAGGTAAa  AACTTCATGa  ACCCTGCGCT  GGCAGGCCGT
451 GCTTTCCTGT  TCTTCGCCTa  CCCTGCCAAc  TTGAGCGGCG  ATGCGGTTTG
501 GACGGCGGTT  GACGGCTATT  CCGGCGCAAc  CGCACTGGCG  CAATGGGCGG
551 CACACGGTGC  AGACGGCCTG  AAAAACGCCG  TAACCGGTCA  AACCATCACT
601 TGGATGGACG  CGTTTATCGG  CAAACTGCCc  GGCTCCATTG  GCGAAGTCTC
651 CACTTTGGCA  CTCTTAATCG  GCGGCGCGTT  TATCGTGTtT  GCCCGCATCG
701 CTTCTTGGCG  CATTATTGCC  GCGTGATGa  TCGGTATGAT  TCGCATGTCT
751 TCGCTGTTCa  ACTTCATCGG  TTCGGACACC  AACGCTATGT  TTGCTATGCC

```

1008

```

801 TTGGTACTGG CACTTGGTGG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCTGTCTCC GCTTCCTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTGCC AACCTGTTT
1001 CCCCATTTC CGACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2030; ORF 630>:

```

m630.pep
1  MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQQNIAND WHYAFANALG
51  INMSSEAGVS DKMLFGAIYF LPIYATVEVV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVTGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLNFFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMLLAILFA NLFAPIFYF VAQANIKRRK
351 ARSNG*

```

m630/g630 93.5% identity in 275 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQQNIANDWHYAFANALGINMSSEAGVS					
g630	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQQSIADHGNALANALGINMSPEAGVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m630.pep	DKMLFGAIYFLPIYATVFVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA					
g630	GKMLFGAIYFLPIYATVFIVGGFWEVLFASVRKHEINEGFFVTSILFALIVPPTLPLWQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m630.pep	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFFAYPANLSGDAVWTAVDGYSGATALA					
g630	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFFAYPANLSGDAVWTAVDGYSGATALA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m630.pep	QWAAHGADGLKNAVTGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
g630	QWAAHGADGLKNAVTGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m630.pep	GVMIGMIAMSSLNFFIGSDTNAMFAMPWYHLVVGGFAIGMLFMATDPVSASFTNVGKWW					
g630	GVMIGMIAMSSLINFIGSDTKAMFAM---HLVHGTTWKDDYHSLYIK.					
	250	260	270	280		
	310	320	330	340	350	
m630.pep	YGALIGVMCVLIRVVNPAYPEGMLLAILFANLFAPIFYFVAQANIKRRKARSNGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2031>:

```

a630.seq
1  ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
51  GTACAACGTC GCGGCACAGG CATTGCGTGC GTTAACGCCC GATTGCTGC
101 AACAAAGCAT CGCCAACGAC TGGCATTACG CCCTTGCCAA CGCTTGGGC
151 ATCAATATGT CGTCTGAAGC GGGCGTGTTC GGCAAAATGC TGTTGCGGCG
201 GATTTACTTC CTGCCGATTT ACGCGACCGT ATTTATTGTC GGCGGTTTCT
251 GCGAAGTTTT GTTCGCCACC GTGCGCAAAC ATGAAATCAA CGAAGGTTTC
301 TTTGTTACCT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCA GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCGT
451 GCCTTCCTGT TCTTCGCCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGCGGTT GACGCTATT CCGCGCAAC CGCGCTGGCG CAATGGCGCG
551 CACACGGTGC AGACGGCCTG AAAAAGCCCA TAACCGGTCA AACCATCACT
601 TGGATGGATG CGTTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG

```

1009

```

701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTCa ACTTCATCGG TCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTGGTTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCCCTTCC GCTTCCTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTGCC AACCTGTTG
1001 CCCCATTTC CGACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

```

a630.pep
1  MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQQSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIDYF VAQANIKRRK
351 ARSNG*

```

m630/a630 98.3% identity in 355 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQQSIANDWHYAFANALGINMSSEAGVS					
a630	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQQSIANDWHYALANALGINMSSEAGVL					
	10	20	30	40	50	60
m630.pep	DKMLFGAIYFLPIYATVFVVGGEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA					
a630	GKMLFGAIYFLPIYATVFIVGGFEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA					
	70	80	90	100	110	120
m630.pep	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
a630	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
	130	140	150	160	170	180
m630.pep	QWAAHGADGLKNAVTGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
a630	QWAAHGADGLKNAITGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
	190	200	210	220	230	240
m630.pep	GVMIGMIAMSSLNFIGSDTNAMFAMPWYHVLVGGFAIGMLFMATDPVSASFTNVGKWW					
a630	GVMIGMIAMSSLNFIGSDTNAMFAMPWYHVLVGGFAIGMLFMATDPVSASFTNVGKWW					
	250	260	270	280	290	300
m630.pep	YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX					
a630	YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

```

g635.seq
1  ATGACCCGGC GACGGGTCGG CAAGCAAAC CGTATTGCCA TCCACTCCGC
51  GCAATACCGA AAAATGGTCG TCTTTGCGGT ATTTAGATA CACGATGACG
101 GGGATTTCa ACTGCGCGAG CTGTCGAAA GACAGGGCAT AGCCTTTCGC
151 CTCAAAACCC AAATCGGGCA TAATGCGCCG CATATCCTCA AACGACGCGC
201 GCATCTGTTT CTTACCCAGT TTTTCAACA CTTCTCTTC CGTCAGCTTT
251 TGCCCGTAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGAG

```

1010

301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCCCGCCGC GCTTTCCAAC  
 351 TCTGCAATTT GATTTTCCG TAAACAACAG GATTATCGTT AACATCGGT  
 401 GCAGCATTCA AACGATAAGA CAAGGGTCTG TACCAGATTA G

This corresponds to the amino acid sequence <SEQ ID 2034; ORF 635.ng>:

g635.pep

1 MTRRRVGKQN RIAIHSAYR KMVVFVFIQI HDDGDFQLRE LFERQGIQIAFR  
 51 LKTQIGHNAP HILKRRALHF LTQFFQHFF RQLLPVKIVQ KRRHRSRPAG  
 101 KIQILLYNIE IPPRFPTLQF DFSVNNRIIV KHRCSIQTIR QGSVPD\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2035>:

m635.seq

1 ATGACCCAGC GACGGGTCGG CAAGCAAAAC CGTATTGCCG TCTATACCGC  
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTCAGATA CACGATGACG  
 101 GGGATTTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCGC  
 151 TTCAAACCC AAATCAGGCA TAATGCGCCG CATATCCTCA AACGACGCGG  
 201 GCATCTGCTC CTTATCCAGT TTTTAAACA CGTCCTCTTC CGTCAGCTTT  
 251 TGCCCGTAAA AATTGTTCAA AAGCGTCACC ACCGAAGCCG CCCCGCAGGA  
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC  
 351 TCTGCACTTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2036; ORF 635>:

m635.pep

1 MTQRRVGKQN RIAVYTAQYR EMILAVFIQI HDDGDLQLCK LLERQGIQIAFR  
 51 FKTQIRHNAP HILKRRGHLL LIQFF\*HVLV RQLLPVKIVQ KRRHRSRPAG  
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D\*

m635/g635 80.0% identity in 130 aa overlap

	10	20	30	40	50	60
m635.pep	MTQRRVGKQNRIAVYTAQYREMIILAVFIQIHDDGDLQLCKLLERQGIQIAFRFKTQIRHNAP					
g635	MTRRRVGKQNRIAIHSAYRKMVVFVFIQIHDDGDFQLRELFERQGIQIAFRKLTQIGHNAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m635.pep	HILKRRGHLLLIQFFXHVLFRLLPVKIVQKRRHRSRPAGKIQILLYNIEIAPFFPTLHF					
g635	HILKRRALHFLTQFFQHFFRQLLPVKIVQKRRHRSRPAGKIQILLYNIEIPPRFPTLQF					
	70	80	90	100	110	120
	130					
m635.pep	DFSISNRIIVDX					
g635	DFSISNRIIVKHRCISIQTIQGSVPDX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2037>:

a635.seq

1 ATGACCCAGC GACGGGTCGG CAAGCAAAAC CGTATTGCCG TCTATACCGC  
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTCAGATA CACGATGACG  
 101 GGGATTTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCGC  
 151 CTCAAACCC AAATCAGGCA TGATGCGCCG CATATCCTCA AACGACGCGC  
 201 GCATCTGCTC CTTATCCAGC TTTTCAACA CGTCCTCTTC CGTCAGCTTT  
 251 TGCCCGTGAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCGCAGGA  
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC  
 351 TCTGCACTTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2038; ORF 635.a>:

a635.pep

1 MTQRRVGKQN RIAVYTAQYR EMILAVFIQI HDDGDLQLCK LLERQGIQIAFR  
 51 LKTQIRHDAP HILKRRALHL LIQLFQHVLF RQLLPVKIVQ KRRHRSRPAG  
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D\*

m635/a635 95.4% identity in 131 aa overlap

10 20 30 40 50 60

1011

```

m635.pep  MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHNAP
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
a635       MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHDAP
          10      20      30      40      50      60

          70      80      90      100     110     120
m635.pep  HILKRRGHLLLIQFFXHVLFRLLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
          |||||:|||||:| ||||||||||||||||||||||||||||||||||||
a635       HILKRRHLLLIQLFQHVLFRLLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
          70      80      90      100     110     120

          130
m635.pep  DFSISNRIIVDX
          ||||||||||||
a635       DFSISNRIIVDX
          130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2039>:

```

g638.seq
1  ATGATTGGCG GACAGTTTAT CGTAGttgGc atGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATA ttgtcGTGAA TAtcGGAATA GTTGACATAG
101 TTAGAGCATGA TGCCCTAATC GCGGCTGCCG ACGGCGATAT TGTCGAACAC
151 TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgcCCACGG
201 AAATATTGCC GCTGacttcg ctgtcgTTGG TGTACATATA GTGGACGGCG
251 AAACGCAGGT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
301 ATTGGA AAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG ccgACGACCT
351 GCGCGccggg CgcgtTCCAA ACGGTAACGC CATTGCCGCG CTCATTCACG
401 CGCAAGGTcg catcgCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGA AGGTATACGC CGAACGAATT ATCAAAAATA TTGTTGTGTT
501 CAACCAGGGC GCGCGGGGCG GCTTTTTCGA GATAAATACC GGCATCCATT
551 GCTGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCTGTGCC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CTTCAATCG TAATCGGTTT GTCGATATAA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGATCGTAT CGCCCGCCCG
751 GGCGCGGGCA AAAATTTCGG CAAGGTTGTC TTGCGGGGAA ACGTGGACGA
801 CGGCTGCCGA TGCCGTCTGA AAAATGCTGC CGGCGGCAAG TATCAGCACG
851 GCCTTCAGCC ATATACGGAG CGCGGATGTG TGCATAGTGT CCCTCTGTTT
901 CGTTCCGGTAT GGCCGAACAA AATAAAGCAT CATTCAAATG TGCCTGTTTT
951 TATACGGAAA CCGCTGAAA CGGTACGGCA ACGGTTTGG CTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```

g638.pep
1  MIGGQFIVVG IVGKNALARF VDNIVVNIGI VDIVEHDALI AAADGDIVEH
51  FEPFGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQVAEA VVFIGVVRAG
101 IGKNAVPPFG NVVADDLRAG RVPNGNAIAA LIHAQGRIAD DFILAHHRIG
151 RTMKVYAERI IKNIIVFNQG ARGGFFEINT GIHCWQAHTG TGNGQVAERY
201 VRRVYGYGTF ALVPFDGCGT VGRPFNRNRF VDIKFGLIYA GSQFDRIARP
251 GAGKNFGKVV LRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGCVHSVPLF
301 RSVWPNKIKH HSNVPVFIAK PPETVRQAVW L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2041>:

```

m638.seq
1  ATGATTGGCG AAAAGTTTAT CGTAGTTGGC ATTATAGGCA AATACGCACT
51  TGCCCTGCCCT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTAGACATAA TGCCCTGATC GCGGCTGCCG ACGGCGATAT TGTCGAATAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACGG
201 AAATATTGCC GCTGATTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAAAT CGCTGAAGCG GTTGTTTTTG TAGGTGTTGT GCGTGCTGGT
301 ATTGGA AAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 GCGCACCGGG TGCGTTCCAA ACGGTAACGC CGTTGCCGCG CTCGTTACAG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGC AGATATACGC CGACCGAATT ATCCAAAATA TTGTTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTCTTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCTGTGCC CCTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CTTCAATCG TAATCGGTTT GTCAATGTGA
701 AGTTTGGTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGGTT CGTGA

```

1012

This corresponds to the amino acid sequence <SEQ ID 2042; ORF 638>:

```

m638.pep
  1  MIGKEFIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY
 51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFGVVVRAG
101  IGKNAVPPFG NVVADDLRTG CVPNGNAVAA LVHAQSRVAD DFILAHHRIG
151  RTMQIYADRI IQNIVVFNQG ARGSSFEINT GIHCGQAHTG TGNQQAERY
201  VRRVYGYGTP APVAFDGCCT VGRPFNRNRF VNVKFGFIYA GSQFERIARP
251  GAGKCGIPIS IIGS*

m638/g638 88.2% identity in 254 aa overlap

      10      20      30      40      50      60
m638.pep  MIGKEFIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY FEPLGKHQHI
g638      MIGGGFIVVG IIVGKNALARF VDNIVVNIGI VDIVEHDALI AAADGDIVER FEFFGKHQHI
      10      20      30      40      50      60

      70      80      90     100     110     120
m638.pep  AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFGVVVRAG IGKNAVPPFG NVVADDLRTG
g638      AHIVAHGNIA ADFAVVGVHI VDGETQVAEAV VVFGVVVRAG IGKNAVPPFG NVVADDLRTG
      70      80      90     100     110     120

      130     140     150     160     170     180
m638.pep  CVPNGNAVAA LVHAQSRVAD DFILAHHRIG RTMQIYADRI IQNIVVFNQG ARGSSFEINT
g638      RVPNGNAIAA LIHAQGRIAD DFILAHHRIG RTMKVYAEIRI KNIVVFNQG ARGSGFEINT
      130     140     150     160     170     180

      190     200     210     220     230     240
m638.pep  GIHCGQAHTG TGNQQAERY VRRVYGYGTP APVAFDGCCT VGRPFNRNRF VNVKFGFIYA
g638      GIHCQAHTG TGNQQAERY VRRVYGYGTP PALVPFDGCCT VGRPFNRNRF VDIKFGFIYA
      190     200     210     220     230     240

      250     260
m638.pep  GSQFERIARP GAGKCGIPIS IIGSX
g638      GSQFDRIARP GAGKNFGK VVLRGNVDDGCRCLKNAAGGKYQHGLQPYTERGCVHVSPLF
      250     260     270     280     290     300

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2043>:

```

a638.seq
  1  ATGATTGGCG GACAGTTTAT CGTAGTTGGC ATTGTAGGCA AAAACGCACT
 51  TGCCCGCTTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101  TTGAGCATGA TGCTTTGGTC GCGGCTGCCG ACGGCGATAT TGTCAAACAC
151  TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCCACGG
201  AAATATTGCC GCTGATTTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
251  AAACGCAAAAT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
301  ATTGGAAGAA ATGCCGTCCC GCCCTTTGGA AATATCGTTG CCGACGACCT
351  GCGCGCCGGG CGCGTTCCAA ACGGTAACGC CATTGCCGCG CTCGTTCCAG
401  CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCCCGCACCA TCGCATCGGC
451  AGAACCATGC AGATAGACGC CGACCGAATT ATCCAAAATA TTATTGTGTT
501  CAATCAGGGC GCGCGGGGCA GTTCTTCGA GATAAATACC GGCATCCATT
551  GCGGCGAGGC TCATACCGGA ACGGTAACGC GTCAGGTTGC GGAGCGTTAC
601  GTCCGCGCGC TGTACGGCTA TGGTACGCCC GCTCCTGTCT CCTTCGATGG
651  TTGACAGACG GTCGCGAGGC CCTCAATCG TAATCGGTTT GTCGATGTGA
701  AGTTTGTTT GATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751  GCGCGGGCA AATCGGGAT ACCGATCAGC ATAATCGACT CATGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2044; ORF 638.a>:

```

a638.pep
  1  MIGGQFIVVG IVGKNALARF VDNVVVNIGI VDIVEHDALV AAADGDIVKH
 51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFIGVVVRAG
101  IGKNAVPPFG NIVADDLRTG RVPNGNAIAA LVHAQSRVAD DFILPHHRIG
151  RTMQIDADRI IQNIIVFNQG ARGSSFEINT GIHCGQAHTG TGNQQAERY
201  VRRVYGYGTP APVSFDGCRT VGRPFNRNRF VDVKFGFIYA GSQFERIARP

```



1013

251 GAGKCGIPIS IIDSW\*

m638/a638 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIVVGIIGKYALACLV	DNVNVNIGIVDIVEHNALIAA	ADGDIVEYFEPLGKHQHI			
a638	MIGGQFIVVGIVGKNALARF	VDNVVNIGIVDIVEHDALVAA	ADGDIVKHFEPLGKHQHI			
	10	20	30	40	50	60
m638.pep	70	80	90	100	110	120
a638	70	80	90	100	110	120
	130	140	150	160	170	180
m638.pep	130	140	150	160	170	180
a638	130	140	150	160	170	180
	190	200	210	220	230	240
m638.pep	190	200	210	220	230	240
a638	190	200	210	220	230	240
	250	260				
m638.pep	250	260				
a638	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTCG TTCGGCGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGCGGTTA CCGTTTGGA
201 CGCGCCCGGC GCGCAGGTCG TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAACT CCTATAAAAA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTT
401 CCGAACGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTACAG ACAATATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTGCCTTA CAATGCCAAC TACGATAAAC
551 TGTCGCGCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CCAGGTCAAA TATGTCAGTA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAAATGGC GCAGGCGCAG TTTCCCGCGG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGGCAG GCGGGAACAC GGTCTTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2046; ORF 639-1.ng>:

g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNIFDNS FGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEVSGN ISVGNMGGYV LMFSERLKVF DNIIVGSRD*
151 GIMLVVNYD DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGMHFTA
201 AIEGTSLHDN SFINNGSQVK YVSTRFLDWS EGGHNGYWSO NSPFDLNGDG
251 FGDSAYRPDG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAO FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLEAET RQSERGRAEN GSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:

1014

## m639-1.seq

```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAATGCCCC
51  GCGCGCCCTG ATTGAACACA ACAATATTTT GGATAATTCG GTCGGCGTAT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AACGGCGTTA CCGTTTGGAA
201 CGCACCCGGT GCGCAGGTGC TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACACA CCTACAAAA CAACCGCTTC
301 AGCGATTTC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCGGTGG GCACAAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTATTC GACAATATCG CCGTCGGCAG CCGCGATCAG
451 GGCATTATGC TCAACTATGT CAACTATTCC GATATTACAG ACAACATTAT
501 CAACAAGGCA GGCAAGTGCG TATTGCCTA TAATGCCAAC TACGATAAAC
551 TTTTCGCCAA TCATTTTGAA AACTGTCAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCTT GCATGACAAT TCCTTTATCA ACAACGAAA
651 CCGGCTCAA TACGTAGCA CGCGCTTCT CGATTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG CCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TTTTGATGAA CAGTCCGCA ATCAGCATCG
851 TCAATGGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGC TACTCAAAGA AGTCGAAACG CGGCAGTCGG
1001 AATGGGCGAG GCGGAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2048; ORF 639-1>:

## m639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWVAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVAVHYM YTNDSSEISGN ISVGNMNGYV LMFSERLKVF DNIIVGSRDQ
151 GIMLNYYVNS DIHDNIINKA GKCVFAYNAN YDKLFANHFE NCQIGIHFTA
201 AIEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPNQ IIDQIWRAP VSRLLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLEKETV RQSEWGRAEN GSLN*

```

g639-1/m639-1 95.9% identity in 344 aa overlap

	10	20	30	40	50	60
g639-1.pep	MSLPAMDAGIYLEKAAPRALVEHNNIFDNSFGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
g639-1.pep	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVAVHYMYTNDSEVSGN					
m639-1	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVAVHYMYTNDSEISGN					
	70	80	90	100	110	120
g639-1.pep	ISVGNMNGYVLMFSERLKVFNDIIVGSRDXGIMLNYYVNSDIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMNGYVLMFSERLKVFNDIIVGSRDQGIMLNYYVNSDIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
g639-1.pep	YDKLSANHFENCQIGMHFTAIEGTSLHDNSFINNGSQVKYVSTRFLDWSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTAIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
	190	200	210	220	230	240
g639-1.pep	NSPFDLNGDGFSDAYRPNQIIDQIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
m639-1	NSAFDLNGDGFSDAYRPNQIIDQIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
	250	260	270	280	290	300
g639-1.pep	DSKPLMKPYAPKIQTRYQAMKDELLEKETVROSERGRAENGSLN					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLEKETVROSERGRAENGSLN					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2049>:

## a639-1.seq

1015

```
1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAC TGCCCC
51  GCGCGCCCTG ATTGAACACA ATAATATTTT GGATAATTCG GTCGGCGTCT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GGGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AATGGCGTTA CCGTTTGGAA
201 CGCGCCCGGC GCGCAGGTCTG TCGGCAACGA TATTTCCAAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACACA CCTATAAAA CAACCGCTTC
301 AGCGATTTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTT
401 CCGAGCGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGACCAA
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTCACG ACAACATTAT
501 CAACAAAGCG GGCAAGTGC G TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAAA TACGTCAGCA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCACC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAAATGGC GCAGGCGCAA TTCCCGCGG TTTTGCCTGG CGGCGTGGTG
901 AIEGTSLHNS FINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
951 TCAGGCGATG AAGGACGGGC TGCTCAAAA AGTCGAAACG CGGCAGTTGG
1001 AATGGGGCAG GCGGAAAAAC GGTTCTTTGA ACTAG
```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

a639-1.pep

```
1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEISGN ISVGNMGMV LMFSERLKVF DNIAGVSRDQ
151 GIMLNYSYNS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGIHFTA
201 AIEGTSLHNS FINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPNG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDGLLKKVET RQLEWGRAEN GSLN*
```

a639-1/m639-1 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
a639-1.pep	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
a639-1.pep	NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
m639-1	NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
a639-1.pep	ISVGNMGMGYVLMFSERLKVF DNIAGVSRDQGIMLNYSYNSDIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMGMGYVLMFSERLKVF DNIAGVSRDQGIMLNYSYNSDIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
a639-1.pep	YDKLSANHFENCQIGIHFTAAIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTAAIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
	190	200	210	220	230	240
a639-1.pep	NSAFDLNGDGFSGDSAYRPNGIIDQIIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
m639-1	NSAFDLNGDGFSGDSAYRPNGIIDQIIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
	250	260	270	280	290	300
a639-1.pep	DSKPLMKPYAPKIQTRYQAMKDGLLKKVETRQLEWGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX					
	310	320	330	340		

1016

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2051>:

```

g640.seq
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGC
51  TATGTCCTGT TTTTCAATCC GCGGTATGTC TCGGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TACCGCCTTT GTCTTTTGA CGGcggcACT GCCCGCTTAT
151 GcggAgcgTc tgcctGATTT TCTGgcgAAA ATacAgcctT CGGAAATTTT
201 TCCGGGTGCG GATCGTTACG GCAAGCCGGA aggcAAGCCT AtggtTGCCC
251 GCgtttACAA AGgcgATGAG CAGCTCGGTT TGGTTTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATCGATA CGCTGATGGC
351 TTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GATCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAAT CCGGTGTGGA TAAGTTCATC
451 GACAAATATA TCGGTCTGAA TTTTATTAAA AATCCGCCGA CCCCGAGCGT
501 GCGCCCGGGC GACATCATCA GcggTGCgAC TgttaCACTG ATGGTGGTTA
551 ACGACAGCAT CCAGCGTTCG TACAAGGTCA TTGCCAACCA ATACCGTCTG
601 GGTTCGGACA AGGCCCTTCA GACGGCATCC GCTTCCGATG TTCGGGAAGC
651 CGCGCCTGCG TCAGAAACCC GTCCGCGCCG TATGGCAAAT CCCGACAAGC
701 AGGATATTTT GTCTTGGGAC GAACTTTTGA AACAAAAGGC CGTCGGCCAT
751 CTGCATATCA CGCTCGATCA AATCAACAAA CTGTTTGAGA AAGGCGGCAA
801 GGCCGGCGTG GCCGATCAGC CCGAACAGGG CGATCCTGAC GATACCTTTA
851 TTGATTTGTA TGTTCCTTGG GTGAGCCAGC CTCCATCGG TAAAAGCCTG
901 CTGGGTGAGG ACGGCTGGGC GCATCTGCAA AAACGGCTGA AACCCGGGCA
951 GCAGGCGGTT TTGGTTGCCG GAGAGGGCCG TTATTCTTGG AAAGGTTCGG
1001 GCTATGTGCG CGGCGGTATT TTCGACCGTA TCGAGATGAT TCAGGGGGAG
1051 AACAGCTTCC GTTTTACCGA TGCCCAACAC GAACGCGTCG TCGAGCTGTC
1101 TGCCGCCGAT GCGCCCGGTT TTAAGAAGT TTCTTGTTT ACCATCCCTG
1151 AAGGCGTAGC GTTGACGGT GCGGAGCCGT GCGGCTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2052; ORF 640.ng>:

```

g640.pep
1  MIHIISILKS IGISGIAMSC FSIRMSAFR ARITAFFTAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAN DGTIAGAKLV DHHEPIMLIG IPQSRVDKFI
151 DKYIGLNFIL NPPTPSVAPG DIISGATVTL MVVNDSIQRS YKVIANQYRL
201 GSKALQTAS ASDVREAAPA SETPRRMAN PDKQDILSWD ELLKQKAVGH
251 LHITLDQINK LFEKGGKAGV ADHAEQGD PDFTIDLYVAL VSQPSIGKSL
301 LGEDGWAHLQ KRLKPGQAV LVAGEGRYSW KSGSYVRGGI FDRIEMIQGE
351 NSFRTDAQH ERVVELSAAD APRFKEVSF TIPEGVAFDG AEPWRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2053>:

```

m640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51  CATGTCCTGT TTTTCAATCA AACGTATGTC CCGGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTTT
201 TCCGGGTGCG GACCGTTACG GCAAGCCGGA AGGTAAGCCT ATGGTTGCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGT
351 GTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GACCATCAGC
401 AACCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2054; ORF 640>:

```

m640.pep (partial)
1  MIHIISILKS IGISGIVMSC FSIKMSAFR ARITAFFAAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMVLAN DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/g640 96.5% identity in 143 aa overlap

	10	20	30	40	50	60
m640.pep	MIHIISILKSIGISGIVMSCFSIKMSAFRARITAFFAAAFVFLTAALPAYAERLPDFLAK					
	:     :     :     :     :					
g640	MIHIISILKSIGISGIAMSCFSIRMSAFRARITAFFTAFVFLTAALPAYAERLPDFLAK					
	10	20	30	40	50	60
	70	80	90	100	110	120

1017

```

m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMVLAN
                |||||
g640          IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMALAN
                70      80      90      100     110     120

                130     140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
                |||||
g640          DGTIAGAKLVDHHEPIMLIGIPQSRVDFIDKYIGLNFIKNPPTPSVAPGDIISGATVTL
                130     140     150     160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a640.seq (partial)
1   ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51  CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTGT
201 TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGGTTGCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGC
351 GTTGGCTAAA GACGGTACGA TAGCCGAGC GAAATTGGTT GATCACCATG
401 AGTCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a640.pep (partial) Length: 143
1   MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFFAF VFLTAALPAY
51  AERLPDFLAK IQPSEIVPGA DRYSKPEGKPMVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHESIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

                10      20      30      40      50      60
m640.pep      MIHIISILKSIGISGIVMSCFSIKRMSAFRRARITAFFFAFVFLTAALPAYAERLPDFLAK
                |||||
a640          MIHIISILKSIGISGIVMSCFSIKRMSAFRRARITAFFFAFVFLTAALPAYAERLPDFLAK
                10      20      30      40      50      60

                70      80      90      100     110     120
m640.pep      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMVLAN
                |||||
a640          IQPSEIVPGADRYSKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMALAK
                70      80      90      100     110     120

                130     140
m640.pep      DGTIAGAKLVDHHEPIMLIGIPH
                |||||
a640          DGTIAGAKLVDHHEPIMLIGIPH
                130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g642.seq
1   ATGCGGTATC CGCCGCAATC GGC GGTTTTC CAGAATGCCG CGCGTTGCCT
51  TTTGCGCCGC CCGAAATCTG CCTGCCGCCG TATTGCCC GCTATCCGCAA
101 TATCGGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
151 GGTGTCTTCG TGTTCCCTCCT GTACGAAGAC AAAAAGTCGG GCGATGATTT
201 TGCCGATGAA GACTTTTTCG AGGGCGCAGG CGTCGGTCAG GGTGTGTTCC
251 TGCAGGAAGC TGCGGATGTC TTCGGGCAAA GCGTAgTCgc gGGCAACGGC
301 GGcaaagcgc ACatcggtTT Gcacggcgtc gagCAGGGgt tggTTTTTGT
351 CCAACTTAAT GCCTGCTTCT TTTTCTTCGG CGGTGGCGCG GACGAACTGG
401 TCGTAAATTT CGGCATAAAG CATATCGTTC GGGCCTTCAA AAATCGTGAA
451 GGGCGCGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAC
501 CCTTCGCGCC CAAGAGTTT TGCAACATTT GCGCGCGGgc gTAAGTGTAT
551 TCCGTGGCGa ggGTTTTGac gatgTTCGCC TCCATCAATT GATGGGCGAc
601 ggGCCGgcacg ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTCCG
651 AAACCTGATG GCGGCGTTGG ATTTCCGGCG GTTCGTAATC GACGAATCTG

```

1018

```

701 ATATCGTTGC GGACATATCG GTTCAGGTTG TCAAGGATGT ATTCCATAAT
751 GCCGTGCGTC ATGCCGATCA GTTGCAGGCG GCTGCGGATA AAGATGTTTT
801 GGAACGCGCG CAAACCGGCA GCGTCGCCCC GGGAGAGTTT CATCAGCGCG
851 GTTGCAGGCA TTTCGGCATC GATGCGGTTG ACGGCGTAAC GGACGGCGCG
901 CAGGCCTTCG GATGCGAGGG TTTGCGAGCG GATGTATGTT TTGGGGACGA
951 GCAGCAGGTC GATGactttg gcgagtttgc Cgtttttgcg ctctttggcg
1001 gcaacgaggA GGAAGTCGCT TTGCGAATTG CCCTGCCAGT ATTTGCGCGC
1051 GttgACGTAA ATGGTTtgtt cgtcgggtata ttcgtagcag gactgcaTTT
1101 CGCGTGCAAT cgCcgcgccg gaggtTtcgg gttcggtaAc gccccaaacgg
1151 cggcttttcgc ctTTGAAAAT CATGTCCAAA CCTGTGCGCA CTTCGccttc
1201 gccgcccgaac tCTTGCAAG GCTGCAACAC CAGCGCGCCT TCGATGCCGG
1251 TACGCAGCGT AACGGGCACG CCGTAATGCC CCGCAATCCT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2058; ORF 642.ng>:

g642.pep

```

1 MRYPPQSAVL QNAARCLLR PKSACRRICP LSAISAVQYI FADV VQEGC
51 GV FVFLLYED KKS GDDFADE DFLQAGAGVQ GVFLQEAADV FGQSVVAGNG
101 GKADIGLHGV EQGLVFVQLN ACFFFFGGGA DELVVNFGIK HIVRAFKNRE
151 GADIDGDIAG WVS AFKTLRA QEF LQHLRGG VSVFRGEGFD DVRLHQLMGD
201 GRDGRNGMAD VAVKDFGNLM AALDFAAFVI DESDIVADIS VQVVKDVFNH
251 AVRHADQLQA AADKDV LERA QTGSVAPGEF HHGGCRHFGI DAVDGVTDGA
301 QAFGCEGFAA DVCFGDEQQV DDFGEFAVFA LFGGNEEEVA LRIALPVFRG
351 VDVNGLFVGI FVAGLHFACN RRAGGF GFGN AQTA AFEN HVQTLCDLRF
401 AAELLQRLQH QRAFDAGTQR NGHAVMPRNP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2059>:

m642.seq (partial)

```

1 GCCTGCCGCC GTATTGCCC GCTACCCGCA ATATCGGCAG TCCAATATAT
51 CTTTGCGGAT GTCGTT CAGC AGGAAGGCTG CGGTGTCTTC GTGTTTCGCC
101 TGTACGAAGA CAAAGAGTCG GCGGATGATT TTGCCGATAA AGACTTTTTC
151 CAGGGCGCAG GCATCGGTCA GGTGTGTTC CTGCAGGAAG CTGCGGATGT
201 CTTCAGGCAA AGTGTAGTCG CGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAAC TTCA TGCCTGCTTC
301 TTTTCTCTCG GCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGTGTGTCTC GCGTCAAAA CCCTTCGCAC CCAAGAGTTT
451 TTGCAACATT TCGCGGCGCG CGTAAGTGA TTCGGTGGCG AGGGTTTTGA
501 CGATGTTCGC CTCCATCAGC TGATGGGCGA CGGGGGCAAC AGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GGCGGCGCGC
601 GATTTCCGGG CGTTCGTAAT CGACGAATTT GATGTCGTTG CGGACGTATC
651 GTTCCAGATT TTCAAGGATG TATTCATAA TGCCGTGCGT CATGCCGATC
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTGCAGGC ATTTGCGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGATAT ATTCGTAGTA GGACTGCATT TCGCGTGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CACCCAAACC GCCGCCCTCG CCTTTGAAAA
1101 TCATCTCCAA ACCTTGCGCG ACTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2060; ORF 642>:

m642.pep (partial)

```

1 ACRRICPLPA ISAVQYIFAD VVQEGCGVVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFRQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VSDIAGGVS AFKTLRTQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGGN RRNGMADVAV KNLGNLMAAP
201 DFAAFVIDEF DVVADVSFQI FKDVFNHNAV HADQLQAAAD KDV LERAQTG
251 SVALGEFHHG GCRHFGIDAV DGVT DGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFVFALEFG GNEEEVALRV ALPVFRGVDV NGLSVDIFVV GLHFACNRRR
351 GGFVFGNTQT AALAFENHLQ TLRDLRFIAE LLQWLQHQRA FDAGTQRNGH
401 AVMPRNP

```

1019

m642/g642 90.4% identity in 407 aa overlap

m642.pep				10	20	30	
				ACRRICPLPAISAVQYIFADV	VQEGCGVFVFR	LYED	
g642	MRYPPQSAVLQNAARCLLRPKSACRRICPLSAISAVQYIFADV	VQEGCGVFVFR	LYED				
	10	20	30	40	50	60	
m642.pep	40	50	60	70	80	90	
	KESGDDFADKDFLQGAGIGQGVFLQEAADVFRQSVVAGDGGKAGIGLQAVEQGLV	FVQLH					
g642	KKSGDDFADEDFLQGAGVGGVFLQEAADVFGQSVVAGNGGKADIGLHGV	EQGLV	FVQLN				
	70	80	90	100	110	120	
m642.pep	100	110	120	130	140	150	
	ACFFFFGGGADKLVNFGIKHIVRAFKNREGADVDS	DIAGGVS	AFKTLRTQ	EFLQHLRGG			
g642	ACFFFFGGGADKLVNFGIKHIVRAFKNREGADIDG	DIAGWVS	AFKTLRAQ	EFLQHLRGG			
	130	140	150	160	170	180	
m642.pep	160	170	180	190	200	210	
	VSVFRGEGFDDVRLHQLMGDGGNRRNGMADVAVK	NLMAALDFAAFV	IDEF	VDVADV			
g642	VSVFRGEGFDDVRLHQLMGDGRDGRNGMADVAVK	DGNLMAALDFAAFV	IDES	DIVADIS			
	190	200	210	220	230	240	
m642.pep	220	230	240	250	260	270	
	FQIFKDVFNHNAVRHADQLQAAADKDVLER	QTGSVALGE	FHHGGCRHFG	IDAVD	GVTDGA		
g642	VQVVKDVFNHNAVRHADQLQAAADKDVLER	QTGSVAPGE	FHHGGCRHFG	IDAVD	GVTDGA		
	250	260	270	280	290	300	
m642.pep	280	290	300	310	320	330	
	QAFGCEGFADVCFGDEQQVDDFGEFAVF	ALFGGNEEEVALR	VALPVFRG	VDVNGLSVDI			
g642	QAFGCEGFADVCFGDEQQVDDFGEFAVF	ALFGGNEEEVALR	IALPVFRG	VDVNGL	LFVGI		
	310	320	330	340	350	360	
m642.pep	340	350	360	370	380	390	
	FVVGHLHFACNRRAGGFGFGNTQTAALAFENH	LQTLRDLRFIAELLQWLQHQRAFDAGTQR					
g642	FVAGLHFACNRRAGGFGFGNAQTAAFAFENH	VQTLCDLRFIAELLQRLQHQRAFDAGTQR					
	370	380	390	400	410	420	
m642.pep	400						
	NGHAVMPRNP						
g642	NGHAVMPRNPX						
	430						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

a642.seq (partial)

1	GCCTGCCGCC	GTATTTGCC	GCTATCCGCA	ATATCGGCAG	TCCAATATGT
51	CTTTGCCGAT	GTCGTTGAGC	AGGAAGGCTG	CGGTGTCTTC	GTGTTCCGCC
101	TGTACGAAGA	CAAAGAGTCG	GCGGATGATT	TTGCCGATAA	AGACTTTTGT
151	CAGGGCGCAG	GCATCGGTCA	GGGTGTGTTT	CTGCAGGAAG	CTGCGGATGT
201	CTTCGGGCAA	AGTGTAGTCG	CGGGCGACGG	CGGCAAAGCG	GGCATCGGTT
251	TGCAGGCGGT	CGAGCAGGGT	TTGGTTTGTG	TCCAACCTCA	TGCCTGCTTC
301	TTTTTCTTCG	GCGGTGGCGC	GGACAACTG	GTCGTAAT	TCGGCATAAA
351	GCATATCGTT	CGGGCCTTCA	AAAATCGTGA	AGGGGCGGAT	GTCGATAGCG
401	ATATTGCCGG	CGGTGTGTCC	GCGTTCAAAA	CCCTTCGCGC	CCAAGAGTTT
451	TTGCAACATT	TGCGCGGCGG	CGTAAGTGTA	TTCCGTGGCG	AGGGTTTGA
501	CGATGTTCCG	CTCCATCAGT	TGATGGGCGA	CGGGTGCAAC	GGGCGAAACG
551	GAATGGCAGA	CGTAGCGGTA	AAGAATCTCG	GAAACCTGAT	GGCGGCGCCG
601	GATTTCCGCG	CGTTCGTAAT	CGACGAATCT	GATGTCGTTG	CGGACGTATC
651	GTTCCAGGTT	TCAAGGGTG	TATTCATAA	TGCCGTGCGT	CATGCCGATC

1020

```

701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCGAGGC ATTTCCGGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGGTAT ATTCGTAGTA AGACTGCATT TCTCGGGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CGCCTAAACC GCCGCCCTCG CCTTTGAAAA
1101 CCATGTCCAA ACCCTGTGCG ATTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2062; ORF 642.a>:

```

a642.pep Length: 407
1 ACRRICPLSA ISAVQYVFAD VVQQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFGQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VSDIAGGVS AFKTLRAQEF
151 LQHLRGVSV FRGEGFDDVR LHQLMGDGCN GRNGMADVAV KNLGNLMAAP
201 DFAAFVIDES DVVADVFSQV FKGVFHNAVR HADQLQAAAD KDLERAQTG
251 SVALGEFHHG GCRHFGIDAV DGVTGGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFVAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVGIFV RLHFSGNRRA
351 GGFGFGNA*T AALAFENHVQ TLCDLRFIAE LLQWLQHQRA FDAGTQRNGH
401 AVMPRNP

```

m642/a642 95.8% identity in 407 aa overlap

```

m642.pep      10      20      30      40      50      60
ACRRICPLSAISAVQYIFADVVQQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF
|||||  ||||||:|||||  |||||||  |||||||  |||||||  |||||||
a642          10      20      30      40      50      60
ACRRICPLSAISAVQYVFADVVQQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF

m642.pep      70      80      90      100     110     120
LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKLNVNFGIKHIV
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
a642          70      80      90      100     110     120
LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKLNVNFGIKHIV

m642.pep     130     140     150     160     170     180
RAFKNREGADVDSIAGGVSAFKTLRTQEFLLQHLRGVSVFRGEGFDDVRLHQLMGDGCN
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
a642         130     140     150     160     170     180
RAFKNREGADVDSIAGGVSAFKTLRAQEFLLQHLRGVSVFRGEGFDDVRLHQLMGDGCN

m642.pep     190     200     210     220     230     240
RRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADVFSQIFKDVFNHNAVRHADQLQAAAD
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
a642         190     200     210     220     230     240
GRNGMADVAVKNLGNLMAAPDFAAFVIDESDVVADVFSQVFKGVFNHNAVRHADQLQAAAD

m642.pep     250     260     270     280     290     300
KDLERAQTGSVALGEFHHGGCRHFGIDAVDGVTGGAQAFGCEGFAADVCFGDEQQVDDF
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
a642         250     260     270     280     290     300
KDLERAQTGSVALGEFHHGGCRHFGIDAVDGVTGGAQAFGCEGFAADVCFGDEQQVDDF

m642.pep     310     320     330     340     350     360
GEFAVFALFGGNEEEVALRVLPVFRGVDVNGLSVDIFVVGLEHACNRRAGGFGFGNTQT
|||||  |||||||  |||||||  |||  |||  |||  |||  |||  |||  |||  |||
a642         310     320     330     340     350     360
GEFAVFALFGGNEEEVALRVLPVFRGVDVNGLSVGIFVVRHLHFSGNRRAGGFGFGNAXT

m642.pep     370     380     390     400
AALAFENHLQTLRDLRFIAELLQWLQHQRAFDAGTQRNGHAVMPRNP
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
a642         370     380     390     400
AALAFENHVQTLCDLRFIAELLQWLQHQRAFDAGTQRNGHAVMPRNP

```



1021

370 380 390 400

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2063>:

```
g643.seq
1   ATGGTGTTCG CTTTGATGTT GTTGGCGACA ATCAGgTcgg CTACGCTGAc
51  gttgtancGt TTGGcaATGt tGaaCAgggt gtcgccTTCT ACAACGCGGT
101 GGATGCTGGC ATGGagcGGG GAGGTTTCGG CTTCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TGCCCGGCGT TtgCCGTCGG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGagatGGTT TCTTCAGCCT GCCGGCGCag gTTGTTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTGGGGGGAt
351 GACCTGCGCg aGTGtTGCGG TTTGGGTTTC agacgGCATG GCAGTCTGTT
401 TTTcggTTTg a
```

This corresponds to the amino acid sequence <SEQ ID 2064; ORF 643>:

```
g643.pep
1   MVLPLMLLAT IRSATLTLXR LAMLN RVSPS TTRWMLAWSG EVSASPSAAL
51  ATRVSKRARR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFGMTCA SVAVWVSDGM AVCFSV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2065>:

```
m643.seq
1   ATGGTGTTCG CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
51  GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAGCGGT
201 ATGTTGCGGA GATGCGGAAA TTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAT
351 GATCTGCGCG AGTGTGCGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTCGGTTTG A
```

This corresponds to the amino acid sequence <SEQ ID 2066; ORF 643>:

```
m643.pep
1   MVLPLMLLAT IRSATLTL*R LAMLN RVSPS TTRWMLAWSG EISASPSAAL
51  ATRVSKRTRR LPSAAVCCG DAEILCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGMICA SVAVWVSDGM AVCFSV*
```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 643 shows 94.9% identity over a 136 aa overlap with a predicted ORF (ORF643.a) from *N. gonorrhoeae*:

m643/g643

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
g643	MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEVSASPSAALATRVSKRARR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFWGMICA					
g643	LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFGMTCA					
	70	80	90	100	110	120
	130					
m643.pep	SVAVWVSDGMVAVCFVSX					
g643	SVAVWVSDGMVAVCFVSX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2067>:

1022

```

a643.seq
1  ATGGTGTTGC CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
51  GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTCCGCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TACCCGCGGT TTGCCGTCGG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC AGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAC
351 GATCTGCGCG AGTGTTCGGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTCGGTTTG A

```

This corresponds to the amino acid sequence <SEQ ID 2068; ORF 643.a>:

```

a643.pep
1  MVLPLMLLAT IRSATLTL*R LAMLRNVSPS TTRWMLAWSG EISASPSAAL
51  ATRVSKRTRR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGTICA SVAVVSDGMA AVCFSV*

```

m643/a643 97.1% identity in 136 aa overlap

	10	20	30	40	50	60
m643.pep	MVLPLMLLAT	IRSATLTLXRL	LAMLRNVSPS	TTRWMLAWSG	EISASPSAAL	ATRVSKRTRR
a643	MVLPLMLLAT	IRSATLTLXRL	LAMLRNVSPS	TTRWMLAWSG	EISASPSAAL	ATRVSKRTRR
	10	20	30	40	50	60
	70	80	90	100	110	120
m643.pep	LPSAAVCCGDAE	ILCSATVSGV	PMTAEMVSSA	CRRLFRATSC	MSSSAACMS	FWGMICA
a643	LPSAATVCCGDE	EMLCSATVSG	VPMTAEMVSS	ACRRRLFRAT	SCMSSAACMS	FWGTICA
	70	80	90	100	110	120
	130					
m643.pep	SVAVVSDGMAV	CFSVX				
a643	SVAVVSDGMAV	CFSVX				
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2069>:

```

g644.seq
1  ATGCCGCTCG AAAGGccgGC GGATTGTTGC CCGGTGCACT TTGTGGTAAA
51  GTTTAGAAAA TTAACCTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CCATGGACAC GGCTGCTTTT TTAAagcaca tcgaatCCGC
201 ATTcCCCCGC ATTTTTCAG ACGGCATCGA CCTGATGCGA TACCTGCCCCG
251 AAGACAAATG GCTTGCCCTG AAGCAGGCGG GTTGTCTGTT GCCCTTCCTC
301 GACAAAAAAC ACGGCGGGCG CAAGGGCAGT CAGTTTGAAA TCCAAGAAGT
351 CCTAAGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACC GGCA
401 TCGAAGGCGC GCTGGTGTG CAGCCTCTGC AAGagttcgg cggcgaagcG
451 CAAGTCGCAC AAGGTTTGGA CATGATTTTC AAaggcgaaa gccgcggttt
501 gggcgTtacc gaacccgaAa cctccggcgc gGcgaTTGCA CGCGAAAtgc
551 agtcctgcta cgaatatacc gacgaacaAA CCATTTACGT caaCGCCGCG
601 AAATACTGGC AGGGCAATTC GCAAAGCGAC TTCCTectcg ttgccgcaaa
651 agagcgcaaaa aacGGcaaac tcgcaaaagt CATCGACCTG CTGCTCGTCC
701 CCAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CCTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAAACTC TCCCGGGGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA
851 TCTTTATCCG CAGCCGCCCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACATCC TTGACAACCT GAACCGATAT GTCCGCAACG ATATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCAACG CCGCCATCAG GTTCCGAAA
1001 TCCTTTACCG CTACGTCTGC CATTCGGTTT CGcccgtegc GCccgTCGCC
1051 CATCAATTGA TGGAGGCGAA catcgtCAAA ACcctCGCCA CGGAATACAC
1101 TTAcgcCGCC GCGCAATGT TGCAAAAAC CTTGGGCGCG AAGGGTTTG
1151 AACCGCGGAC CCCAGCCGGC AATATCGCCA TCGATATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACA TATGCTTTAT GCCGAAATTT ACGACCAAGT
1251 CGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATTAAG TTGGACAAAA
1301 accaaaCCCT Gctcgaagcc gtgCAAAccg atGTCEgctt tgcCGCGGTT
1351 GCCcgGacT ACGCTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCTGACC GACGCTGCG CCCTGCAAAA AGTCTTCATC GGCAAAATCA

```

1023

1451 TCGGCCGACT TTTGTCTTC GTACAGGAGG AACACGAAGA CACCACAGCC  
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG  
 1551 ATAG

This corresponds to the amino acid sequence <SEQ ID 2070; ORF 644.ng>:

g644.pap  
 1 MPSERPADCC PVHFFVKFRK LTLNCGRRFD RPPINGNRQR KPMIHTEPSA  
 51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL  
 101 DKKHGGRRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGGEEA  
 151 QVAQGLDMIF KGESRRLGVT EPETSGAAIA REMQSCYEYD DEQTIYVNAA  
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA  
 251 VRYAVNRIDA EMPATAVMKL SRGDAAGLRA FQNI FIRSRL QLIGMTHGIM  
 301 EYILDNLNRY VRNDIRFVDY ERREIQRHQQ VSEILYRYVC HSVSPVAPVA  
 351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHAPG NIAIDIRPFT  
 401 IFEGPNMPLY AEIYDQFVRA TAEKEAGIK LDKNQTLDDA VQTDVRFPAV  
 451 ARDYALPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQEEHEDTTA  
 501 FLNDIRKDI LDCRYCG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2071>:

m644.seq  
 1 ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA  
 51 GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA  
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG  
 151 CAGCCGTCAG CTATGGACAC GGCTGCTTTT TTAAGACACA TCGAATCCGC  
 201 ATTCCGCGCG ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCCG  
 251 AAGACAAATG GCTTGCCCTG AAGCAGGCGG GTTGTCTGTT GCCCTTCCTC  
 301 GACAAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TCCAAGAAAT  
 351 CcTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA  
 401 TCGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG  
 451 CAAGTCGCGC AAGGTTTGA GATGATTTT AAAGGCGAGG GCGGCGGTTT  
 501 GGGTGTATAC GAACCCGAAA CCTCCGGCGC GCGGATTGCA CGCGAAATGC  
 551 AGTCCTACTA CGAATATATC GACGGACAAA CCATTACGT CAACGCCGCG  
 601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA  
 651 AGAGCGCAAA AACGGCAAA TCGCCAAAAGT CATCGACCTG CTGCTCGTCC  
 701 CCAAAACATA CATCCGCTGC GAAACCTCG CATCCGAAAG CTGCGCGCC  
 751 GTCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT  
 801 GATGAAACTG TCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA  
 851 TCTTTATCCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG  
 901 GAATACATCC TTGAAAATCT GGAACGATAC GTCCGCAACG ACATCAAATT  
 951 CGTCGATTAC GAACGCCGCG AAATCCGCGC CGGCCATCAG GTTCCGAGA  
 1001 TTCTTTACCG CTACGCTGCG CATTCGTTT CGCCTGTTGC CCCCCTCGCC  
 1051 CATCAGCTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC  
 1101 TTACGCCGCG CCGCAATGT TGCAAAAACCT CTTGGGTGCG AAGGGTTTTG  
 1151 AACCGCGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG  
 1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAGTT  
 1251 TGTCGCGCGC ACCGCCGAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA  
 1301 ACCAAACCTT GCTCGACCGC CTGCAAAACCG ATGCCCGCTT TGCCGCCGTC  
 1351 GCCCGCGACT ACACTTTGCC TGAAGACATC CGCAGCTTCC TGCAGGAACA  
 1401 CACCCGTGAC GATGCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA  
 1451 TCGCCGACT CTTGTCTTC GTACAGGCGA AACACGAAGA CACCGCAGCC  
 1501 TTCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG  
 1551 GTAG

This corresponds to the amino acid sequence <SEQ ID 2072; ORF 644>:

m644.pap  
 1 MPSERSADCC PAHFFVKFRK STLNCGRRFD RPPINGNRQR KPMIHTEPSA  
 51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL  
 101 DKYGGRRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGDEA  
 151 QVAQGLEMIF KEGGGGLGVT EPETSGAAIA REMQSYEYI DGQTIYVNAA  
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA  
 251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNI FIRSRL QLIGMTHGIM  
 301 EYILENLERY VRNDIKFVDY ERREIQRHQQ VSEILYRYVC HSVSPVAPVA  
 351 HOLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHATG NIAIDIRPFT  
 401 IFEGPNMPLY AEIYDQFVRA TAEKEAGMK LDKNQTLDDR LQTDARFAAV  
 451 ARDYTLFEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQAKHEDTAA  
 501 FLNDIRKDI LDCRYCG\*

m644/g644 94.6% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pap	MPSERSADCCPAHFFVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
	:					
g644	MPSERPADCCPVHFFVKFRKLTNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					

1024

	10	20	30	40	50	60
m644.pep	70	80	90	100	110	120
	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLPFLDKKYGGRKGSQFEIQEVLRI					
g644	:     :     :     :     :					
	70	80	90	100	110	120
	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLPFLDKKYGGRKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	130	140	150	160	170	180
	AGHYGVPVTLRTGIEGALVLPLOEFGDEAQAQGLEMIFKGEGGGLGVTEPETSGAAIA					
g644	:     :     :     :     :					
	130	140	150	160	170	180
	AGHYGVPVTLRTGIEGALVLPLOEFGGGAQAQGLDMIFKGESRRLGVTEPETSGAAIA					
	130	140	150	160	170	180
m644.pep	190	200	210	220	230	240
	REMQSYEYIDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
g644	:     :     :     :     :					
	190	200	210	220	230	240
	REMQSCYEYTDQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	250	260	270	280	290	300
	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM					
g644	:     :     :     :     :					
	250	260	270	280	290	300
	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSRGDAAGLRAFQNI FIRSRLQLIGMTHGIM					
	250	260	270	280	290	300
m644.pep	310	320	330	340	350	360
	EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMANIVK					
g644	:     :     :     :     :					
	310	320	330	340	350	360
	EYILDNLNRYVRNDIRFVDYERREIQRRHQVSEILYRYVCHSVSPVAPVAHQLMANIVK					
	310	320	330	340	350	360
m644.pep	370	380	390	400	410	420
	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
g644	:     :     :     :     :					
	370	380	390	400	410	420
	TLATEYTYAAAQMLQKLLGAKGFERGHPAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
m644.pep	430	440	450	460	470	480
	TAEKEAGMKLDKNQTLDRQLQTDARFAAVARDYTLPEDIRSFLQEHTLTDACALQKVFI					
g644	:     :     :     :     :					
	430	440	450	460	470	480
	TAEKEAGIKLDKNQTLDAVQTDVRFVAARDYALPEDIRSFLQEHTLTDACALQKVFI					
	430	440	450	460	470	480
m644.pep	490	500	510			
	GKIIARLFVVFQAKHEDTAFLNDIRKDILDCRYCGX					
g644	:     :     :     :     :					
	490	500	510			
	GKIIARLFVVFQEEHEDTTAFLNDIRKDILDCRYCGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2073>:

```

a644.seq
1  ATGCCGTCCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAA
51  GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAG CTATGGACAG GGCTGCTTTT TTAAGCACA TCGAATCCGC
201 ATTCCGCCGC ATTTTTCGAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
301 GACAAAAAAT ACGCGGGCGC CAAGGGCAGC CAGTTTGAAA TTCAGGAAGT
351 CTTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTANNNNN NNNNNNNNNN
401 NNGAAGCGCG GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
451 CAAATCGCAC AGGTTTGGG CATGGTTTTC AAAGGCGAGG GCGGCGGTTT
501 AGGCGTTACC GAACCGGAAA CCTCCGGCGC GCGGATTGCC CGAGAAATGC
551 AGTCTTACTA CGAATATACC GACGGACAAA CCATTACGT CAACGCCGCG
601 AAATACTGGC AGGGCAATC GCAAAGCGAC TTCCTCTCG TTGCCGCCAA
651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACGCCCGT
801 GATGAACTC TCCAGAGCG ACGTGCCCGG TTGCGCGCG TTCCAAACAA

```

1025

```

851 TCTTTATCCG CAGCCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCGCGC CGCCCATCAG GTTTCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCCGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGCGCGC AAGGGTTTTG
1151 AACCGCGACA CACCGCCGGC AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAAGT
1251 TGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
1301 ACCAAACCCT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCCGTC
1351 GCCCGCGACT ACACTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCCGACT CTTTGTCTTC GTACAGGCGG AACACGAAGA CACCGCAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG

```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

```

a644.pep
1  MPSERSADCC PAHFVVKFRK STLNCGRFRD RPPINGNRQR KPMIHTEPSA
51  QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKKYGGRKGS QFEIQEVLRI AGHYGVPVXX XXXXEGALVL QPLQEFGDEA
151 QIAQGLDMVF KEGGGGLGVT EPETSGAAIA REMQSYEYTDGQTIYVNA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNI FIRSRL QLIGMTHGIM
301 EYTLNLERY VRNDIRFVDY ERREIRRRHQ VSEILYRYVCHSVSPVAPVAH
351 QLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDDR LQTDARFAAV
451 ARDYTLPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*

m644/a644 97.3% identity in 517 aa overlap

      10      20      30      40      50      60
m644.pep  MPSERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644      MPSERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
      10      20      30      40      50      60

      70      80      90      100     110     120
m644.pep  LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI
a644      LKHIESAFRRIFADGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI
      70      80      90      100     110     120

      130     140     150     160     170     180
m644.pep  AGHYGVPVTLRGTGIEGALVLQPLQEFGDEAQVAQGLEMI FKGEGGGLGVTEPETSGAAIA
a644      AGHYGVPVXXXXXEGALVLQPLQEFGDEAQIAQGLDMVFKGEGGGLGVTEPETSGAAIA
      130     140     150     160     170     180

      190     200     210     220     230     240
m644.pep  REMQSYEYIDGQTIYVNAAKYWGNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC
a644      REMQSYEYTDGQTIYVNAAKYWGNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC
      190     200     210     220     230     240

      250     260     270     280     290     300
m644.pep  ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM
a644      ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM
      250     260     270     280     290     300

      310     320     330     340     350     360
m644.pep  EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK
a644      EYTLNLERYVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK

```

1026

	310	320	330	340	350	360
	370	380	390	400	410	420
m644 .pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
a 644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m644 .pep	TAEKEAGMKLDKNQTLDRLOTDAFAAVARDYTLPEDIRSFLQEHTLTACALQKVFI					
a 644	TAEKEAGMKLDKNQTLDRLOTDAFAAVARDYTLPEDIRSFLQEHTLTACALQKVFI					
	430	440	450	460	470	480
	490	500	510			
m644 .pep	GKIIARLFVQAKHEDTAAFLNDIRKDILDCRYCGX					
a 644	GKIIARLFVQAEHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2075>:

g645 .seq

```

1  ATGATGATGG TGTGGCGTT GGGGATGTCG ATGCCGTTT CGATGATGGT
51  GGAACAGAGC AACACATTGA ATCTTGTCTG CAAAAGTTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCAGCG AGTTGTCCGT GCGCCACGCC GATACGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTCTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAata cCTGTCTCC CCGTTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTGACAAA GGTTTTCACG
301 GCGAGGCGGC GGCTCGGTGC AGTGGTAATC AGCGAGAAGT CGCGCAGACC
351 TTCGAGCGCC ATGCTGAGGG TCGCGGAAT CCGCGTGGCG GTCATGGTTA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGTGCGACG
451 CCGAAGCGGT GTTCTTCATC GATAATCAAT AAACCTAAGT TTTTGAATTT
501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACGATA TCGACAGTAC
551 CGTCCGCCAT GCCTTCGAGC GTGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTGCGGCGC AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGAAG GCGGACTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACA AGTCGGTCCA TCGGCTTCGC
801 CTGCGTCAA TCTTTAATCA CGGcggcgat ggcggcggc TGGTCTTCGG
851 TTTCTCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2076; ORF 645.ng>:

g645 .pep

```

1  MMMVLALGMS MPVSMMEQS NTLNLCCKKS RMTCSRSSR SCPCATPIRA
51  SGRSVSSRSR IFSIVSTSLC RKNTPPRLS SRNTASRLP SLNGLTKVFT
101 ARRLGAVVI SEKSRFPSSA MLVRGIGVA VMVRMSTLAR RRLSCSFCRT
151 PKRCSSSIIN KPKFLNFMSS CTNLCVPITI STVPSAMPSS VALVALLLLK
201 RERLATFTGK SAKRSKAFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT SRSIGFACVK SLITAAMAAA WSSVSS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2077>:

m645 .seq

```

1  ATGATGATGG TGTGGCGTT GGGGATATCG ATACCGTTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAGTTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTTTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAATA CCTGTCTCC CCGTTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGTAAAGG GTTGACAAA GGTTTGACG
301 GCGAGGCGGC GGCTGGGCGC GGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAACGCC ATACTTAAAG TACGCGGAAT CCGCGTGGCG GTCATGGTAA
401 GGATATCAAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCGACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTAAGT TTTTGAATTT
501 GATGTCGTCC TGCACAGTT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCTGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGCGCG TGCTGCTCGA CCAAAAGCGT GGTGCGGAGC AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGCAG GCGGACTTCG
751 GTTTTGCCGA AGCCGACATC GCCGCACACA AGGCGATCCA TCGGCTTCGC
801 TTGCGTCAA TCTTTAATCA CGGCGCGCAT GCGGCGGCC TGGTCTTCGG

```

1027

851 TTTCCTCGTA G

This corresponds to the amino acid sequence &lt;SEQ ID 2078; ORF 645&gt;:

```

m645.pep
1  MMMVLALGIS IPVSMMEQSN TLNRCCKKS RMTCSRSSR SCPCATPMRA
51  SGRVSSRSR IFSIVSTSLC RKNTCPRLS SRNTASRTLP SLKGLTKVLT
101 ARRLGAVVI SEKSRSPSNA ILKVRGIGVA VMVRISTLAR RRLSCSF*RT
151 PKRCSSSIIT KPKFLNLMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSKFCA CCSTKSUVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/g645 93.7% identity in 286 aa overlap

	10	20	30	40	50	60
m645.pep	MMMVLALGISIPVSMMEQSN	TLNRCCKKS	RMTCSRSSR	SCPCATPMRA	SGRVSSRSR	
g645	MMMVLALGMSMPVSMMEQSN	TLNRCCKKS	RMTCSRSSR	SCPCATPIRAS	SGRVSSRSR	
	70	80	90	100	110	120
m645.pep	IFSIVSTSLCRKNTCP	PRLSSRNTASRTLP	SLKGLTKVLTARRRL	GAVVISEKSRSPSNA		
g645	IFSIVSTSLCRKNTCP	PRLSSRNTASRTLP	SLNGLTKVFTARRRL	GAVVISEKSRSPSNA		
	130	140	150	160	170	180
m645.pep	ILKVRGIGVAVMVRIST	LARRRLSCSFXRTP	PKRCSSSIITKPKFLN	LMSSCTSLCVPITI		
g645	MLRVRGIGVAVMVRIST	LARRRLSCSFCRTP	PKRCSSSIINKPKFLN	FMSSCTNLCVPITI		
	190	200	210	220	230	240
m645.pep	STVPSAMPSSAALVALL	LKRERLATFTGKSAKRS	KFCACCSTKSUVGAS	TATCLPPIT		
g645	STVPSAMPSSVALVALL	LKRERLATFTGKSAKRS	KFCACCSTRSVVGAS	TATCLPPIT		
	250	260	270	280		
m645.pep	ATNAARRATSVLPKPTSP	HRRSIGFACVKSLITA	AMAAWSSVSSX			
g645	ATNAARRATSVLPKPTSP	HRSIGFACVKSLITA	AMAAWSSVSSX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2079>:

```

a645.seq
1  ATGATGATGG TGTGGCGTT GGGAAATGTCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCACGC ATGTTTTCGA TGGTATCCAC
201 TTCATTGTGC AGGAAAAATA CTTGCCCGCC GCGTTTGAGT TCGCGCAATA
251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTTTGACG
301 GCGAGGCGGC GGCTGGGCGC AGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAGCGCC ATACTTAAAG TACGCGGAAT CGGCGTAGCG GTCATGGTAA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTACGT TTTTGAATTT
501 TATGTCGTCC TGCACCAGTT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCCGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTGTTTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAGC GGTGCGCAAA
651 ATTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTGCGTGCG AGTACGGCAA
701 CTTGTTTGCC ACCCATTACC GCCACAAACG CGGCGCGCAG GCGCATTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACG AGGCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTTAATCA CGGCGGCGAT GCGGCTGCC TGGTCTTCGG
851 TTCTTTCGTA G

```

This corresponds to the amino acid sequence &lt;SEQ ID 2080; ORF 645.a&gt;:

```

a645.pep
1  MMMVLALGMS IPVSMMEQSN TLNRCCKKS RMTCSRSSR SCPCATPMRA

```

1028

```

51  S GSRVSSRSR MFSMVSTSLC RKNTCPPLRS SRNTASRTLPSLNGLTKVLT
101 ARRLGAVVI SEKSRSPSSA ILKVRGIGVA VMVRMSTLAR RRLSCSF*RT
151 PKRCSSSIIT KPTFLNFMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSAKFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/a645 96.9% identity in 286 aa overlap

```

              10      20      30      40      50      60
m645.pep      MMMVLALGISIPVSMVSEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645          MMMVLALGMSIPVSMVSEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
              10      20      30      40      50      60

              70      80      90     100     110     120
m645.pep      IFSIVSTSLCRKNTCPPLRSSRNTASRTLPSLTKVLTARRRLGAVVISEKSRSPSNA
              :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645          MFSMVSTSLCRKNTCPPLRSSRNTASRTLPSLNGLTKVLTARRRLGAVVISEKSRSPSSA
              70      80      90     100     110     120

              130     140     150     160     170     180
m645.pep      ILKVRGIGVAVMVRISTLARRRLSCSEFXRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645          ILKVRGIGVAVMVRMSTLARRRLSCSEFXRTPKRCSSSIITKPTFLNFMSSCTSLCVPITI
              130     140     150     160     170     180

              190     200     210     220     230     240
m645.pep      STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCACCSTKSVVGASTATCLPPIT
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645          STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSKFCACCSTRSVVGASTATCLPPIT
              190     200     210     220     230     240

              250     260     270     280
m645.pep      ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645          ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAWSSVSSX
              250     260     270     280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2081>:

```

g647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAGGTGTCGA
51  TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCT
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAGTAGGCGT AGTTGATGAC ACCGATGCCG
251 AGCGAACGGC GGTCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2082; ORF 647.ng&gt;:

```

g647.pep
1  MQRLAADGIQ IFFVGVGDQF ALRINGLVKE RARSVFFGKV CRCFEQVILY
51  GFKGTGVGQTE RGTVAADTV FRQIVGVDD TDAERTAVHS RGRGFYRIS
101 LII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2083>:

```

m647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAAGTGTCGA
51  TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAATAAGCAT AGTTAATCAC GCCGATGCCG
251 AGCGAACGGC GGCCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2084; ORF 647&gt;:

```

m647.pep
1  MQRLAADGIQ IFFVSDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY

```



1029

51 GFKGTVGQTE RGTAVADTV FRQIISIVNH ADAERTAHS RGTRGFYRIS  
101 LII\*

m647/g647 91.3% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSVGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	:     :     :     :     :     :					
g647	MQRLAADGIQIFFVSVGQFALRINGLVKERARSVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTAVADTVFRQIISIVNHADAERTAHSRGTRGFYRISLIIX					
	:     :     :     :     :					
g647	RGTAVADTVFRQIVGVDDTDAERTAVHSRGTRGFYRISLIIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2085>:

a647.seq  
1 GTGCAAAGGC TCGTTACACA CAGCGTCCAA GTCTTTTTTG TAGGTGTCGA  
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTTAAAGAG CGTGCACGCA  
101 CCGTATTCTT TGGCAAAGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT  
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAGCCG TCGCTGTAGC  
201 GGACACCGTT TTTCGCCAAA TAATACGCAT AGTTGATCAC GCCGATACCG  
251 AGCGAACGGC GGCCCATAGT GGAGGTACGC GCGGCTTCTA CCGGATATCC  
301 CTGATAATCT AA

This corresponds to the amino acid sequence <SEQ ID 2086; ORF 647.a>:

a647.pep  
1 VQRLVTHSVQ VFFVGVGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY  
51 GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADTERTAHS GGTRGFYRIS  
101 LII\*

m647/a647 87.4% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSVGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	:    : :  :     :     :     :     :     :					
a647	VQRLVTHSVQVFFVGVGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTAVADTVFRQIISIVNHADAERTAHSRGTRGFYRISLIIX					
	:     :     :     :     :					
a647	RGAVAVADTVFRQIIRIVDHADTERTAHSRGTRGFYRISLIIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2087>:

g648.seq  
1 ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT  
51 CGACGTTTTG AATGTAGATG CGCCCGGTCC CGGCACGCTC CTGCATCAGC  
101 GTGGAACAAC GGTGCGCAGC CGGAATGATA CGCTTGCGTA TGTTGCGGTC  
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA  
201 ACGCTTCGTA CAACCCCGAA ACCTCGTTGG GCGAAAACAG CGTAATGTTG  
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTG GCACGCCATA  
301 ATCAAGCTGG CGGATACGGT TGTCTTCCAC GCCCGGTTG TTTTCAACA  
351 CCAGCAGGCT TTCGGCTTCA ATATGCCACA AGGGGTAGAA CAAGGTTGCC  
401 GCGCCGCCGC GCACGCCACC TTGCGAACAA GATTGACCG CCGCCTGAAA  
451 CATCTTAAAG AAGGGAATGC AGCCGGTATG CCGGGCTTCA CCGCCCCGGA  
501 TTTCGCTGTC CAGCCCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCG  
551 CGTTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGCCAT TGATGGAATC  
601 CAACTATCG TCGCATTCAA TCAGCACACA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2088; ORF 648.ng>:

g648.pep

1030

```

1  MNRRNARIER AVRIAVIDVL NVDAPGPGTL LHQRGKQVGS RNDTLAYVRV
51  LLVFRIEPLK FVLVGKKRFV QPRNLVGRKQ RNVAALNQAG VQQAVDLHAI
101 IKLADTVVFH APVVFQHQQA FGFNMPQGV E QGCRAAAHAT LRTFRDRRLK
151 HLKEGNAAGM PGFTAPDFAV QPADTSGIDA DARALGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2089>:

```

m648.seq
1  ATGAACAGGC GCGACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTTG AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCGGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAA TCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCAC ACCGCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCGCC TTGCGAACAG GATTGACCG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGCGCTTCG CCGCCCCGGA
501 TTTCGCTGTC CAAACCGCGG ATACGTCGGG CATTGATGCC GATGCCCGCA
551 CGCTGGGAAA CGTATTTTAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGCATTCAA TCAGCACACA GCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2090; ORF 648>:

```

m648.pep
1  MNRRDARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
51  LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVDLHAV
101 IKLADTVVFH TAVVFQHQQA FGFDMPPQGV E QGCRAAAHAA LRTGFDRRLK
151 HFKEGNAAGM PRFAAPDFAV QTADTSGIDA DARTLGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

m648/g648 91.5% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
	:       :       :       : :					
g648	MNRRNARIERAVRIAVIDVLNVDAPGPGTLLHQRGKQVGSRNDTLAYVRVLLVFRIEPLK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVDLHAVIKLTDTVVFHTAVVFQHQQA					
	:       :       :       :       :					
g648	FVLVGKKRFVQPRNLVGRKQRNVAALNQAGVQQAVDLHAIKLDATVVFHAPVVFQHQQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m648.pep	FGFDMPPQGVQGCRAAAHAALRTGFDRRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA					
	:       :       :       :       :					
g648	FGFNMPPQGVQGCRAAAHATLRTFRDRRLKHLKEGNAAGMPGFTAPDFAVQPADTSGIDA					
	130	140	150	160	170	180
	190	200	210			
m648.pep	DARTLGNVFHNRRAGSGIDGIQTIVAFNQHTAX					
	:       :       :       :					
g648	DARALGNVFHNRRAGSGIDGIQTIVAFNQHTAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2091>:

```

a648.seq
1  ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTTG AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCGGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAA TCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCAC GCCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCACC TTGCGAACAG GATTGACTG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGTGCTTCG CCGCCCCGGA

```

1031

501 TTTCGCTGTC CAGTCCGCGG ATACGTCGCG CATTGATGCC GATGCCCCGA  
 551 CGCTGGGAAA CGTATTTTAC AATCGCGCTG GTAGTGGCGT TGATGGAATC  
 601 CAGGCTGTCT TCGCATTCTGA TCAATACGCA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

a648.pep  
 1 MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV  
 51 LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAAALNQAG VQQAVIDLHAV  
 101 IKLTDTVVFH APVVFQHQQA FGFDMPQGV E QGCRAAAHAT LRTGFDCLRK  
 151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI  
 201 QAVVAFDQYA A\*

m648/a648 93.8% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
a648	:					
	10	20	30	40	50	60
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAAALNQAGVQQAVIDLHAVIKLTDTVVFHAPVVFQHQQA					
a648						
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAAALNQAGVQQAVIDLHAVIKLTDTVVFHAPVVFQHQQA					
a648						
	70	80	90	100	110	120
m648.pep	FGFDMPQGV E QGCRAAAHATLRTGFDRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA					
a648	:                             :					
	130	140	150	160	170	180
m648.pep	FGFDMPQGV E QGCRAAAHATLRTGFDRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA					
a648	:                             :					
	130	140	150	160	170	180
m648.pep	DARTLGNVFHNRAGSGIDGIQTIVAFNQHTAX					
a648	:    :    :					
	190	200	210			
m648.pep	DARTLGNVFHNRAGSGVDGIQAVVAFDQYAA					
a648	:    :    :					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

g649.seq  
 1 ATGCTTGCCA TACTGTTGTC TGCAATACTG GGACTGGTAT CAACAACCTGC  
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG ACATACCAAA CATATCAGCA  
 101 AGGCAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC  
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGGAAAA  
 201 CAAAAAGGCG CGCAAAGCAT TCCGCACCCT GCCTTATGCG GAACAGAAAA  
 251 TCCAATGCCG GCGGCTTAT GAGGCTTCG ATGATTTCGA CCGCGGCAGG  
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

g649.pep  
 1 MLAILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECRKYLER  
 51 RAAWYRSQGN VQELRENKKA RKAFRTLPHY EQKIQCAAAY EAFDDFDGGR  
 101 FRR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

m649.seq  
 1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACCTGC  
 51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA  
 101 AGGCAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC  
 151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGGAAAA  
 201 CAAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA  
 251 TCCAATGCCG GCGGCTTAT GAGGCTTCG ATGATTTCGA CCGCGGCAGT  
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649.pep

1032

```

1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51  RAAWYRSQGN VQELRENKKA RKAFRSLPYA EQKIQCRAAY EAFDDFDGGS
101 FRR*

```

m649/g649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
g649           MLAILLSAILGLVSTTAAAGTSEPAHRHTKHISKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||||
g649           VQELRENKKARKAFRTLPHYAEQKIQCRAAYEAFDDFDGGRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2097>:

```

a649.seq
1  ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACGTC
51  CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAA CATATCCGCA
101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGA AAA
201 CAAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATAAG GAACAGAAAA
251 CCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCAGCAGG
301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2098; ORF 649.a&gt;:

```

a649.pep
1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51  RAAWYRSQGN VQELRENKKA RKAFRSLPYK EQKTQCRAAY EAFDDFDGSR
101 FRR*

```

m649/a649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
a649           MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||||
a649           VQELRENKKARKAFRSLPYKEQKTQCRAAYEAFDDFDGSRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2099>:

```

g550.seq
1  ATGTCCAAAC TCAAAACCAT CGCCCTGACC GCATCAGGTC TGTCCGTTTG
51  TCCGGGTTTC CTATATGCCC AAAACACCTC ATCACACCAA GTCGGTTTAG
101 CGATTATGCG GTTAAACTCT TCAATACTCG ACCTGCCACC GACAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGGACGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCGAG CTATTTCGAC AGGTCGTCA ACCGGAGCCG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCG CCGAAGCCGC
351 CTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGTACCGG CAGGCATTAC
451 GGCTTGAAA AAACaccgGT TTACGacgGc aggcacGacG TtacgcaGc
501 taccgatgcc gcacTCAACT AtctGcAATA TCTCTatggA CTGTTcGGCG
551 ACTGGCCGCT CGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCGTC ACCGCGCCCG CGACCAAGGG CTCGAACCGA CCTACGAAAA
651 CTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCAAG CTGCTCGCCG
701 TCGCAACAT TATTGCCACC CCCCAATCTT TCGGCATGAA TATCAGCGAC

```

1033

```

751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGGCC GTCCGCTCGA
801 caacGAagc ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTGAATCC TGCATTCAAC GTCCCCGCGt tcatCCCCAA AAacaaacgc
901 aaacTGCTGC TTCCTGTCCG GTCCGTCCAA ACCTTccaaa gcaACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAA GCCTCAACAA CCTGAACGGC AACCTTGTCa ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAat
1151 ccGTCTGTTT CATCGACATC GACAATACGC CcgacacCTa ccgttccaaT
1201 ATGCcggcag gcaCGGTGAA CGTCAGCATT gccCgaatcc aacCCgcccgc
1251 cgcaCAGACA gcggacatta ccgtcgcacc ttgcccga gaaaccgtcc
1301 gtacgggaac ccgatccctt tgtccgcaTt accgaaccgc ccctTGGCAG
1351 AGCCGCAGCG CaacctCAAA ccgAAAAACA GACTGCCATG CcgtctGA

```

This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

```

m650.pep
1 MSKLTIALT ASGLSVCPGF LYAQTSSHQ VGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWDE LRQGRFMGEV NPFLVRRHES KFIASRSYFD RVNRSRPYM
101 YHIANEVKKR NMPAEALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGENVG
201 RAVNRARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPGRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKNKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSIDI DNTPDITYRSN
401 MPAGTVNVSI ARIQPAQAQT ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

```

m650.seq
1 ATGTCCAAAC TCAAAACCAT CGCTCTGACC GCATCAGGTC TGTCCGTTTG
51 TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCCCC GACAAAACAA
151 TATTCCCAAT CCGGCAGCCT GTGGGGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGCG AATATGCCCG CCGAAGCCGC
351 CCTGCTTTCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGCTACCGG CAGGCATTAC
451 GGCTTGGAAC AAACACCGGT TTACGACGGC AGGCACGACG TTACGCGCGC
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGGC
551 ATCTGGCCGCT TGCCCTTTGCC GCCTACAACG GGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCTCAAG CTGCTCGCCG
701 TGCGCAACAT TATTGCCACT CCCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCTTAAACCC CGCATTCAAC GTCCCCGCGT TTATCCCCAA AAGCAAACGC
901 AAATGCTGCT TTCCTGTCCG GTCCGTACAA ACCTTCCAAA GCAACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAA GCCTCAACAA CCTGAACGGC AACCTTGTCa ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCGCG
1251 CGCAGAGACA GCGGACATTA CCGTCGCACC TTTGCCGCGA AAAACCGTCC
1301 GTACGG.AAC CCGATCCCTT TGTCCGTATT GCCGAACCTG CCCTTGGCGAC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

```

m650.pep
1 MSKLTIALT ASGLSVCPGF LYAQTSSHQ IGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWGE LRQGRFMGEV NPFLVRRHES KFIASHSYFN RVNRSRPYM
101 YHIANEVKKR NMPAEALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPDITYRSN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451 SRSATSNRKT DRHAV*

```

m650/g650 96.1% identity in 465 aa overlap

1034

	10	20	30	40	50	60
m650.pep	MSKLKTI	ALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE				
g650	MSKLKTI	ALTASGLSVCPGFLYAQNTSSHQVGLAIMRLNSSILDLPPTKQYFQSGSLWGE				
	10	20	30	40	50	60
	70	80	90	100	110	120
m650.pep	LRQGF	RMGEVNP	ELVRRHESKFIASHSYFN	RVINRSR	PYMYHIANEVKKRNMPAE	AALLP
g650	LRQGF	RMGEVNP	ELVRRHESKFIASRSYFDRV	VNRSR	PYMYHIANEVKKRNMPAE	AALLP
	70	80	90	100	110	120
	130	140	150	160	170	180
m650.pep	FIESAF	VTKAKSHV	GASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQVLYG			
g650	FIESAF	VTKAKSHV	GASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQVLYG			
	130	140	150	160	170	180
	190	200	210	220	230	240
m650.pep	LFGDW	PLAFAAYNW	GEGNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT			
g650	LFGDW	PLAFAAYNW	GEGNVGRAVNRARDQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT			
	190	200	210	220	230	240
	250	260	270	280	290	300
m650.pep	PQSFG	MNISDIDN	KPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKSKR			
g650	PQSFG	MNISDIDN	KPYFQAVEPGRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKNKR			
	250	260	270	280	290	300
	310	320	330	340	350	360
m650.pep	KLLLP	VASVQTFQSNYLNAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG				
g650	KLLLP	VASVQTFQSNYLNAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG				
	310	320	330	340	350	360
	370	380	390	400	410	420
m650.pep	NLVN	AGRSILVAKNGKTLQTASESVV	SIDIDNTPD	TYRSNMPAGTVNVGIARIRPAA	AQT	
g650	NLVN	AGRSILVAKNGKTLHTASESVV	SIDIDNTPD	TYRSNMPAGTVNVSIARIQPAA	AQT	
	370	380	390	400	410	420
	430	440	450	460		
m650.pep	ADITV	APLPQKTV	RTXTRSPCPYCRTCPCDSRSATS	SNRKTD	DRHAVX	
g650	ADITV	APLPQETV	RTGTTRSPCPHYRTRPCDSRSATS	SNRKTD	CHAVX	
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2103>:

```

a650.seq
1  ATGTCCAAC TCAAAACCAT CGCCCTGACC GCGTCAGGTC TGTCCGTTTG
51  TCCGGGTTTC CTATACGCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGAGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
451 GGCCTGGA AAACACCGGT TTACGACGGC AGGCACGACA TTTACGCCGC
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGGC
551 ACTGGCCGCT CGCCTTTGCC GCCTACAACT GGGTGGAAG CAACGTCGGA
601 CGCGCATCA ACCGCGCCCG CGCCCAAGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTTCCTAAG CTGCTCGCCG
701 TGCGCAACAT CATTGCCGCC CCCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCGTATTT TCAGGCAGTC GAACCGGACC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTAAACCC CGCATTCAAC GTCCCGCGT TCATCCCCAA AAGCAAACGC

```

1035

```

901  AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951  CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CAAAACCAG CTTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAA GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCAGC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

```

a650.pep
1  MSKLKTIALT ASGLSVCPGF LYAQNTSSHQ IGLAIMRLNS SILDLPPTKQ
51  YFQSGSLWSE LRQGRMGEV NPVELRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDIIYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAINRARAQG LEPTYENLRM PNETRNVVPK LLAVRNIIAA PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTNYSRN
401 MPAGTVNVGI ARIRPAAQQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451 SRSATSNRKT DRHAV*

m650/a650 99.1% identity in 465 aa overlap

          10          20          30          40          50          60
m650.pep  MSKLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE
          |||||
a650      MSKLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWSE
          10          20          30          40          50          60

          70          80          90          100         110         120
m650.pep  LRQGRMGEVNPVELRRHESKFIASHSYFN RVINRSRPYMYHIANEVKKRNMPAEALLP
          |||||
a650      LRQGRMGEVNPVELRRHESKFIASHSYFN RVINRSRPYMYHIANEVKKRNMPAEALLP
          70          80          90          100         110         120

          130         140         150         160         170         180
m650.pep  FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG
          |||||
a650      FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDIYAATDAALNYLQYLYG
          130         140         150         160         170         180

          190         200         210         220         230         240
m650.pep  LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNVVPKLLAVRNIIAT
          |||||
a650      LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNVVPKLLAVRNIIAA
          190         200         210         220         230         240

          250         260         270         280         290         300
m650.pep  PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
          |||||
a650      PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
          250         260         270         280         290         300

          310         320         330         340         350         360
m650.pep  KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
          |||||
a650      KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
          310         320         330         340         350         360

          370         380         390         400         410         420
m650.pep  NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTNYSRNMPAGTVNVGIARIRPAAQQT
          |||||
a650      NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTNYSRNMPAGTVNVGIARIRPAAQQT

```

1036

	370	380	390	400	410	420
	430	440	450	460		
m650.pep	ADITVAPLPQKTVRTXTRSPCPYCRTPCDSRSATSNRKTDRAVX					
a 650	ADITVAPLPQKTVRTXTRSPCPYCRTPCDSRSATSNRKTDRAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2105>:

```

g652.seq
1  ATGATCGAAT TGGACGGTAC TGAACAACAAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTTCTATGCG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGCGC CAGGTCGGAT GTCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGTAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAG AAGCCCTGCA ACTGATGGTC GAAGCGGCCG
401 AAGCCGCCGG CTACAAGGCG GCGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCATTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGGCGA ATACTTGGA GGCTTGGTTA
551 ACGAATTTCC GATTATTTCC ATTGAAGACG GGATGGACGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATG GCGAAAAAG TTCAATTGGT
651 CGGCGACGAC TTGTTCTGTA CCAATCCGAA AATTCTTGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAACGCA TTGCTGGTCA AAGTCAACCA AATCGGTACT
751 TTAAGCGAAA CCCTGAAAGC cgtcgatctg gCAAAATGCA accgctacGc
801 cagCGTGATG AGCCACcgct ccggCGAAAC CGAAGACAGT Accattgccc
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TTAACccgG TTCTTTGAGc
901 cgtTCCGACC GCATGGCGAA ATACAACCAa ctGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCGcgctACT ACCCGGCGAA AGCCGCATTC TACCAACTGG
1001 GCAATAAA

```

This corresponds to the amino acid sequence <SEQ ID 2106; ORF 652.ng>:

```

g652.pep
1  MIELDGTENK GNLGANATLA VMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNLSNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EAAEAAGYKA GEDVLFALDC
151 ASSEFYKDCK YHLEAEGRSY TNAEFAEYLE GLVNEFPIS IEDGMDENDW
201 EGWKLLEKL GKQVQLVGGD LFTNPKILA EGIEKGVANA LLVKVNIQGT
251 LSETLKAVDL AKCNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAYNQ LLRIEELAE AAYYPGKAAF YQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2107>:

```

m652.seq
1  ATGATCGAAT TGGACGGTAC TGAACAACAAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTTCTATGCG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGCGC CAGGTCGGAT GTCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCCGG CTACAAGGCG GCGAAGACG TATTATTCGC ATTGGACTGC
451 GCCTCCAGCG AGTTCTACAA AGACGGCAAA TACCATTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGGCGA ATATCTGGA GGCTTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GCATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAACTG GGCGGTAGAG TTCAATTGGT
651 TGCGGACGAC TTGTTCTGTA CCAATCCAAA AATCTTGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAACGCA TTGCTGGTCA AAGTCAATCA AATCGGTACT
751 TTGAGCGAGA CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCCGACC GCATGGCGAA ATACAACCA CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCGCGCGACT ACCCGAGCAA AGCCGCATTC TACCAACTGG
1001 GCAATAAA

```

This corresponds to the amino acid sequence <SEQ ID 2108; ORF 652>:

```

m652.pep
1  MIELDGTENK GNLGANATLA VMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNLSNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC

```



1037

```

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW
201 EGWKLLETKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAYNQ LLRIEEELAE AADYPSKAAF YQLGK*

```

m652/g652 98.2% identity in 335 aa overlap

```

              10      20      30      40      50      60
m652.pep      MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
g652          MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
              10      20      30      40      50      60

              70      80      90      100     110     120
m652.pep      EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN
g652          EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN
              70      80      90      100     110     120

              130     140     150     160     170     180
m652.pep      SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
g652          SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
              130     140     150     160     170     180

              190     200     210     220     230     240
m652.pep      GLVNEFFIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
g652          GLVNEFFIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
              190     200     210     220     230     240

              250     260     270     280     290     300
m652.pep      LLVKVNQIGTLETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
g652          LLVKVNQIGTLETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
              250     260     270     280     290     300

              310     320     330
m652.pep      RSDRMAYNQ LLRIEEELAE AADYPSKAAF YQLGKX
g652          RSDRMAYNQ LLRIEEELAE AAYYPGKAAF YQLGKX
              310     320     330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

```

a652.seq
1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51  GACTTTGGCG GTTCTATGCG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGCGGCG CAGGCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCCGG CTACAAAGCG GGCGAAGACG TATTATTCGG ATTGACTGCG
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCATTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCGCGA ATATCTGGAA GGCCTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GGATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAACTG GCGGCGAAAG TCCAACTCGT
651 TGGCGACGAC CTCTTCGTTA CCAACCGGAA AATCCTTGCC GAAGGCATTG
701 AAAAAGGCGT GGCAACGCA CTATTGGTCA AAGTCAACCA AATCGTACT
751 TTGAGTGAAG CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCGACG GCATGGCGAA ATACAACCAA CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCGCGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2110; ORF 652.a&gt;:

```

a652.pep
1  MIELDGTENK GNLGNATLA VSMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC

```

1038

151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW  
 201 EGWKLLETKL GGVQLVGGD LFTNPKILA EGIEKGVANA LLVKVNOIGT  
 251 LSETLKAVDL AKRNRYSVM SHRSGETEDS TIADLAVATN CMQIKTGSLS  
 301 RSDRMAKYNQ LLRIEELAE AADYPSKAAF YQLGK\*

m652/a652 99.7% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNL	GANATLAVSMAVARAA	EDSGLPLYRYLGGAGPMSL	PVPMNVINGG		
a652	MIELDGTENKGNL	GANATLAVSMAVARAA	EDSGLPLYRYLGGAGPMSL	PVPMNVINGG		
	10	20	30	40	50	60
m652.pep	EHANNSLNIEF	MIMPVGA	KSFREALRCGAE	IFHALKKL	CDSKGFP	TTVGDEGGFAPNLN
a652	EHANNSLNIEF	MIMPVGA	KSFREALRCGAE	IFHALKKL	CDSKGFP	TTVGDEGGFAPNLN
	70	80	90	100	110	120
m652.pep	SHKEALQLMVE	EATAAGYKAG	EDVLFALDCAS	SEFYKDGKYH	LEAEGRSY	TNAEFAEYLE
a652	SHKEALQLMVE	EATAAGYKAG	EDVLFALDCAS	SEFYKDGKYH	LEAEGRSY	TNAEFAEYLE
	130	140	150	160	170	180
m652.pep	GLVNEFFIIS	IEDGMDENDW	EGWKLLTE	KLTKLGG	RVQLVGGD	LFTNPKILAEGIEKGVANA
a652	GLVNEFFIIS	IEDGMDENDW	EGWKLLTE	KLTKLGG	RVQLVGGD	LFTNPKILAEGIEKGVANA
	190	200	210	220	230	240
m652.pep	LLVKVNOIGT	LSETLKAVD	LAKRNRYS	VM SHRSGET	EDSTIADL	AVATNCMQIKTGSLS
a652	LLVKVNOIGT	LSETLKAVD	LAKRNRYS	VM SHRSGET	EDSTIADL	AVATNCMQIKTGSLS
	250	260	270	280	290	300
m652.pep	RSDRMAKYNQ	LLRIEELAE	AADYPSKA	AFYQLGKX		
a652	RSDRMAKYNQ	LLRIEELAE	AADYPSKA	AFYQLGKX		
	310	320	330			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2111>:

g652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACCA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GTGCGGCCGT ACCGAGCGGC GCATCCACCG GTCAGAAAGA AGCTTTGGAA
151 CTTGCGGACG GCGACAAATC CCGCTATTCC GGCAAAGGCG TATTGAAGGC
201 CGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATC GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTGGG TGCGAATGCG ACTTTGGCGG TCTCTATGGC
351 GGTTCACGCG GCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGGGGCGC AGGTCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTCCGCGA AGCGTTGCGC TGCGGTGCGG
551 AAATTTTCCA CGCCTTGAAA AACTGTGCG ACAGTAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AAGCGGCCGA AGCCGCCGGC TACAAGGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGGG AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TACTTGGGAG GCTTGGTTAA CGAATTCCCG ATTATTCCA
851 TTGAAGACGG GATGGACGAA AACGACTGGG AAGGTGGGAA ACTGTGACC
901 GAAAAATTGG GCAAAAAAGT TCAATTGGTC GCGCAGCACT TGTTCGTAAC
951 CAATCCGAAA ATTCTTGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGTGCAA AGTCAACCAA ATCGGTACTT TAAGCGAAAC CCTGAAAGCC
1051 GTCGATCTGG CAAAATGCAA CCGCTACGCC AGCGTGATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGTA CCATTGCCGA CTGGCAGTC GCCACCAACT
1151 GTATGCAGAT TAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCTACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2112; ORF 652-1.ng>:

## g652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYSGKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNATLAVSMAVAR AAAEDSGLPL YRYLGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAAEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMD E NDWEGWKLLT
301 EKLGGKQVLV GDDLFTVNP ILAEGIEKGV ANALLVKVNO IGTLSSETLKA
351 VDLAKNRNYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAAYPGK AAFYQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

## m652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTGCCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCCGCGAG GCGACAAATC CCGTTATTCC GGCAAGGGCG TATTGAAGGC
201 GGTGCAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTGGCGG TTTCTATGGC
351 GGTGTCACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGGCG AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGCGGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCGAAAT CTTCCCGCGA AGCGTTGCGC TGCGGTGCGG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGCAAGG CTTCCGAGC
601 ACAGTCGGCG ACGAAGGCGG TTTGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCCGGC TACAAAGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGGCAAT ACCACTTGGG AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGATTCCCC ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAAATCG GCGGTAGAGT TCAATTGGTT GCGGACGACT TGTTCGTAAC
951 CAATCCAAAA ATCTTGGCCG AAGGCATCGA AAAAGGGCTA GCAACCGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGCGAGAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

## m652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYSGKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNATLAVSMAVAR AAAEDSGLPL YRYLGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMD E NDWEGWKLLT
301 EKLGGKQVLV GDDLFTVNP ILAEGIEKGV ANALLVKVNO IGTLSSETLKA
351 VDLAKNRNYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEADYPSK AAFYQLGK*

```

m652-1/g652-1 98.6% identity in 428 aa overlap

	10	20	30	40	50	60
m652-1	MSAIVDIFAREILDSRGNPTVECDVLESVMGRAAVPSGASTGQKEALELRDGDKSRYSGKGVLKAVEH VNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR					
g652-1	MSAIVDIFAREILDSRGNPTVECDVLESVMGRAAVPSGASTGQKEALELRDGDKSRYSGKGVLKAVEH VNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652-1	GKGVLKAVEH VNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR					
g652-1	GKGVLKAVEH VNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652-1	AAAEDSGLPLYRYLGAGPM SLPVPMNVI NGGEHANNSL NIQEFMIMPV GAKSFREALR					
g652-1	AAAEDSGLPLYRYLGAGPM SLPVPMNVI NGGEHANNSL NIQEFMIMPV GAKSFREALR					
	130	140	150	160	170	180

1040

```

      190      200      210      220      230      240
m652-1  CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
      |||||
g652-1  CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEAAEAAGYKAGEDVLFA
      190      200      210      220      230      240

      250      260      270      280      290      300
m652-1  LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFFIISIEDGMDENDWEGWKLLT
      |||||
g652-1  LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFFIISIEDGMDENDWEGWKLLT
      250      260      270      280      290      300

      310      320      330      340      350      360
m652-1  EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKNRNYA
      |||||
g652-1  EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKNRNYA
      310      320      330      340      350      360

      370      380      390      400      410      420
m652-1  SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEADYPSK
      |||||
g652-1  SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEADYPSK
      370      380      390      400      410      420

      429
m652-1  AAFYQLGKX
      |||||
g652-1  AAFYQLGKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2115>:

```

a652-1.seq
1  ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACCA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAGA GGCTTTGGAA
151 CTTCGCGACG GCGACAAATC CCGTTATTCG GGCAAGGGCG TATTGAAGGC
201 GGTGGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAAATCA TGATCGAATT GGACGGTACT
301 GAAACAAAG GCAATTTGGG TGCGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTGACGCG GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AAGCGGCGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTCGCCGCA AGCGTTGCCG TCGGTTGCCG
551 AAATTTTCCA CGCCTTGAAA AAAGTGTGCG ACAGCAAAGG CTTCGCCGAC
601 ACAGTCGCGC ACGAAGGCGG TTTCGCCCGC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTGC AGGCGACCGA AGCCGCGCGC TACAAAGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCGCC ATCATCTCCA
851 TCGAAGACGG GATGGATGAA AACGACTGGG AAGGCTGAA ACTGCTGACC
901 GAAAAAAGTG GCGGCAAAGT CCAACTCGTT GCGGACGACC TCTTCGTTAC
951 CAACCCGAAA ATCCTTGCCG AAGGCATTGA AAAAGCGGTG GCAAACGCAC
1001 TATTGGTCAA AGTCAACCAA ATCGGTACTT TGAGTGAAAC CCTGAAAGCC
1051 GTCGACTTAG CCAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTGGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAA GCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2116; ORF 652-1.a>:

```

a652-1.pep
1  MSAIVDIFAR EILDSRGNPT VECDEVLES VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGA NA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIEQFMIMPV GAKSFREALR CGAEIFHALK KLDCSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFF IISIEDGMDE NDWEGWKLLT
301 EKLGGKVQLV GDDLFTNPK ILAEGIEKGV ANALLVKVNQ IGTLSLTKA
351 VDLAKNRNYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEADYPSK AAFYQLGK*

```

m652-1/a652-1 99.8% identity in 428 aa overlap

10 20 30 40 50 60

1041

```

m652-1      MSAIVDIFAREILDSRGNPTVECDVLESVGMGRAAVPSGASTGQKEALELRDGDKSRY
a652-1      MSAIVDIFAREILDSRGNPTVECDVLESVGMGRAAVPSGASTGQKEALELRDGDKSRY
              10      20      30      40      50      60

              70      80      90      100     110     120
m652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
a652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
              70      80      90      100     110     120

              130     140     150     160     170     180
m652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMEVGA
a652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMEVGA
              130     140     150     160     170     180

              190     200     210     220     230     240
m652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAG
a652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAG
              190     200     210     220     230     240

              250     260     270     280     290     300
m652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPPIISIEDGMDENDW
a652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPPIISIEDGMDENDW
              250     260     270     280     290     300

              310     320     330     340     350     360
m652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNIQIGTLSETLKAVDLA
a652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNIQIGTLSETLKAVDLA
              310     320     330     340     350     360

              370     380     390     400     410     420
m652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEADY
a652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEADY
              370     380     390     400     410     420

              429
m652-1      AAFYQLGKK
a652-1      AAFYQLGKK

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

```

g653.seq
1  ATGGCGGcgccg aaccgatgag gAtgccggag gtaAcgtaCG GTTTTCCGG
51  ATCGTTCGGG ATGGCGTTT TGTtgacggT GATGTGCGCt ttgccccAAG
101 CGGCTtcggc ggctttgcCg gtgaTTTCA TCGGTTGCAG GtcgacgaGG
151 AAaactgTGC TTTCGGTGC GCGGAAacg atgcgCaaac cgCGTttaac
201 caactcttcc gcCATGACGG CAGCATTGAT TTCACTTGT TTTGCGTATT
251 GTTTGAactC GGGTTGcaac gcttctTTAA acgctACGGC TttgGCGGCG
301 ATAACGTgca tcaACGGAcc gCCTTGcAGG CTTGGGAAGA TGGAAGAGTT
351 CAGCGCTTT TCGTGGGTAT TGTCACGGCA CAAATCACA CCGCCGCGAG
401 GGCCGCGTAG GGTTTGTGG GTGGTAGTgG ttACgaaGTc GCAGAatggc
451 ACGGGgttag gatattcgcc gccGGCAACC AgtccgGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

```

g653.pep
1  MAAPPMRME VTYGFSGSFG MAFLLTVMCA LPKAASALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNS AMTAAIFTC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGKMEEFSAF SWVLSRHKIT PPRGPRRVLW VVVVTKSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

```

m653.seq
1  ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51  ATCGTTCGGA ATGGCGTTT TGTGACGGT GATGTGCGCT TTGCCAAAG
101 CGGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCACGAGG

```

1042

```

151 AAAACGTGGC TTTGGGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCATTGT TTTGCGTATT
251 GTTTGAACTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGACC GCCTTGCAGG CTTGGGAAGA TGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTGCGGCA CAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TCACGAAGTC GCAGAACGGC
451 ACCGGGTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2120; ORF 653>:

```

m653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWLSRHKIT PPRGPRRLW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/g653 96.9% identity in 163 aa overlap

	10	20	30	40	50	60
m653.pep	MAAEPMRMPEVTGKFSGSFGMAFLLTMCAALPKAASAALPVIFIGCRSTRKTWLSVRPET					
g653	MAAEPMRMPEVTYGFSGSFGMAFLLTMCAALPKAASAALPVIFIGCRSTRKTWLSVRPET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m653.pep	MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF					
g653	MRKPRLTNSSAMTAALIFTCFAYCLNSGCNASLNATALAAITCINGPPCRLGKMEEFSAF					
	70	80	90	100	110	120
	130	140	150	160		
m653.pep	SWLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX					
g653	SWLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATSPAX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2121>:

```

a653.seq
1  ATGCGCGCGG AACGATGCG GATGCCGAG GTAACGAAGG GTTTTCCGG
51  ATCATTCCGG ATGCGGTTTT TGTGACAGT GATGTGCGCT TTGCCCAAAG
101 CAGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCAACGAGG
151 AAAACGTGGC TTTGGGTGCG GCCGGAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCATTGT TTTGCGTATT
251 GTTTGAACTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGGCC ACCTTGCAGG CTTGGGAAGA TGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTGCGGCA CAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TAACGAAGTC GCAGAACGGC
451 ACGGGATTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2122; ORF 653.a>:

```

a653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWLSRHKIT PPRGPRRLW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/a653 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m653.pep	MAAEPMRMPEVTGKFSGSFGMAFLLTMCAALPKAASAALPVIFIGCRSTRKTWLSVRPET					
a653	MAAEPMRMPEVTGKFSGSFGMAFLLTMCAALPKAASAALPVIFIGCRSTRKTWLSVRPET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m653.pep	MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF					
a653	MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF					
	70	80	90	100	110	120
	130	140	150	160		
m653.pep	SWLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX					
a653	SWLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX					

130                      140                      150                      160

g656.seq

```
1 ATGCCGCGTT TCTCCGGTTC GATTTCCTCG ATGATTTCCTCA TCGCGCGGAC
51 TTTtggcGCG CCGGAGAGTG TGCcggcagg gAAGGTGGCG GCGAGGATGT
101 CCATATTGGT AACGCCCTCT TTCAAACAGc ctTCGACGTT GGAACGATG
151 TGCATCACAT GGGAGTATTT TTCATACACC ATTTTGTCCG TGACTTTGAC
201 TTCGCTGTT TTGCTGATGC GTCGACATC GTTGGCGCCC AAATCGATAA
251 GCATAACGTG TTCGGCgatt TCTTTGGCGT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGCT CTTCCGGCGG GGTTTTGGCG CGCAGGCCGCG TGCCGGCGAT
351 GGGGCGGAGC ATGACGTcat CGCGTTCGCG CGGGAGCÄGG ATTTCGGGCG
401 AGGAACCGAC GATGTGGAAT TCCGGCAAAAT CGTAG
```

g656.pep  
1 MPRFSGSISS MISIARTFGA PESVPAGKVA ARMSILVTPS FKQPSTLETM  
51 CITWEYFSIT ILSVLTSPV LLMRPTSLRP KSISITCSAI SLASLNKSCS  
101 LARSSAGVLP RRRVPMGRT MTSSRSRRR ISGEEPTMWK SPKS\*

```
m656.seq
1  ATGCCGCGTT  TGCTCGGTTT  GACTTCTTCG  ATGATTTCCA  TGCGCGGAC
51  TTTGGGTGCG  CCGAGAGAGT  TGCCGGCAGG  GAAGGTAGCG  GCGAGGATGT
101 CCATGTTGGT  CATGCCGTCT  TTCAGACGGC  CTTCCAGCTT  GGAAACGATG
151 TGCATTACAT  GGGAGTATTT  TTCATACACC  ATTTTGTGCG  TAACTTTGAC
201 TTCGCCGGTT  TTA CTGATGC  GGCCGACGTC  GTTGCCTCCT  AAGTCAATCA
251 ACATGACGTG  TTCGGCGATT  TCTTTGGCAT  CGCTTAACAA  ATCTTGTTCT
301 TTGGCAAGGT  CTTCGGCGGG  GGTTTTGCCG  CGCAGGCGCG  TGCCGGCGAT
351 GGGGCGGACG  ATAACGTCGT  TGCCTTCGCG  TCGGACGAGG  ATTTGGGGCG
401 AGGAGCCGAC  GATGTGAAAA  TCGCCGAAAT  CGTAG
```

m656.pep  
1 MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRPSTLETM  
51 CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KsinMTCSAI SLASLNKSCS  
101 LARSSAGVLP RRRVPA MGRT ITSLSR RRT R ISGEPTMWK SPKS\*

Homology with a predicted ORF from *N. gonorrhoeae*

m656/g656 91.0% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLG	STSSM	ISMART	LGAPES	VPAGK	VAARMS
	:	:	:	:	:	:
g656	MPRFSG	SISSM	ISIART	TFGAPES	VPAGK	VAAARMS
	10	20	30	40	50	60
	70	80	90	100	110	120
m656.pep	ILSVTL	TSPVLL	MRPTSL	RPKSIN	MTCSAIS	LASLNK
	:	:	:	:	:	:
g656	ILSVTL	TSPVLL	MRPTSL	RPKSI	SITCSAIS	LASLNK
	70	80	90	100	110	120
	130	140				
m656.pep	ITSLRS	RRTRIS	GEEPTM	MWKSP	KPSKX	
	:	:	:	:	:	
g656	MTSSRS	RRTRIS	GEEPTM	MWKSP	KPSKX	
	130	140				

1044

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2127>:

```
a656.seq
1  ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCTA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTCGACGTT GGAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCGG TAACTTTGAC
201 TTCGCCGTT TACTGTATGC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTGCGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACATCGT CGCGTTCGCG GCGGACGAGG ATTTCGGGCG
401 AGGAGCCGAC GATGTGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2128; ORF 656.a>:

```
a656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP K SINMTCSAI SLASLNKSCS
101 LARSAGVLP RRRVPAMGRT MTSSRSRRT R ISGEEPTMWK SPKS*
```

m656/a656 98.6% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRPSTLETMCITWEYFSIT					
a656.	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRPSTLETMCITWEYFSIT					
	10	20	30	40	50	60
m656.pep	ILSVTLTSPVLLMRPTSLRPSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
a656	ILSVTLTSPVLLMRPTSLRPSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLRPSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
a656	ILSVTLTSPVLLMRPTSLRPSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
	130	140				
m656.pep	ITSLRSRRT R ISGEEPTMWKSPKSX					
a656	MTSSRSRRT R ISGEEPTMWKSPKSX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2129>:

```
g657.seq
1  ATGAACACAC CCCCCATCCT TCCTCCCGCC ATGCTCGGCA TCCTCGGCGG
51  CGGACAATTa ggcagAATGT TTGCCGTGCG CGCTAAACC ATGGGCTACA
101 AAGTAACCGT TCTCGATCCC GACCCGAATG CGCCGGCGGC GGAATTGCGC
151 GACCGCCATT TGTGCGCGCC GTTGTACGAC CGGGCCGCGT TGGACGAATT
201 GGCAAAATGC GCGCGGTTa cgACCGAATT TGAAAacgtc aaTGCCGACG
251 CGATGCGCTC TCTGGCAAAG CATACCAACG TTTCCCCCAG CGGCGACTGC
301 GTGTCCATTG CACAAAACCG CATTCAGGAA AAAGCGTGGA TACGCAAAGC
351 AGGCTTGCAA ACCGCGCCGT ATCAGGCGGT TTGCAAGGCC GAAGACATTA
401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
451 GGCTACGACG GCAAAGGTCA AATCCGCGTC AAAACGTTGG ACGAACTCAA
501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTTG GAAAAAATGG
551 TGGACTTGCG CGGCGAGATT TCCGTGATCG TATGCCGTCT GAACGATGAA
601 AACGTGCAAA CTTTCGACCC CGCCGAAAAC ATCCACGAAA ACGGCATCTT
651 GGCTTattc ATCGTCcccg CGCGGCTGAG TGCCGACGTG CAGCAACAGG
701 CGCGGCAGAC GCGCAACGc tTGGCGGACG AATTGGATTA TGTCGGCgta
751 TTGGCGGTAG AAATGTTTGT TGTGCGCGAC ACACATGAAT TGCTCGTCAA
801 TGAACCGGCC CGCGCACGC ACAATTCCGG CCACCATACG ATAGATGCCT
851 GCGCCGACAG CAGTTCCAA CAGCAGGTAC GCATTATGTG CAAcctGCCG
901 cccGccgACA CCAAATTATT aTCCCTtgC TGTATGGCGA ATATTTTGg
951 CGACGTTTGG CAGGAAGATG GCGGCGAACC GGATTGGCTG CCGTTGCAAA
1001 GCCGGCCGAA TGCACACCTG CACCTATACG GAAAAAAAC CGCACAGAAA
1051 GGTCCGAAAA TGGGACACTT TaccgTTTTG ACCACCGATT CGGACaccgC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2130; ORF 657.ng>:



1045

g657.pap

1	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA
51	DRHLCAPFDD	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC
101	VSIAQNRIQE	KAWIRKAGLQ	TAPYQAVCKA	EDITEASAQF	LPGILKTATL
151	GYDGKGQIRV	KTLDLKAFF	AEHGGVDCVL	EKMVDLRGEI	SVIVCRLNDE
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQQARQTAQR	LADELDYVGV

251 LAVEMFVVGD THELLVNETA PRTHNSGHHT IDACAAQDQF QQVRIMCNLF  
301 PADTKLLSPC CMANILGDVW QEDGGEPDWL PLQSRPNAHL HLYGKKTAAQK  
351 GRKMGHFTVL TTDSDTAFOE AKKLHOSL\*

m657.seq

1	ATGAAAAACA	TATCTCTTTC	TCCGCCCGCC	ATGCTTGGCA	TCTCTCGGCG
51	CGGACAATTA	GGCAGAAATG	TTACCGTTGC	CGCCAAACC	ATGGGCTACA
101	AAGTAAACCG	TCTGCACCCC	GATCCGGAGC	CGCCGGCAGC	AGAATTTTGCC
151	GACCGCCATT	TGTGCGGCGC	GTTTAACGAC	CAAGCTGCTT	TGGACGAATT
201	GGCAAAATGC	GCGGCGGTGA	CCATTGAATT	TGAAAACGTC	AATGCCGATG
251	CGATGCGCTT	TTTGGCAAAA	CATACCAATG	TTTCCCCTAG	CGGCGATTGT
301	GTGGCGATTG	CACAAAACCG	CATTCAAGAA	AAGCGATTGA	TACGCAAAAGC
351	GGGATTGCAA	ACCGCGCCGT	ATCAAGTGGT	TTGTAAGGCT	GAAGACATCA
401	CTGAAGCAAG	CGCGCAATTT	TGCGCCGCGA	TCTGAAAAAC	GGCTACGTTA
451	GGCTACGACG	GCAAAGGTCA	AATCCGCGTA	AAAACATTGG	TGGAACTCAA
501	AGCCGCGTTT	GCCGAACACG	GCGGCGTGGA	TTGCGTTTTG	GA AAAAATGG
551	TGGATTTGCG	CAGTGAATTT	TCCGTAAATG	TATGCCGTTT	GAACAATGAC
601	AACGTGCAAA	CTTTGCAACC	TGCCGAAAAC	ATCCACGAAA	ACGGCTACTT
651	GGCTTATTCC	ATCGTCCCCG	CGCGACTGAG	TGCCACGAGT	CAGCAACAGG
701	CGCGGCAGAT	GGCGCAACGC	TTGGCGGACG	AATTGGATTA	TGTTCGGCGTA
751	TTGGCGGTAG	AAATGTTTGT	TGTCCGTGAC	ACGCATGAAT	TGGTCGTCAA
801	CGAAATCGCC	CCGCGCCCCG	ACAATTCGGG	ACACCATACG	ATAGATGCCT
851	GCGCAGCAGA	CAGTTCCAG	CAGCAGGTAC	GCATTATGTG	CAACCTGCCG
901	CCTGCCGATA	CCAAATTACT	GAGTCTTTGC	TGATGGCAA	ATATTTTGGG
951	CGACGTTTGG	CAGGAAGACG	GCGGCGAACC	GGATTGGCTG	CCCTTGCAAA
1001	GCCATCCGAA	TGCACACCTG	CACCTTTACG	GCAAAAAAAC	CGCGCACAAA
1051	GGGCGGAAAA	TGGGCACTT	TACCGTTTTA	ACCACCGATT	CGGACACCCG
1101	ATTTCAAGAA	GCAAAAAAAC	TGCATTCAGT	CCTATAA	

m657.pcp

1	MKNISLSPPA	MLGILGGGQL	GRMFTVAAKT	MGYKVTVLDP	DPDAPAAEFA
51	DRHLCAQRIED	QAALDELAKC	AAVTTEFENV	NADAMRFLAK	HTNVSPSGDC
101	VAIAQNRIQE	KAWIRKAGLO	TAPYQVVCKA	EDITESAQF	LPGILKTATL
151	GYDGGKQIRV	KTLDLKAFAF	AEHGGVDVCL	EKMVDLRSEI	SIVVLCRLND
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQQARQMAQR	LADEL DYGVV
251	LAVEMFVVGD	THELVVNETA	PRPHNSGHTH	IDACAADQFQ	QQVRIMCNLP
301	PADTKLLSSC	CMANILGDVW	QDGGEGDHWL	PLQSHPNAHL	HLYGKKTAAHK
351	GRKMGHFTVL	TTDSDTAFQE	AKKLHSL*		

### Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m657.pep	MKNISLSP	PAMLGIL	GGGQLGR	MFTVAAK	TMGYKVT	VLDPDPD
	APAAEFAD	RHLCAP	FND			
	::	:				
g657	MNTPPIL	PPAMLGIL	GGGQLGR	MFVA	AAKTMGYK	VTVLDP
	DPNAPAA	EFADRHLC	APFND			
	10	20	30	40	50	60
	70	80	90	100	110	120
m657.pep	QAALDE	LAKCAA	VTTEF	ENVNAD	AMRFLA	KHTNV
	SPSGDC	VAIAQ	NRIQE	KAWIR	KAGLQ	
	:					
g657	RAALDE	LAKCAA	VTTEF	ENVNAD	AMRSLA	KHTNV
	SPSGDC	VSIAQ	NRIQE	KAWIR	KAGLQ	
	70	80	90	100	110	120
	130	140	150	160	170	180
m657.pep	TAPYQV	VCKAE	DITEA	SAQFLP	GILKTAT	LGYDGK
	QIRVKT	LDELKA	AAFAE	HGGVDC	VL	
		:				
g657	TAPYQV	CKAE	DITEA	SAQFLP	GILKTAT	LGYDGK
	QIRVKT	LDELKA	AAFAE	HGGVDC	VL	
	130	140	150	160	170	180

1047

	190	200	210	220	230	240
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQARQMAQR					
g657	EKMVDLRGEISVIVCRLNDENVQTFDPAENIHENGILAYSIVPARLSADVQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657.pep	LADEL DYVGV LAVEMFVVGDTHELVVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP					
g657	LADEL DYVGV LAVEMFVVGDTHELVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSRPNAHLHLYGKKTAAKGRKMGHFTVL					
g657	PADTKLLSPCCMANILGDVWQEDGGEPDWLPLQSRPNAHLHLYGKKTAAKGRKMGHFTVL					
	310	320	330	340	350	360
	370	379				
m657.pep	TTDSDTAFQEAKKLHQSXLX					
g657	TTDSDTAFQEAKKLHQSXLX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

```

a657.seq
1  ATGAAAAACA TATCTCTTTC TCCGCCGCC ATGCTCGGCA TTCTTGCGCG
51  CGGACAATTA GGCAGAAATGT TACTGTTGC TGCCAAAACC ATGGGCTACA
101 AAGTAACCGT ACTCGATCCC AACCCGAATG CGCCGGCAGC GGAATTTGCC
151 GACCGCCATT TGTGTGCGCC GTTTGACAAC CAAACCGCTT TGGAGAATTT
201 GGCAAAATGT GCGGCTGTTA CGACCGAGTT CGAAAACGTC AATGCCGATG
251 CGATGCGTTT TCTCGCCAAA CATACCAATG TTTCCCCAG CGGCGACTGC
301 GTTGCCATCG CGCAAAACCG CATTCAAGAA AAGGCATGGA TACGCAAAGC
351 AGGCCTGCAA ACCGCGCCGT ATCAAGCAAT TTGCAAAGCC GAAGACATCA
401 CTGAAGAAAG CATACAATTT CTGCCCGGCA TCCTGAAAAC CGCTACATTG
451 GGCTATGACG GCAAAAGCCA AATCCGCGTC AAAACGGTGG ATGAACTCAA
501 AGCCGCGTTT GCCGAACACC GCGGCGTGGA TTGCGTTTTC GAAAAAATGG
551 TGGACTTGCG CGGCGAAATT TCCGTTATCG TATGCCGCTCT GAACAATGAC
601 AACGTGCAAA CTTTCGATCC TGCCGAAAAC ATTCACGAAA ACGGTATCCT
651 CGCTACTCC ATCGTCCAG CCCGACTGAG TGCCGACATT CAGCAACAGG
701 CGCGACAAAT GGCGCAGCGT TTGGCCGATG AATTGAACTA CGTCGGCGTA
751 TTGGCGGTAG AAATGTTTGT TGTGCGCGAC ACGCATGAAT TGGTCGTCAA
801 CGAAATCGCG CCGCGTCCGC ACAATTCCGG CCACCATAAC GTCGACGCCT
851 GCGCGGCAGA CCAATTCCAG CAACAGGTCC GCCTGATGTG CAACCTGCCA
901 CCTGCTGACA CCAAATGCT GAGTTCTTGC TGTATGGCGA ATATTTTGGG
951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGTTT CCCCTGCAAA
1001 GCGGCGCGGA CGCGCACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
1051 GGGCGGAAAA TGGGACACTT TACCATTTTA AGCACCGATT CGGACACCGC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

```

a657.pep
1  MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP NPNAPAAEFA
51  DRHLCAPFDN QTALEELAKC AAVTTEFENV NADAMRFLAK HTNVSFSGDC
101 VAIAQNRIQE KAWIRKAGLQ TAPYQAICKA EDITEESIQF LPGILKTATL
151 GYDGKGQIRV KTVDELKAAF AEHRGVDCVL EKMVDLRGEI SVIVCRLNND
201 NVQTFDPAEN IHENGILAYS IVPARLSADI QQARQMAQR LADELNYVG
251 LAVEMFVVGDTHELVVNEIA PRPHNSGHHT VDACAADQFQ QQVRLMCNLP
301 PADTKLLSSC CMANILGDVW QEDGGEPDWL PLQSRPDAHL HLYGKKTAAK
351 GRKMGHFTIL STDSDTAFQE AKKLHQSXL*

```

m657/a657 94.2% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPAPAAEFADRHLCAFPND					

[illegible]

g658.seq

This corresponds to the amino acid sequence <SEQ ID 2136; ORF 658.ng>:

g658 . pep

1 MVAGIVRARG GFIDEQFMCV ADNKHFYRQY ADIIQFVRQA LRRLPRLLLH  
51 VGTQPRGDDG ISQDAVEVDV FGGVEGLHVF IVQTAYDHGN LAAQVHHFFQ

1049

```

101 NAIHAAVFGK RGFEFVQRF ADLTFVVAQ RSRFQDAGQK LRACFSNVFG
151 LANRLIRRLG QACFAYPRFF LNAVLCNGHA VAAGGNVGM LQRAHRVIGID
201 VFKFGRNRRR FCQFVQRPV VKRRAQMAVG KFRRRRIRVG IENGYFVAHG
251 FSGNGKHSAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2137>:

```

m658.seq
1 ATGGTGTCCG GAATTGTGCG GCGCGGGGCG GATTCGTTG ACGACCAATT
51 CATGCGTGTC ACCGACAACA AACATTCTA CCGCCAATAC GCCGACATAA
101 TCCAATTTCGT CCGCCAAGCG TTGCGCCATC TGCCGCGCCT GTTGCTGCAC
151 GTCGGCACTC AGTCGCGCGG GGACGATGGA ATAAGCCAAG ATGCCGTTTT
201 CGTGGATGTT TTCGGCAGGG TCGAAAGTTT GCACGTTGTC ATTGTTCAAA
251 CCGCATACGA TTACGGAAAT TTCACTGCGC AAATCCACCA TTTTTCCTAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAAA CGCGGCTTTG AGTTCATCCA
351 ATGTTTTTAC GCGGATTGGA CCTTGCCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CCGGCAAAA TTGCGCGCTT GCTTCAGTGA TGTCTTCAGC
451 CTTACAAACC ACTTGATACG GCGCGGTTG CAATCCCGCT TTGCGTATCC
501 ATGCTTTTTC CTGAATGCGG TTTGTGCAA TCGCCACACA ATCGCCGCTA
551 GGGGAAACAT TGGTATGTTT TGCCAAAAG CGCATCGCAT CCGCATTGAC
601 GTTTTCAAAT TCAGTGGTCA CCGCCGCGCA TTTTGCCAAT TCGTCCAAAG
651 CAGCTTGGTC GTTAAACGGC GCGCACAAAT GCGCGTCGGC AAATTCTGCT
701 GCGGCGCGT CCGGATCGGG GTCGAGAACG GTTACTTTGT AGCCCATGCT
751 TTTGCGGCA ACGGTAAACA TTCTGCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2138; ORF 658>:

```

m658.pep
1 MVSGIVRARG DFVDDQFMRV TDNKHFYROY ADIIQFVRQA LAHLPRLLLH
51 VGTQSRGDDG ISQDAVFVDV FGRVESLHV IVQTAYDYG NFTAQIHFFQ
101 NAIHAAVFGK RGFEFIQCFY ADLTFVVAQ RSRFQDAGQK LRACFSDVFS
151 LTNHLIRRLG QSRFAYPCLF LNAVLCNRHT IAARGNIGMF CQKAHRIGID
201 VFKFSGHRRR FCQFVQSSLV VKRRAQMAVG KFCCRRVRIG VENGYFVAHG
251 FGGNGKHSAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m658/g658 82.2% identity in 259 aa overlap

	10	20	30	40	50	60
m658.pep	MVSGIVRARGDFVDDQFMRVTDNKHFYROYADIIQFVRQALRHLPRLLLHVGTQSRGDDG					
g658	MVAGIVRARGGFIDEQFMCVADNKHFYROYADIIQFVRQALRRLPRLLLHVGTQPRGDDG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m658.pep	ISQDAVFVDVFGGRVESLHVIVQTAYDYG NFTAQIHFFQNAIHAAVFGKRGFEFIQCFY					
g658	ISQDAVFVDVFGGVEGLHVFIVQTAYDHGNLAAQVHFFQNAIHAAVFGKRGFEFVQRF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m658.pep	ADLTFVVAQRSRFQDAGQKLRACFSDFSLTNHLIRRLGQSRFAYPCLFLNAVLCNRHT					
g658	ADLTFVVAQRSRFQDAGQKLRACFSNVFGLANRLIRRLGQACFAYPRFFLNAVLCNGHA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m658.pep	IAARGNIGMFCQKAHRIGIDVFKFSGHRRAFQCFVQSSLVVKRRAQMAVGKFCCRRVRIG					
g658	VAAGGNVGM LQRAHRVIGIDVFKFGRNRRAFQCFVQRPVVKRRAQMAVGKFRRRRIRVG					
	190	200	210	220	230	240
	250	260				
m658.pep	VENGYFVAHGFSGNGKHSAX					

1050

g658  
 :|||||||:|||||||  
 IENGYFVAHGFGNGKHSAX  
 250 260

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2139>:

a658.seq  
 1 ATGGTGGCCG GAATTGTGCG GACGCGGCGC GATTTCGTTG ACGACCAATT  
 51 CATGCGTGTC GCCGACAACA AACATTTCTA CCGCCAATAC GCCGACGTAG  
 101 TTCAATTCAT CGGCCAAACG CTGCGCCATT TGTCGCGCCT GTTGCTGAAT  
 151 GTCGGCACTC AGTCGGGCTG GGACGATGGA GTAGGCGAGG ATACCGTTTT  
 201 CGTGAATGTT TTCGGCAGGA TCGAAAGTTT GCACGTTGTC ATTGTTTCAGA  
 251 CGGCATACGA TAACGGAAT TTCGCCGCGC AAGTCCACCA TTTTTCCTAA  
 301 AACGCAATCC ACGCGCGCGT GTTCGGCAAA CGCGGCTTTG AGTTCATCCA  
 351 CCCTTTTGAC GCGGATTTGG CCTTTGCCGT CATAGCCCAA TGTCGCGTT  
 401 TTCAGGATGC CGGGCAGAAA TTGTATGCTT TCTTCAGTGA TGTCTTCGGC  
 451 TTTGCAAAAT GCTTGATACG GCGCGGTTTG CAGGCCTGCT TTGCGTATCC  
 501 ATGCCTTTTC CTGAATGCGG TTTTGCGCGA TGGCAACGCA GTCGCGCGTG  
 551 GGGGAAACAT TGGTATGTTT GGCGAGAAAA CGCATCGCAT CGGCATTGAC  
 601 GTTTTCGAAC TCGGTCGTAA CAGCCGCACA TTTTGCCAA TCTTCCAAAG  
 651 CGGTTTGTT GTCAAACGCG GCACACAAAT GGCGGTCGGC AAATTCGCGT  
 701 GCCGGCGCAT TCGGTTGGG ATCGAGTACG GTTACTTTGT AGCCCATGGT  
 751 TTTGGCAGCA ACAGTAAACA TTCTGCCTAA

This corresponds to the amino acid sequence <SEQ ID 2140; ORF 658.a>:

a658.pep  
 1 MVAGIVRTRR DFVDDQFMRV ADNKHFYRQY ADVVQFIGQT LRHLRLLLN  
 51 VGTQSGWDDG VGEDTVFVNV FGRIESLHV IVQTAYDNGN FAAQVHHFFQ  
 101 NAIHAAVFGK RGFEFIHRFD ADLAFAVIAQ CSGFQDAGQK LYAFFSDVFG  
 151 FANCLIRRLG QACFAYPCLF LNAVLRDNGA VAAGGNIGMF GEKTHRIGID  
 201 VFELGRNSRT FCQFFQSGLV VKRRTQMAVG KFCRRIRRVG IEYGYFVAHG  
 251 FGSNSKHS\*

m658/a658 75.3% identity in 259 aa overlap

	10	20	30	40	50	60
m658.pep	MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLLVGTQSRGDDG					
a658	:    :       :     :     :    : : :            :					
	10	20	30	40	50	60
	70	80	90	100	110	120
m658.pep	ISQDAVFVDVFGRVESLHVIVQTAYDNGNFTAQIHFFQNAIHAAVFGKRGFEFIQCFY					
a658	:::    :    :     :          : : :       :     :     :					
	70	80	90	100	110	120
	130	140	150	160	170	180
m658.pep	ADLTFAVVAQRSRFQDAGQKLRACFSDVFSLTNHLIRRLGQSRFAYPCLFLNAVLCNRHT					
a658	:    :               :       :      :      :       : ::					
	130	140	150	160	170	180
	190	200	210	220	230	240
m658.pep	IAARGNIGMFCQKAHRIGIDVFKFSGHRRAFQCFVQSSLVVKRRQMAVGKFCRRVRIG					
a658	:         :  :     : : :    :       :     :          : :					
	190	200	210	220	230	240
	250	260				
m658.pep	VENGYFVAHGFGGNGKHSAX					
a658	:       : :					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2141>:

1051

```

g661.seq
1  ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GGCGGGCATT GCGACAAAC CCTTCGCCG CCTCTGTCGG GCGTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGCCA GCGATCCGAC GCTCAGGAAT
151 ACCGGA AAAA CCTgcaccg cagtgaTTTt gccgatgaag gCGGCATCGT
201 TGCCGTGCAG ATTGCCGGCA GCGACCcga acaGATGGCG Gatgcggcgc
251 gttacAACGT CGGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC
301 ccgcccgaGA AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA
351 CGAGccgctg gttgcCgcca tTTtgaggc ggtggtcAAG GCGGCGGcg
401 TACCCGTAC cctCAAAACc cgtTtggtt ggcacgacga cgatcaaac
451 ctgcCcgccg tcgccaaaat cgccgaagat tgcggcattg ccgccCttgc
501 cgttccacgg gcgCGCgcgC ACGCAAATGT ACAAAGGCGA GGCgcGTTAC
551 Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCGG cctGggtCAA
601 CCGCGACATC actTCgcccgc AAAAAGCCGC CGcgcTCTC AAACAAACCG
651 CCGCCGACGG CATCATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTT
701 TTCCGCGATT TGAAGCATTG TGCCGAACAC GCGGTTTAC CGCTGCCTT
751 GAGTTTGGCA GAATGCAGAG CCGCCATTTT GAACCACATC CGCGCCATGC
801 ACGCGTTTGA TGGTGAGACC GTCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGCGGAAAT GCGGACGGC GAACAGGCGC GGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

```

g661.pep
1  MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN
51  TGKTLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC
101 PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDDQDN
151 LPAVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ
201 RRHHFAAKSR RRPQTNRRRR HHDRARRARQ AVVFPRFEAL CRTRRFTACL
251 EFGRMQSRHF EPHPRHARVL WXDRCARHT QTHRLVHRRN ARRTGAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

```

m661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GGCGGGCATT ACCGACAAAC CGTTCGCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGACCCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTGTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCGCTG GTTGCGCCA TTTTGAAGC CGTCGTCCGT GCGGCAGGCG
401 TACCCGTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCGTCA TCGCCAAAT CGCCGAAGAT TGCGGCATCG CCGCCCTTGC
501 CGTCC.AC GG ACGCACGCGT ACGCAAATGT ACAAAGGCGA AGCGCGTTAC
551 GAACATCATCG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CCGCGACATT ACTTCGCCG AAAAAGCCCA AGCGTCTCTC AAACAAACCG
651 CCGCGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTC
701 TTCCGCGATT TGAACATTA TGCCGAACAC GGTGTTTTGC CGCTGCCTT
751 GAGTTTGGCA GAATGCGCG CCGCTATTTT GAACCACATC CGCGCCATAC
801 ACGCGTTTGA CCGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCGGACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

```

m661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDDHQN
151 LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ
201 RRYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPREFEL CRTRCFACL
251 EFGRMRRRYF EPHPRHTRVL RRHRRCAHRT QTHRLVHRRN ARRTDTS*

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 88.5% identity in 295 aa overlap

1052

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					
g661	MHIGGYFIDNPIALAPMAGIADKPFRLCRAFGAGWAVCEMLASDPTLRNTGKTLHRSDF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m661.pep	ADEGGIVAVQIAGSDPQOMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL					
g661	ADEGGIVAVQIAGSDPEQMADAARYNVGLGAQVIDINMGCPAKKVCNVQAGSALMQDEPL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m661.pep	VAAILEAVVRAAGVPVTLKTRLGWDDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR					
g661	VAAILEAVVKAAGVPVTLKTRLGWDDHQNLPVAKIAEDCGIAALAVPRARAHANVQRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m661.pep	SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRNRRHYDRARRARQAVVLPFRFETL					
g661	GALRTHRRDQKPSHPGLGQRRHHFAAKSRRRPQTNRNRRHHRARRARQAVVFPFRFEAL					
	190	200	210	220	230	240
	250	260	270	280	290	299
m661.pep	CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX					
g661	CRTRRFTACLEFGRMQSRHFEPHPRHARVLWXDRRCAHRTQTHRLVHRRNARRRTGAAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2145>:

```

a661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GCGCGGCATT ACCGACAAAC CGTTCCGCGG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTGACACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGGAGGC GGTGGTCAA GCGGCGGGCG
401 TACCCGTTAC CCTCAAACCC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCCGTC TCGCCAAAT CGCCGAAGAT TGCGGCATTG CCGCCCTTGC
501 CG.TCCACGG ACGCACGCGC ACGCAATGT ACAAAGCGCA AGCGGCTTAC
551 GACCTGATTG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CCGCGACATT ACCTCGCCGC AAAAAGCCCA AGCCGTCCTC AAACAAACCG
651 CCGCAGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG ACCGTGGTTC
701 TTCCGCGATT TGAAACATTA CGCCGAACAC GGTGTTTAC CGCCTGCCTT
751 GAGTTTGCA GAATGTACCG CCACTATTTT GAACCATATC CGAGCCATGC
801 ACGCGTTTTC CGGCGACACC GCCGTGTGTC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2146; ORF 661.a>:

```

a661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVK AAGVPVTLKT RLGWDDHQN
151 LPVIAKIAED CGIAALAXPR THAHANVQRR SGLRPDCRNQ MPSEHPGLGQ
201 RRYLAAKSP SRPQTNRNRR HYDRARRARQ TVVLPFRFETL RRTRCFACIL
251 EFGRMYRHYF EPHPSHARVL RRHRRCAHRT QTHRLVHRRN ARRTDTS*
  
```

m661/a661 94.6% identity in 298 aa overlap

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					



1053

```

a661      MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
           10      20      30      40      50      60

           70      80      90      100     110     120
m661.pep  ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           |||||
a661      ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           70      80      90      100     110     120

           130     140     150     160     170     180
m661.pep  VAAILEAVVRAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
           |||||:|||||
a661      VAAILEAVVKAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
           130     140     150     160     170     180

           190     200     210     220     230     240
m661.pep  SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPFRFETL
           |||||:|||||
a661      SGLRPDCRNQMPSEHPGLGQRRHYLAAKSPSRPQTNRRRRHYDRARRARQTVVLPFRFETL
           190     200     210     220     230     240

           250     260     270     280     290     299
m661.pep  CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
           |||||:|||||
a661      RRTRCFTACLEFGRMYRHYFEPHPSHARVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
           250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

```

g663.seq
1  ATGTGTACCG AGATGAAATT TATATTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCTGATC GGTTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTTGGCA
151 AAATGTTTTT CCGAATGGGA CGAAGAAAAG CGTAAAACCG TGTTGAAACA
201 GCATTTCAAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
251 ACGCGtctGC CAAATGCCTG AAATCGCTGG TCGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GGCGGGGGAA AAAGTCATCA TCCTGTACCC
351 GCACTTTACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATGTCC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAg gccgcaACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAagggctg cgCGCCctcg TCAAACAGTT CCGCAAAAGC AGTGCGCCGT
551 TCCTGTATCT GCCCGATCAG GATTTCGGAC GCAACAATTC GGTTTTGTG
601 GATTTTTCG GCATtcagaC GGCAACGATT ACCGCTTGA GCCGATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCCTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAA TTCTATCCCG CTTGGAAATC CTTCCGAGT
751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCGCTTA TCGAAGAACG
801 CGTGCCGCGA CACCCGGAAC AATATTTCTG GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

```

g663.pep
1  MCTEMKFIFF VLYVLQFLPF ALLHKIAGLI GSLAYLLVKP RRRIGEINLA
51  KCFPEWDEEK RKTVLKQHFH HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALAAGE KVILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGNNNSVFEV
201 DFFGIQTATI TGLSRIAALA NAKVIPAI PV READNTVTLQ FYPWKSFFPS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

```

m663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGACCTGACG GGTTTGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTTGGCA
151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAAACCG TGTTGAAACA

```

1054

```

201 GCATTTCAAA CACATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGGCGCTGC CGGACGTTTG AAATCGCTGG TGGCTACCG CAATAAGCAT
301 TATTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATATCC
401 CGCTGATCAG TATGTATTCC CATCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCGCGATCAG GATTTCCGAC GCAACGATTC GGTTTTTGTG
601 GATTTTTTCG GTATTCAGAC GGCAACGATT ACCGGATTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCTGTC CGCGAGGCAG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTGGAAATC CTTTCCGGGT
751 GAAGACGCGA AAGCCGACGC GCAGCGCATG AACCGTTTGA TCGAAGACAG
801 GGTGCGCGAA CATCCGGAAC AATATTTTGG GCTGCACAAG CGTTTTTAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2150; ORF 663>:

```

m663.pep
1  MCIEMKFIFF VLYVLQFLPF ALLHKIADLT GLLAYLLVKP RRRIGEINLA
51  KCFSEWSEEK RKTVLKQHFK HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDIPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVFV
201 DFFGIQTATI TGLSRIAALA NAKVIPAIPV READNTVTLH FYPAWSFPG
251 EDAKADAQRM NRFIEDRVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m663/g663 94.9% identity in 293 aa overlap

m663.pep	10	20	30	40	50	60
	MCIEMKFIFFVLYVLQFLPFALLHKIADLTGLLAYLLVKPRRRIGEINLAKCFSEWSEEK					
g663	10	20	30	40	50	60
	MCTEMKFIFFVLYVLQFLPFALLHKIAGLIGSLAYLLVKPRRRIGEINLAKCFPEWDEEK					
m663.pep	70	80	90	100	110	120
	RKTVLKQHFKHMAKLMLEYGLYWYAPAGRLKSLVRYRNKHLYLDDALAAGEKVIILYPHFT					
g663	70	80	90	100	110	120
	RKTVLKQHFKHMAKLMLEYGLYWYASAKCLKSLVRYRNKHLYLDDALAAGEKVIILYPHFT					
m663.pep	130	140	150	160	170	180
	AFEMAVYALNQDIPLISMYSHQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS					
g663	130	140	150	160	170	180
	AFEMAVYALNQDVPLISMYSHQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS					
m663.pep	190	200	210	220	230	240
	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALANAKVIPAIPVREADNTVTLH					
g663	190	200	210	220	230	240
	SAPFLYLPDQDFGRNNSVFVDFFGIQTATITGLSRIAALANAKVIPAIPVREADNTVTLQ					
m663.pep	250	260	270	280	290	
	FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX					
g663	250	260	270	280	290	
	FYPAWSFPSDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2151>:

```

a663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAAGT
51  TCTGCCGTTT GCGCTGCTGC ACAAACTTGC TGATCTGACA GGCTTGCTCG
101 CCTACCTTTT GGTCAAACCC CGCCGCCGTA TCGGCGAAAT CAATTGGCA

```

1055

```

151 AAATGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAACCG TGTTGAAACA
201 GCATTTCAAA CATATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCCCG CGGGCGTTTG AAATCACTGG TCGCTACCG CAACAAACAT
301 TATTTGGACG ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAAC GTTTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCCGATCAG GATTTCGGAC GCAACGATTC GGTTTTGTTC
601 GATTTCTTCG GTATTCGGAC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATCCCTGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAT TTCTACCCCTG CTTGGGAATC CTTTCCGAGT
751 GAAGATGCGC AGGCCGACGC GCAGCGCATG AACCGTTTGA TCGAGGAACG
801 CGTGC CGCGAA CATCCGAGC AGTATTTTGT GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:

```

a663.pep
1  MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA
51  KCFPEWDGKK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGNRDSVFV
201 DFFGIRTATI TGLSRIAALA NAKVIPAIPV READNTVT LH FYPAWESFPP
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

m663/a663 96.2% identity in 293 aa overlap

          10      20      30      40      50      60
m663.pep  MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP RRRIGEINLAKCFSEWSEEK
a663      MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP RRRIGEINLAKCFPEWDGKK
          10      20      30      40      50      60

          70      80      90      100     110     120
m663.pep  RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH YLDDALAAGEKVIILYPHFT
a663      RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH YLDDALAAGEKVIILYPHFT
          70      80      90      100     110     120

          130     140     150     160     170     180
m663.pep  AFEMAVYALNQDIPISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS
a663      AFEMAVYALNQDIPISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS
          130     140     150     160     170     180

          190     200     210     220     230     240
m663.pep  SAPFLYLPDQDFGNRDSVFVDFFGIQTATITGLSRIAALANAKVIPAIPVREADNTVT LH
a663      SAPFLYLPDQDFGNRDSVFVDFFGIQTATITGLSRIAALANAKVIPAIPVREADNTVT LH
          190     200     210     220     230     240

          250     260     270     280     290
m663.pep  FYPAWKSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX
a663      FYPAWESFPSEDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX
          250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2153>:

```

g664.seq
1  ATGATACATC CGCACCACCT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51  AGAAATTGTT CATCTCCTCA TAGCTGACgg gCGGCACCGG ATGGGCGGTC
101 GGGCTGCGT CTTGGGGGAA CTGGTCTGG CGCAGCAGGC GGATGTTCTC
151 GATGCGGCGC ACGGCGCGGC CGGCGCGGTC GCCGAAAC TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCTGTGC CGACCACGGA
301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCGAGGA
351 CGAACTTGGT GTTAAAAATG TTCAAACCTT TGTTTTCCAT CGCGCCCAT
401 TTGAAATCGC CTACGGCGAC GACCATGAaa atatccaagt cataTTCaa
451 cCgaagcgc gtttcgtcCc acttcacgc gtTTTTTCAA cgaTTCACG
501 GCAAAGCCGA CCTTGGGTTT GTCCGCTTCG GTGGGTGAAA ACTCGATTTT

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2155>>:

This corresponds to the amino acid sequence <SEQ ID 2156; ORF 664>:

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2157>:

a664.seq

1	GTGATACATCT	CGCACCACTT	CCGCGCCTTT	TTCATAAACG	GTCATGGTGT
51	AGAAATTCGTT	CATCTCCTCA	TATCGCTCGG	GGCGCACCGG	ATGTGCGGTC
101	GGACCTGCGT	CTTCGGGGAA	CTGTGTGCTG	CGCAGCAGGC	GGATGTTTTT
151	GATACGGCGC	ACGGCGCGGC	TGGCGCGGTC	GCGCGAAATC	TCTTGGTTCG

```

a664.pep
1  VIHPHHFRAF  FINGHGVEIV  HLLISGGAHR  MCGRTC VFGE  LVLAQQADVF
51  DTAHGAAGAV  AGKFLVAEHG  QPFLQRLKLE  PVAAGHAVAR  PVEIFVSDHG
101 FDAFKIGIGG  GTAVGKDELG  VKDVQTLVFH  RTHIEIAHGD  DHENIQVVFQ
151 TEARFVPLHC  VFXAIPRQSR  FWACPLRWCK  TRF*

```

		10	20	30	40	50	60
m664.pep		VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGGRCVFGELVLAQQADVFDAAHGAAGAV					
		:     :     :     :     :     :     :     :					
a664		VIHPHHFRAFFINGHGVEIVHLLISGGAHRMCGRTC VFGEVLVLAQQADVFDTAHGAGAV					
		10	20	30	40	50	60
		70	80	90	100	110	120
m664.pep		AGKFLVAEHGQPF LQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAVGKDELG					
		:     :     :     :     :     :     :					
a664		AGKFLVAEHGQPF LQRKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGTAVGKDELG					
		70	80	90	100	110	120
		130	140	150	160	170	180
m664.pep		VKDVQTLVFHRAHIEIAHGDDHENIQVVFQTEARFVPFHRVFXTPQRSRPWACPLRWCK					
		:     :     :     :     :     :     :					
a664		VKDVQTLVFHRT HIEIAHGDDHENIQVVFQTEARFVPLHCVFEXAIQRSRPWACPLRWCK					
		130	140	150	160	170	180
m664.pep	TRFX						
a664	TRFX						

g665.seq

```
1 atgaagtGgGg acgaaacgcg cttcgGgttg GAAtatgact tggatatattt
51 CATGGTCGTC GCCGTAGGCG ATTTCAATAT GGGCGCGATG GAAACAAGG
101 GTTTGAACAT TTTTCAACCC AAGTTCGTCC TCGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTCGAAGG CATGTAATCC GTGGTCGGAC ACGAATATTT
201 CCACAAC TGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAGTT TTCCGGCGAC
301 CGCGCCGGCC CCGCCGTGCG CCGCATCGAG AACATCGGCC TGCTGCGCCA
351 GAACCACTT CCGCAAGACG CAGGCCGAC CGCCATCCG GTGCGCcccg
401 TCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAA
451 GGC CGGAAG TGGT GCGGAT GTATCATACC CTGCTCGCGC AAGAGGGCTT
501 CCAAAAAGGC ATGAAGCTAT ATTTCCaacy CCACGACGGA CAGGCAGTGA
551 CCTGCGACGA TTTCGCGCGG GCGatgvcgg ATGCGAACGG CATCAATCTC
601 GACCACTTCG CCTTG TGTA CAGCCAGTGG GGCACGCCCG TTTTGGAAGC
651 CGAAGGCcGT CTGAAAAACA ATGTTTTCTGA GTTAACCATT AAACAAACCG
701 TGCCGCCCAC GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
751 AAAGTCGGGC TTCTGAACCG CAACGGCGAA GCGGTGGCAT TCGATTATCA
801 GGGCAAAACG GCAACCGAAG CCGTGTGCT GATACCGAA GCCGAACagg
851 CCTTCCCGCT CGAAGGTGTA ACCGAAGCCG TCGTTCCTC ACTGCTGCGC
901 GGGTTCAGCG CGCCAGTGTA TCTGAAC TCTGTAACGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCCACG ACAGCGACGC TTTCAGGTGC TGGGAAGCCG
```

```

1001 CCCAAACGCT CTACCGTCGC GCCGTCGCCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCATCG GGTTCGGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TGGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCGTC CGAAGCCGAa ctGTGGGACG GCACGAAAA CATcgaCCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGtcCG
1251 CttcctgcCG AAATGGCACG AATTGGaccg tcaggcggcg aagCaggaaa
1301 accaaagtTA CGAATACAGC CCCGAAACCG CCGACTGGCG CACGCTGCGC
1351 AACGTCTGCC GCGCCTtctgt cctGCGCGCC GACCCGCGC acatcgAAAC
1401 TGTTGCCGAA Aaatacggcg AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCATACGCG CAACTGCCTG
1501 CTGGCGCAGT TTGCCGAcaa gTtttcAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTCGCC CTTATCGGCT CAAGccgccc cagCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAATTCA GTCTCGAAAA CCCCAACAAA
1651 GCCCGTTCGC TCATCGGCAG CTTTCAGCCG AACGTCCCGC ATTTTCACGC
1701 ACAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA cccGCaggtc gccGCCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTgGTGAAAC AAGAATTGCA
1851 GTGCATTCCG GCGCAGGAAG GATTGTCGAA AGacGTGGC GAaatcgtCG
1901 GCAAGATTTT GGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2160; ORF 665.ng>:

g665.pep

```

1 MKWDETRFGL EYDLDFIMV AVGDFNMGM ENKGLNIFNT KEVLADSRTA
51 TDTFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RAGRAVRRIE NIRLLRQNF PEDAGPTAHP VRPVSYEEMN NFYTMTVYEK
151 GAENVVMYHT LLGEEGFQKG MKLYFORHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAEGR LKNNVFELTI KQTVPTPDM ADKQPMPIPV
251 KVGLLNRNGE AVAFDYQGR ATEAVLLMTE AEQAFPLEGV TEAVVPSLLR
301 GFSAPVYLYN PYSDDDL LLL LAHDSDAFTC WEAQOTLYRR AVAANLAALS
351 DGIGLPKHEK LLAAVEKVIS DDLDNAFKA LLGVPSEAE LWDGTENIDP
401 LRYHQAREAL LDTLAVRFLP KWHELDRAA KQENQSYEYS PETADWRTLRL
451 NVCRAFLVLA DPAHIETVAE KYGEMAQNM HEWGILSAVN GNESDTRNCL
501 LAQFADKFS DALVMDKYFA LIGSSRRSDT LQQVQTALQH PKFSLENPNK
551 ARSLIGFSFR NVPHFHAQDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQELQCIR AQEGLSKDVG EIVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2161>:

m665.seq

```

1 ATGAAATGGG ACGAAACGCG CTTCCGTTTG GAATACGACT TGGATATTTT
51 CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTCGAAGG CATCGAATCC GTGGTCGGAC ACGAGTATTT
201 CCACAACTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAATT TTCCGGCGAC
301 CGCGCCAGCC GCGCCGTGCG CCGCATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCACTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCCCCG
401 CCAGCTATGA GGAGATGAAC AATTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TAGTGCGGAT GTATCACACC CTGCTCGGCG AAGAGGGCTT
501 CCAGAAAGGC ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCCGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGCGG ACGCGAACGG CATCAATCTC
601 GACCACTTCG CTTGTGGTA CAGCCAGGCG GGCAGCCCCG TTTTGAAGC
651 GGAAGGTCGT CTGAAAAACA ATATTTTCGA GTTGACCGTC AAACAAACCG
701 TGCCGCCAC GCGCATATG ACGGATAAAC AGCCGATGAT GATTCCCGTC
751 AAGGTCGGGC TGCTGAACCG CAACGGCGAA GCGGTGGCAT TCGACTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CTTTCTGCT CGAAGGCGTA ACCGAAGCCG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGTGCA TCTGAATAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCCATG ACAGCGACGC CTTACGCGC TGGGAAGCCG
1001 CCCAAACGCT CTACCGCCGC GCCGTCGCCG CCAACCTTGC CACGCTTTCA
1051 GACGGCGTTG AGCTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TAGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCATC CGAAGCCGAG CTGTGGGACG GCGCAGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGTCCA
1251 CTTCTGCGC AAATGGCACG AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAATACAGC CCCGAAGCCG CCGGCTGGCG CACGCTGCGC

```

```

1351 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCCGCGC ACATCGAAAC
1401 CGTTGCCGAA AAATACGGCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCGAACCGC CTTGCAGCAT CCGAAATTCA GCCTCGAAAA CCCCAACAAA
1651 GCCCGTTCGC TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA CCCGCAGGTC GCCGCCCGCT TAGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTTCG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

```

m665.pep
  1  MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIFNT KFVLADSRTA
 51  TDITDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101  RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPASYEEMN NFYTMVYEK
151  GAENVVRYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201  DQFALWYSQA GTPVLEAEGR LKNNIFELTV KQTVPPTPDM TDKQPMIPV
251  KVGLLNRRGE AVAFDYQGKR ATEAVLLTE AEQTFLEGV TEAVVPSLLR
301  GFSAPVHLNY PYSDDDLILL LAHDSDAFTR WEAAQTLYRR AVAANLATLS
351  DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLGVPSAE LWDGAENIDP
401  LRYHQAREAL LDTLAVHFLP KWHELNQRAA KQENQSYEYS PEAAGWRTL
451  NVCRAFLRA DPAHIETVAE KYGEMAQNM HEWGILSAVN GNESDTRNRL
501  LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLENPNK
551  ARSLIGSFSR NVPHFAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601  CNKLEPHRKN LVKQALQRIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

m665.pep	10	20	30	40	50	60
	MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRTATDITDFEGIES					
g665	MKWDETRFGL EYDLDFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRTATDITDFEGIES					
	10	20	30	40	50	60
m665.pep	70	80	90	100	110	120
	VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF					
g665	VVGHEYFHNW TGNRVTCRDW FQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQNOF					
	70	80	90	100	110	120
m665.pep	130	140	150	160	170	180
	PEDAGPTAHPVRPASYEEMN NFYTMVYEKGAENVVRYHTLLGEEGFQKG MKLYFQRHDG					
g665	PEDAGPTAHPVRPASYEEMN NFYTMVYEKGAENVVRYHTLLGEEGFQKG MKLYFQRHDG					
	130	140	150	160	170	180
m665.pep	190	200	210	220	230	240
	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPPTPDM					
g665	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPPTPDM					
	190	200	210	220	230	240
m665.pep	250	260	270	280	290	300
	TDKQPMIPV KVGLLNRRGE AVAFDYQGKRATEAVLLTEAEQTFLEGVTEAVVPSLLR					
g665	ADKQPMIPV KVGLLNRRGE AVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLR					
	250	260	270	280	290	300

	310	320	330	340	350	360
m665.pep	GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEAAQTLYRRAVAANLATLSDGVELPKHEK      :     :     :     :     :					
g665	GFSAPVYLNYPYSDDDLLELHAHDSDAFTCWEAAQTLYRRAVAANLAALSDGIGLPKHEK 310          320          330          340          350          360					
	370	380	390	400	410	420
m665.pep	LAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHELFP      :     :     :     :     :					
g665	LAAVEKVISDDLLDNAFKALLLGVPSAEELWDGTENIDPLRYHQAREALLDTLAVRELF 370          380          390          400          410          420					
	430	440	450	460	470	480
m665.pep	KWHELNRQAQKENQSIEYSPEAGWRTRLRNVCRAFVLRADPAHIETVAEKYGEMAQNMT      :     :     :     :     :					
g665	KWHELDRQAQKENQSIEYSPETADWRTRLRNVCRAFVLRADPAHIETVAEKYGEMAQNMT 430          440          450          460          470          480					
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSSDALVMDKYFALVGSSRRSDTLQQVRTALQH      :     :     :     :     :					
g665	HEWGILSAVNGNESDTRNCLLAQFADKFSSDALVMDKYFALIGSSRRSDTLQQVQTALQH 490          500          510          520          530          540					
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPFHFAEDGSGYRFIADKVIEDRFNPQVAARLVQAFNL      :     :     :     :     :					
g665	PKFSLENPNKARSLIGSFSRNVPFHFAQDGSFYRFIADKVIEDRFNPQVAARLVQAFNL 550          560          570          580          590          600					
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQRIRAEGLSKDVGEIVGKILD      :     :     :     :     :					
g665	CNKLEPHRKNLVKQELQCIRAEGLSKDVGEIVGKILGX 610          620          630					

a665.seq

1	ATGAAGTGGG	ACGAAACGCG	CTTCGGTTTG	GAATACGACT	TGATATTTT
51	CATGGTCGTC	GCCGTGGGCG	ATTCAATAT	GGGTGCGATG	GAAAAACAAGG
101	GTTTGAACAT	CTTTAACACC	AAGTTCGTCC	TTGCCGACAG	CCGTACCGCC
151	ACCGATACCG	ATTTTGAAGC	CATCGAATCC	GTGGTCGGAG	ACGAATATTT
201	CCACAACCTG	ACGGCGAACG	GGGTGACCTG	CCGCGACTGG	TTCACGTTT
251	CGCTGAAGGA	AGGGTTGACC	GTGTTCCGCG	ACCAAGAAAT	TTCCGGCGAC
301	CGCGCCAGCG	GCCGCGTGCG	CGGTATCGAA	AACATCCGCC	TGCTGCGCCA
351	GCACCACTTC	CCCGAAGACG	CAGGTCCGAC	CGCACATCCG	GTGCGCCCGC
401	CCCGATATGA	GGAGATGAAC	AATTTCTACA	CCATGACCTT	TTATGAAAAA
451	GGCGCGGAAG	TGGTGCGGAT	GTATCACACC	TTGCTCGGG	AAGAGGGGCTT
501	CCAAAAAGGT	ATGAAGCTCT	ATTTCCAACG	CCACGACGGA	CAGGCTGTTA
551	CCTGCGACGA	TTTCCGCGCG	GGCATGGTGG	ACGCGACAAG	CATCAACCTC
601	GACCAATTTC	CTTGTGTGTA	GACCCAAGCA	GGTAGCCCGG	TTTTAGATCG
651	TCAAGGGCGT	CTGAAAAACA	ATGTTTTCGA	GTTAACCATC	AAACAAACCG
701	TGCCGCCAC	GCCGATATG	GCGGACAAAC	AGCCGATGAT	GATTTCCGTC
751	AAATCTGGGG	TGCTGAACCT	CAACGCGGAA	GCGGTGGCAT	TTGATTATCA
801	GGGCAAAACG	GCGAAGCAAG	CCGTGTTGCT	GCTGACCGAA	GCCGAAACAGA
851	CCTTCCAGTT	CGAAGAGGTA	ACCGAAGCCG	TCGTTCCCTC	GCTGCTGCGC
901	GGGTTCAGCG	CGCCGGTGCA	TCTGAACAT	CCGTACAGCG	ACGACGACCT
951	GCTGCTTCTG	CTCGCCCATG	ACAGCGACGC	CTTACGCGC	TGGGAAGCCG
1001	CACAAACGCT	CTACCGCCGT	GCCGTGCGCG	CCAACTTTGC	CGCGCTTTCA
1051	GACGGCGTCG	AGTTGCCGAA	ACACGAAAAA	CTGCTTGCCG	CCGTGCGAAA
1101	AGTCATTTCA	GACGACCTCT	TAGACAACGC	TTTCAAGGCC	CTGCTTTTGG
1151	GTGTGCCGTC	TGAAGCCGAG	CTGTGGGACG	GCGCGGAAAA	CATCGACCCG
1201	CTGCGCTACC	ATCAGGCGCG	CGAAGCCTTG	TTGGATATAC	TTGCCGTCCG
1251	CTTTGTCGCG	AAATGGCAGC	AATTGAACCG	TACGGCGGCG	AAGCAGGAAA
1301	ACCAAGAGCTA	CGAGTACAGC	CCCGAAGCCG	CCGCTTGGCG	CACGCTGCGC
1351	AATGTCTGCC	GCGCCTTCGT	CCTGCGCGCC	GATCCCGCGC	ACATCGAAAC



1061

```

1401 CGTTGCCGAG AAATACGCCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTC AAC GCGAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTCGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTCAGCAT CCGAAGTTCA GCCTCGAAAA TCCCAACAAA
1651 GCCCGCTCGC TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTTAA CCCGCAGGTC GCGCCCGGCC TGGTGACGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTCCG GCGCAGGAAG GATTGTGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2164; ORF 665.a>:

```

a665.pep
1 MKWDETRFGL EYDLDFMVV AVGDFNMGM ENKGLNIFNT KFLVADSRTA
51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPARYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMVDANGINL
201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPTPDM ADKQPMPIPV
251 KIGLLNCNGE AVAFDYQGKR ATEAVLLLTE AEQTFQFESV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAAQTLYRR AVAANLAALS
351 DGVELPKHEK LLAAVEKVIS DLLLONAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDILAVRFLP KWHELNROAA KOENQSYEYS PEAAGWRTLRL
451 NVCRAFLVLA DPAHIETVAE KYAEMAQNM HEWGILSAVN GNESDTRNRL
501 LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVQTALQH PKFSLNPKN
551 ARSLIGSF SR NVPHFAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQRI AQEGLSKDVG EIVGKILD*

```

m665/a665 97.3% identity in 638 aa overlap

m665.pep	10	20	30	40	50	60
	MKWDETRFGL EYDLDFMVV AVGDFNMGM ENKGLNIFNT KFLVADSRTA TDTDFEGIES					
a665	MKWDETRFGL EYDLDFMVV AVGDFNMGM ENKGLNIFNT KFLVADSRTA TDTDFEGIES					
	10	20	30	40	50	60
m665.pep	70	80	90	100	110	120
	VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD RASRAVRRIE NIRLLRQHOF					
a665	VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD RASRAVRRIE NIRLLRQHOF					
	70	80	90	100	110	120
m665.pep	130	140	150	160	170	180
	PEDAGPTAHP VRPARYEEMN NFYTMTVYEK GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG					
a665	PEDAGPTAHP VRPARYEEMN NFYTMTVYEK GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG					
	130	140	150	160	170	180
m665.pep	190	200	210	220	230	240
	QAVTCDDFRA AMADANGINLDQFALWYSQA GTPVLEAEGRLKNNIFELTVKQTVPTPDM					
a665	QAVTCDDFRA AMVDANGINLDQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPTPDM					
	190	200	210	220	230	240
m665.pep	250	260	270	280	290	300
	TDKQPMPIPV KIGLLNCNGE AVAFDYQGKR ATEAVLLLTE AEQTFQFESV TEAVVPSLLR					
a665	ADKQPMPIPV KIGLLNCNGE AVAFDYQGKR ATEAVLLLTE AEQTFQFESV TEAVVPSLLR					
	250	260	270	280	290	300
m665.pep	310	320	330	340	350	360
	GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAAQTLYRR AVAANLAALSDG VELPKHEK					
a665	GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAAQTLYRR AVAANLAALSDG VELPKHEK					
	310	320	330	340	350	360

1062

	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNFAKALLGVPSEAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
a665	LLAAVEKVISDDLLDNFAKALLGVPSEAEELWDGAENIDPLRYHQAREALLDILAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEAQNMT					
a665	KWHELNROAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYAEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQH					
a665	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNPVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
a665	PKFSLENPNKARSLIGSFSRNPVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILDX					
a665	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILDX					
	610	620	630			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2165>:

g665-1.seq

```

1  ATGAGCAAAA CCGTCCGTTA TCTGAAAGAT TACCAAACGC CTGCCTACCG
51  CATTCCTGAA ACCGAAGTGC ATTTCCGACAT TGCCGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTC GAGCCGCGA GGGCGGGCGA GCCCGTGGTG
151 TTGACCGGTT CGGCAAAACT CTTGTCCGTC AAAATCAACG GCGCGGCGGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCAGAC GTACCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAACAACAA
301 TCGCTGATGG GCGTGATGTC TTCCGGCGGC AATCTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGCAACAA AATCGACGGC GCGGAGTTT CAGACGGCGC
501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTTCG GGGCGATTG GCGGTAACGG AAGACCGTTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGCAAAACC
651 CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAGTGGGACG
701 AAACGCGCTT CGGGTTGGAA TATGACTTGG ATATTTTCAT GGTCGTCGCC
751 GTAGGCGATT TCAATATGGG CGCGATGGAA AACAAGGGTT TGAACATTTT
801 TAACACCAAG TTCGTCCTCG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT TGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAGTTTTC CGCGGACCGC GCCGGCCCGC
1001 CCGTGCGCCG CATCGAGAAC ATCCGCCTGC TGCGCCAGAA CCAGTTCGCC
1051 GAAGACGCAG GCCCGACCGC CCATCCGGTG CGCCCGTCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGGC GCGGAAGTGG
1151 TGCGGATGTA TCATACCCCTG CTCGGCGAAG AGGGCTTCCA AAAAGGCATG
1201 AAGCTATATT TCCAACGCCA CGACGGACAG GCAGTGACCT GCGACGATT
1251 CCGCGCGGGC ATGGCGGATG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CCAGGCGGGC ACGCCCGTTT TGAAGCCGA AGGCCGTCTG
1351 AAAACAATG TTTTCGAGTT AACCATTAAA CAAACCGTGC CGCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAAA GTCGGGCTTC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTTC ATTATCAGGG CAAACGCGCA
1501 ACCGAAGCCG TGTGCTGAT GACCGAAGCC GAACAGGCCT TCCCGCTCGA
1551 AGGTGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CAGTGTATCT GAATATCCG TACAGCGACG ACGACCTGCT GCTCTGCTC
1651 GCCCACGACA GCGACGCTTT CACGTGCTGG GAAGCCGCC AAACGCTCTA
1701 CCGTCGCGCC GTCGCGCCA ACCTTGCCGC GCTTTCAGAC GGCATCGGGT

```

```

1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTGG ACAACGCCCTT CAAAGCCCTG CTTTGGGGCG TGCCGTCCGA
1851 AGCCGAACCTG TGGGACGGCA CGGAAACAT CGACCCGCTG CGCTACCATC
1901 AGCGCGCGCA AGCCTTGTTG GATACGCTTG CCGTCCGCTT CCTGCCGAAA
1951 TGGCACAAT TGGACCGTCA GCGCGCGAAG CAGGAAACC AAAGTTACGA
2001 ATACAGCCCC GAAACCGCCG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAC CCGCGGCACA TCGAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTGCCCTTT
2251 ATCGGCTCAA GCCGCGCGAG CGACACCCCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAATTCAGTC TCGAAAAACC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC-
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGTCCGCC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAGCTCG
2501 AGCCGCACCG CAAAACTTG GTGAAACAAG AATTGCAGTG CATTGGGCGG
2551 CAGGAGGAT TGTCGAAAGA CGTGGCGGAA ATCGTCGCGA AGATTTTGGG
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

g665-1.pep

```

1 MSKTVRYLKD YQTPAYRILE TELHFDIAEP QTVVKSRLTV EPQRAGEPLV
51 LDGSAKLSV KINGAAADYV LEGETLTIAD VPSEFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRPV
151 LLSNGNKIDG GEFSDGRHWV KWEDPFAKPS YLFALVAGDL AVTEDRFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL YDLDFMVVA
251 VGFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDFW QLSLKEGLTV FRDQEFSGDR AGRVRRRIEN IRLLRNQFP
351 EDAGPTAHVP RPVSYEEMNN FYTMTVYKAG AEVVRMYHTL LGEEGFQKGM
401 KLYFORHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNVFELTIK QTVPPTPDMA DKQPMIPVK VGLNLRNGEA VAFDYQKRA
501 TEAVLLMTEA EQAFPLEGVT EAVVPSLLRG FSAPVYLNYP YSDDDLLELL
551 AHDSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVISD
601 DLLDNFAKAL LLGVPSEAE LWDGTENIDPL RYHQAREALL DTLAVRFLPK
651 WHELDROQAAK QENQSYEYSP ETADWRTLRLN VCRAFVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSRRSDTL QVQVQALQHP KFSLENPNKA RSLIGSFSRN VPHFHAQDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQELQCIRA
851 QEGLSKDVG EIVKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

m665-1.seq

```

1 ATGAGCAAAA CCGTGCATTA TCTCAAGAC TATCAACGC CCGCTACCA
51 TATTCTCAAA ACCGATTAC ATTTGATAT TAATGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTT GAGCCGAGA GGGTAGGGGA GCCGCTGGTG
151 TTGGACGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GGGCGGCGGC
201 GGATTATGTT TTGGAAGGAG AGACGCTGAC GATTGCGGGC GTGCCGTCCG
251 AACGCTTAC CGTCGAAGTG GAAACCGAAA TCCTGCCGCG GGAAACAAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATTTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
401 TGTCGAAGTT CACCACCACC ATCGTCGCGC ACAAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGCAGTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTTC CAAACCGAGC TATCTGTTTG
551 CTTTGGTCCG GGGCGATTTG GCGGTAACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTGGGCGATT TCAATATGGG CCGCATGGAA AACAGGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACAG AGTATTTC AACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCG TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAAATTTT CCGCGACCGC GCCAGCCGCG
1001 CCGTGCGCCG CATCGAAAC ATCCGCTGTC TGCGCCAGCA CCAGTTCCCC
1051 GAAGACGCG GCGCGACCGC CCATCCGGTG CCGCCCGCCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGGC GCGGAAGTAG
1151 TGCGGATGTA TCACACCCTG CTCGGCGAAG AGGGCTTCCA GAAAGGCATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCCGTTACCT GCGACGATTT
1251 CCGCGCGCGC ATGGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CCAGCGGGC ACGCCCGTTT TGGAAGCGGA AGGTCTGCTG
1351 AAAACAATA TTTTCGAGTT GACCGTCAAA CAAACCGTGC CGCCACGCC
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCGCTCAAG GTCGGGCTGC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTG ACTATCAGG CAAACGCGCG

```

1501 ACCGAAGCCG TGTGCTGCT GACCGAAGCC GAACAGACCT TCCTGCTCGA  
1551 AGGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC  
1601 CGGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC  
1651 GCGCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCCC AACGCTCTA  
1701 CGCGCCGCCG GTCGCCGCCA ACCTTGCCAC GCTTTCAGAC GCGGTTGAGC  
1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTCAGAC  
1801 GACCTCTTAG ACAACGCCTT CAAAGCCCTG CTTTGGGCG TGCCATCCGA  
1851 AGCCGAGCTG TGGGACGGCG CAGAAAACAT CGACCCGCTG CGTACCATC  
1901 AGGCGCGCGA AGCCTTGTTG GATACGCTTG CCGTCCACTT CCGCCGAAA  
1951 TGGCAGCAAT TGAACCGTCA GCGCGCGAAG CAGGAAAACC AAAGCTACGA  
2001 ATACAGCCCC GAAGCCGCCG GCTGGCGCAC GCTGCGCAAC GTCTGCCCGG  
2051 CCTTTGTCTT GCGCGCCGAC CCGCGCGACA TCGAAACCGT TGCCGAAAAA  
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGCA TCCTGTCCGC  
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCTGCTG GCGCAGTTG  
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTTGCCTC  
2251 GTCGGCTCAA GCCGCGCAG CGACACCTG CAACAGGTTT GAACCGCCTT  
2301 GCAGCATCCG AAATTCAGCC TCGAAAAACC CAACAAAGCC CGTTCGCTCA  
2351 TCGGCGAGCT CAGCCGCAAC GTCCCGCATT TCCACGAGA AGACGGCAGC  
2401 GGTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC  
2451 GCAGGTCGCC GCCCGCTTAG TGCAGGCGTT CAACCTCTGC AACAAGCTCG  
2501 AGCCGCAACG CAAAACTTG GTGAAACAAG CATTGCAGCG CATTGGGCG  
2551 CAGGAAGGAT TGTGAAAGA CGTGGCGGAA ATCGTCGGCA AAATTTTGA  
2601 TTGA

This corresponds to the amino acid sequence <SEQ ID 2168; ORF 665-1>:

m665-1.pep

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV  
51 LDGSAKLLSV KINGAAADYV LEGETLTIAG VPSEFTVEV ETEILPAENK  
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV  
151 LLSNGNKIDG GEFSDGRHWV KWEDPFSKPS YLFALVAGDL AVTEDYFTTM  
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGLE YDLDFMVVA  
251 VGDFNMGAME NKGLNIFNTR FVLADSRTAT DTDPEGIESV VGHEYFHNWT  
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLRQHQFP  
351 EDAGPTAHPV RPASYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGPKQGM  
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL  
451 KNNIFELTVK QTVPPTPDMT DKQPMIPVK VGLLNRNGEA VAFDYQGKRA  
501 TEAVLLLTEA EQTFLLLEGVT EAVVPSLLRG FSAPVHLNYP YSDDDDLLLLL  
551 AHDSDAFTRW EAAQTLYRRA VAANLATLSD GVLEPKHEKL LAAVEKVID  
601 DLLDNFAKAL LLGVPSEAEL WDAENIDPL RYHQAREALL DTLAVHFLPK  
651 WHELNQAAK QENQSYEYSP EAAGWRTLRLN VCRAFVLRAD PAHIETVAEK  
701 YGEMAQNMTH EWGILSAVNG NESDTRNRL ALQFADKFSDD ALVMDKYFAL  
751 VGSRRSDTL QQVRTALQHP KFSLENPNKA RSLIGSFSRN VPHFAEDGS  
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQRIRA  
851 QEGLSKDVG EIVGKILD\*

m665-1/g665-1 96.1% identity in 866 aa overlap

m665-1.pep	10	20	30	40	50	60
m665-1.pep	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTVVKSRLTV	EPQRVGEPLV	LDGSAKLLSV
g665-1	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTVVKSRLTV	EPQRVGEPLV	LDGSAKLLSV
m665-1.pep	70	80	90	100	110	120
m665-1.pep	KINGAAADYV	LEGETLTIAG	VPSEFTVEV	ETEILPAENK	SLMGLYASGG	NLFTQCEPEG
g665-1	KINGAAADYV	LEGETLTIAG	VPSEFTVEV	ETEILPAENK	SLMGLYASGG	NLFTQCEPEG
m665-1.pep	130	140	150	160	170	180
m665-1.pep	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFSDGRHWV	KWEDPFSKPS
g665-1	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV	LLSNGNKIDG	GEFSDGRHWV	KWEDPFSKPS
m665-1.pep	190	200	210	220	230	240
m665-1.pep	YLFALVAGDL	AVTEDYFTTM	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGLE
g665-1	YLFALVAGDL	AVTEDYFTTM	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGLE
m665-1.pep	250	260	270	280	290	300
m665-1.pep	YDLDFMVVAV	GDENMGAMEN	KGLNIFNTR	KFVLADSRTAT	DTDPEGIESV	VGHEYFHNWT
g665-1	YDLDFMVVAV	GDENMGAMEN	KGLNIFNTR	KFVLADSRTAT	DTDPEGIESV	VGHEYFHNWT

1065

	250	260	270	280	290	300
m665-1.pep	310	320	330	340	350	360
	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV					
g665-1						
	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV					
	310	320	330	340	350	360
m665-1.pep	370	380	390	400	410	420
	RPASYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQXGMKLYFQRHDGQAVTCDDFRAA					
g665-1						
	RPVSYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQXGMKLYFQRHDGQAVTCDDFRAA					
	370	380	390	400	410	420
m665-1.pep	430	440	450	460	470	480
	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPPTPDMTDKQPMMPVK					
g665-1						
	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTPPTPDMADKQPMMPVK					
	430	440	450	460	470	480
m665-1.pep	490	500	510	520	530	540
	VGLLNRRNGEAVAFDYQGKRATEAVLLLTAEQTFLEGVTEAVVPSLLRGFSAPVHLNYP					
g665-1						
	VGLLNRRNGEAVAFDYQGKRATEAVLLMTEAQAFPLEGVTEAVVPSLLRGFSAPVHLNYP					
	490	500	510	520	530	540
m665-1.pep	550	560	570	580	590	600
	YSDDDLLLLLAHDSDAFTRWEAAQTLYRRVAANLATLSDGVELPKHEKLLAAVEKVISD					
g665-1						
	YSDDDLLLLLAHDSDAFTCWEAAQTLYRRVAANLAALSDGIGLPHKEKLLAAVEKVISD					
	550	560	570	580	590	600
m665-1.pep	610	620	630	640	650	660
	DLLDNAFAKALLGVPSAEALWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELNQAAK					
g665-1						
	DLLDNAFAKALLGVPSAEALWDGTENIDPLRYHQAREALLDTLAVRFLPKWHELDQAAK					
	610	620	630	640	650	660
m665-1.pep	670	680	690	700	710	720
	QENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMTHWGLSAVNG					
g665-1						
	QENQSYEYSPEADWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMTHWGLSAVNG					
	670	680	690	700	710	720
m665-1.pep	730	740	750	760	770	780
	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTLQHPKFSLENPNKA					
g665-1						
	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTLQHPKFSLENPNKA					
	730	740	750	760	770	780
m665-1.pep	790	800	810	820	830	840
	RSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCKLEPHRKNL					
g665-1						
	RSLIGSFSRNVPHFAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNLCKLEPHRKNL					
	790	800	810	820	830	840
m665-1.pep	850	860				
	VKQALQIRIRAQEGLSKDVGEIVGKILD					
g665-1						
	VKQELQCIRIRAQEGLSKDVGEIVGKILGX					
	850	860				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAAA ACCGATTAC ATTTGATAT TAACGAACCG CAACCATTTG
101 TGAAGTCGCG TTTGACGGTC GAGCCGAAGA GGGTGGGAGA GCCGCTGGTG
151 TTGACGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG CGGTGGCGGC
201 GGATTATGTG TTGAAGGCG AGACGCTGAC GATTGCGGAC GTGCCGTCGG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAAACAAA
301 TCGCTGATGG GGCTGTATGC GTCCGCCGGT AACCTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA TATCGACCGT CCGGATGTCA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAACG CTATCCCGTT
451 TTGCTCTCCA ACGGCAACAA AATCGACGGC GGCGAGTATT CAGACGGCCG

```

1066

```

501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTCGC GGGCGATTTG GCGGTCACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCCGGC TTGCGCGTGG AATCGCTGAA AAACGCAATG AAGTGGGACG
701 AAACGCGCTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTGGGCGATT TCAATATGGG TCGATGGGAA AACAAGGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTGG CCGACAGCCG TACCGCCACC GATACCGATT
851 TTGAAGGCAT CGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TGACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GTTGACCGTG TTCCGCGACC AAGAAATTTT CGGCGACCGC GCCAGCCCGC
1001 CCGTGGCGCG TATCGAAAAC ATCCGCCTGC TGGCCAGCA CCAGTTCCCC
1051 GAAGACGCGG GTCCGACCGC ACATCCGGTG CGCCCGCCCC GATATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGGC GCGGAAGTGG
1151 TGCGGATGTA TCACACCTTG CTCGGCGAAG AGGGCTTCCA AAAAGGTATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCTGTACCT GCGACGATT
1251 CCGCGCGGCG ATGGTGGACG CGAACGGCAT CAACCTCGAC CAATTGCGCT
1301 TGTGTACAG CCAAGCAGGT ACGCCGGTTT TAGATGCTCA AGGGCGTCTG
1351 AAAAACAATG TGTTGAGATT AACCATCAA CAAACCGTGC CGCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAA ATCGGGCTGC
1451 TGAATGCAA CGCGGAAGCG GTGGCATTG ATTATCAGGG CAAACCGCGC
1501 ACCGAAGCCG TGTTGCTGCT GACCGAAGCC GAACAGACCT TCCAGTTTCA
1551 AAGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CGGTGCATCT GAACATCCG TACAGCGACG ACGACCTGCT GCTTCTGCTC
1651 GCCCATGACA GCGACGCGCT CACGCGCTGG GAAGCCGCAC AAACGCTCTA
1701 CCGCCGTGCC GTCGCGGCCA ACCTTGCCGC GCTTTCAGAC GCGCTCGAGT
1751 TGCCGAAACA CGAAAAATG CTTGCCGCGC TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTAG ACAACGCTTT CAAAGCCCTG CTTTGGGTG TGCCGTCTGA
1851 AGCCGAGCTG TGGGACGGCG CGGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATATACTTG CCGTCCGCTT TCTGCCGAAA
1951 TGGACGGAAT TGAACCGTCA GCGCGCGAAG CAGGAAAACC AAAGCTACGA
2001 GTACAGCCCC GAAGCCGCGG GTTGGCGCAC GCTGCGCAAT GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCGCAT CCCGCGCACA TCGAAACCGT TGCCGAGAAA
2101 TACGCGGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTGCGCCTC
2251 GTCGGCTCAA GCGCGCGCAG CGACACCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAGTTAGGCC TCGAAAAATC CAACAAAGCC CGCTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTTAACCC
2451 GCAGCTCGCC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAAGCTCG
2501 AGCCGCAACG CAAAAACTTG GTGAAACAAG CATTGCAGCG CATTGCGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGGCGAA ATCGTCGCGA AAATTTTGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2170; ORF 665-1.a>:

a665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV
51 LDGS AKLLSV KINGVAADYV LEGETLTIAD VPSEFTVEV ETEILPAENK
101 SLMGLYASAG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEYSDGRHWV KWEDPFAKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGLE YDLDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRTAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDOEFSGDR ASRAVRRIEN IRLLRQHQP
351 EDAGPTAHPV RPARYEEMNN FYTMTVYKGG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MVDANGINLD QFALWYSQAG TPVLDAGQRL
451 KNNVFELTIK QTVPTPDMA DKQPMMPVK IGLLNCNGEA VAFDYQGKRA
501 TEAVLLLTEA EQTFQFESVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAETRW EAAQTLYRRA VAANLAALSD GVLEPKHEKL LAAVEKVISD
601 DLLDNAFKAL LLGVPSEAEI WDGAENIDPL RYHQAREALL DILAVRFLPK
651 WHELNQAAK QENQSYEYSP EAAGWRTLRL VCRAFVLRAD PAHIETVAEK
701 YAEQAQNMTH EWGILSAVNG NESDTRNRL AQFADKFSDD ALVMDKYFAL
751 VGSSRRSDTL QVQVQALQHP KFSLENPNKA RSLIGSFSRN VPHFAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQRIRA
851 QEGLSKDVGE IVGKILD*

```

a665-1/m665-1 97.2% identity in 867 aa overlap

	10	20	30	40	50	60
a665-1.pep	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTIVKSRLTV	EPKRVGEPLV	LDGS AKLLSV
m665-1	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTIVKSRLTV	EPKRVGEPLV	LDGS AKLLSV
	70	80	90	100	110	120

1067

a665-1.pep	KINGVAADYVLEGETLTIADVPSEFTVEVETEILPAENKSLMGLYASAGNLFTQCEPEG
m665-1	KINGAAADYVLEGETLTIAGVPSEFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG
	70 80 90 100 110 120
a665-1.pep	130 140 150 160 170 180
m665-1	FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEYS DGRHWVKWEDPFAKPS
	130 140 150 160 170 180
a665-1.pep	190 200 210 220 230 240
m665-1	YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTEADKPKVGFVAVESLKNAMKWDTRFGLE
	190 200 210 220 230 240
a665-1.pep	250 260 270 280 290 300
m665-1	YLDLIFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATDTDFEGIESVVGHEYFHNWT
	250 260 270 280 290 300
a665-1.pep	310 320 330 340 350 360
m665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRRIENIRLLRQHQPEDAGPTAHPV
	310 320 330 340 350 360
a665-1.pep	370 380 390 400 410 420
m665-1	RPARYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDGQAVTCDDFRAA
	370 380 390 400 410 420
a665-1.pep	430 440 450 460 470 480
m665-1	MVDANGINLDQFALWYSQAGTPVLDAQGRKNNVFELTIKQTPPTPDMDKQPMIIPVK
	430 440 450 460 470 480
a665-1.pep	490 500 510 520 530 540
m665-1	IGLLNCNGEAVAFDYQGKRATEAVLLLTEAEQTFQFESVTEAVVPSLLRGFSAPVHLNYP
	490 500 510 520 530 540
a665-1.pep	550 560 570 580 590 600
m665-1	YSDDDLLELLLAHDSDAFTRWEAAQTLRYRAVAANLAALSDGVLPKHEKLLAAVEKVISD
	550 560 570 580 590 600
a665-1.pep	610 620 630 640 650 660
m665-1	DLLDNAFKALLGVPSEAEIWDGAENIDPLRYHQAREALLDILAVRFLPKWHELNROAAK
	610 620 630 640 650 660
a665-1.pep	670 680 690 700 710 720
m665-1	QENQSYEYSPAAAGWRTLNRVCRAFLRADPAHIETVAEKYAEQAQNMTHWGLSAVNG
	670 680 690 700 710 720
a665-1.pep	730 740 750 760 770 780
m665-1	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQHPKFSLENPNKA
	730 740 750 760 770 780
a665-1.pep	790 800 810 820 830 840
m665-1	RSLIGSFSRNVPHFHAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL
	790 800 810 820 830 840

	790	800	810	820	830	840
	850	860				
a665-1.pep	VKQALQRI	RAQEGLSK	DVGEIVGK	ILD		
m665-1	VKQALQRI	RAQEGLSK	DVGEIVGK	ILD		
	850	860				

g666.seq

1	ATGCTTTGTA	TGAATTATCA	ATCAAACCTCA	GGCGAAGGAG	TGCTTGTAGC
51	TAAACATAT	TTATTGACTG	CATTGATAAT	GTCTATGGTA	ATCTCCGGAT
101	GTCAAGTCAT	CCATGCCAAT	CAAGGTAAGG	TTAATACTAA	TTCTGCTGTC
151	ATCGCAGGTG	CAGACGCTCA	CACGCCCTGAA	CATGTAACGG	GACTGACCGA
201	ACAAAGCAG	GTGATTGCAA	GTGATTTTAT	AGTAGCGTCA	GCCAAATCCAT
251	TAGCAACACA	AGCTGGCTAT	GATATCTTAA	AGCAAGGCGG	TAGCGCTGCA
301	GATGCGATGG	TGGCGGTGCA	GACGACACTA	AGCTTGGTAG	AGCCACAGTC
351	GTCAGGCTTG	GGCGGTGGTG	CATTTGTGTT	GTATTGGGAC	AATACCGCCA
401	AAACATTGAC	CACATTTGAT	GGGCGTGAGA	CGGCACCGAT	CGGTGCGACG
451	CCAGAATTAT	TTTTGGATAA	AGATGGTTAA	CCATTGAAAT	TTATGGAAGC
501	GGTGGTCGCT	CGGTAGGTAC	GCCTGCTATC	CCTAAACTGA	

g666.pep

1	MLCMNYQSNS	GEGVLVAKTY	<u>LLTALIMSMV</u>	ISGCQVIHAN	QGVNTNSAV
51	IAGADAHTPE	HVTGLTEQKQ	VGGAFVLYWD	ANPLATQAGY	DILKQGGGSA
101	DAMVAVQTTL	SLVEPQSSGL	GGAADFVLYD	NTAKLTTFD	GRETAPMRAT
151	PELFLDKDGX	PLKFMEAVVA	RXXRLLSLN*		

m666.seq

```
1 ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTGGC
51 TAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAGGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CACGCGCTGAA CATGCAACGG GACTGACCGA
201 ACAAAAGCAG GTGATTGCAA GTGATTTTTT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTTGTGTT GTATTGGGAT AATACCGCCA
401 AAACATTGAC CACATTTGAT CGGCGTGAGA CGGCACCGAT GCGTGCGACG
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGGTAGCGCT GCTATCCCTA AACTGA
```

m666.pep

1	MFCMNHQSNS	GEGVLVAKTY	<u>LLTALIMSMT</u>	<u>ISGCQVIHAN</u>	QGVNTHSAV
51	ITGDAHTPE	HATGLTEPKQ	VIASEFMVNS	ANPLATQAGY	DILKQGSAA
101	DAMVAQTTL	SLVEPQSSGL	GGGAFVLYWD	NTAKTLTTFD	GRETAPMRAT
151	PELFLDKDGO	PLKFMEAVVV	VARVWRLLSI	N*	

m666/g666 93.9% identity in 181 aa overlap

```
m666.pep      10          20          30          40          50          60
MPCMNHQSNSEGGVLAQTYLLTALIMSMITSGCQVIHANQGKVNTHSAVITGADAHTPE
| |:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
g666          MLCMNYSNQSNGEGVLAKTYLLTALIMSMIVISGCQVIHANQGKVNTNSAVIAGADAHTPE
              10          20          30          40          50          60

m666.pep      70          80          90         100         110         120
HATGLTEQKQVIASDFMVASANPLATQAGYDILKGGSAAADAMVAVQTTLSLVEPQSSGL
```



a666.seq

```
1 ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTGGC
51 TAAACATAT TTATGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAAAGTCAT CCATGCCAAT CAAGGTAAAGG TTAATACTCA TTCTGCTGTC
151 ATACACAGGTG CAGACGCTCA CAGCGCTGAA CATGCAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGCGGG TAGCGTGCA
301 GATCGCATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGGGTGGTG CATTTGTGTT GTATTGGGAT AATACCGCCA
401 AAACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGGCAGC
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CATTGAAAT TTATGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA
```

```
a666.pep
1 MPCMNHQSNS GEGVLAKTY LLTALIMSMT ISGCGVIHAN QGKVNTHSAV
51 ITGADVAQTHE HATGLTEQKQ VIASDFMVAS ANPLATOAGY DILKQGGSA
101 DAMVAVQTTT SLVPEQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT
151 PELFLDKDGQ PLKFMEAVVV VARVWRLLSL N*
```

		10	20	30	40	50	60
m666.pep		MPCMNHQSN	SGEGLVAK	TYLLTALIM	SMTISGCQVI	HANQGKVN	THSAVITGADAHTPE
a666		MPCMNHQSN	SGEGLVAK	TYLLTALIM	SMTISGCQVI	HANQGKVN	THSAVITGADAHTPE
		10	20	30	40	50	60
		70	80	90	100	110	120
m666.pep		HATGLTEQ	KQVIASDF	MVASANPLA	TQAGYDIL	KQGGSAAD	AMVAVQTTL
a666		HATGLTEQ	KQVIASDF	MVASANPLA	TQAGYDIL	KQGGSAAD	AMVAVQTTL
		70	80	90	100	110	120
		130	140	150	160	170	180
m666.pep		GGGAFVLY	WDNTAKTL	TTTFDGR	ETAPMRAT	PELFLDKD	GQPLKFME
a666		GGGAFVLY	WDNTAKTL	TTTFDGR	ETAPMRAT	PELFLDKD	GQPLKFME
		130	140	150	160	170	180
m666.pep	NX						
a666	- NX						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2177>:

```
g667.seq
1   atgcggtttg tcttctgttt gggcgGAGAG ATAGtttctg atccgtgtga
51  tttccAtttg gtattcgtcc gcgtcgaatc tgccgctgAc CAGAcagaaa
101 cgCAGataca tCaaatacgt attcacggca tcggtttcgc aatAAattgcg
151 GAtttccttc agcgtgcccc cgtgGAacgc ttcccacact ttgctgccgt
201 ccataCCCAg ctTGCCCGGA AAGCCGCACA GTTTCgcCat atcgtccagC
251 GGCACATTcg ccctcggetG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCActtg AAATCGCGGC
351 tgtcgccgAA ATCGccgTCG CCGTATCCC AATAGCGCGC GGC GTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGGTCGA AACCGCGCC
451 GTTCCAGCTG ACCAGTTGCG GCGTATGTTT TTCAACCAAT TCGAAAACT
501 TGGCAATCAC GACTTCTTCG CCATCGTCCA TCTCGCCGAT GGTGCCGACA
551 TGAACCTTGT CCTGCCCCCA GCGCATACAG CAGGAAACCG CCACAACCTG
601 ATGGAGGTGG TGCTGCATAA AATCGCCGCC GGTCTGTGCG CGGCGTTCT
651 GCTGCGCGAA CAGCACCCT TCGTCATCCG GCAGGAAGA CGGCAAGTCA
701 TACAACGTAC GGATACCTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTA TTCATGGCag tACCTTGCAT tcaAAAACAG ActTGCGCCT
801 ATTgTgtcaT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2178; ORF 667.ng>:

```
g667.pep
1   MRFVFLGGE IVSDPCDFHL VFVRVESAAD QTETQIHQIR IHGIGFAIIA
51  DFLQARVER FPHFAAVHTQ LARKAAQFRH IVQRHIRPRL VKREQIHQIA
101 VALVITADV VPLEIAAAVE IAVARIPIAR GVDVYQGA V MQYGQVETAA
151 VPADQLRRMF FNQFEKLG NH DFFAIVHLAD GADMLVLP P AHTAGNRHNL
201 MEVVLHKIAA GLCAAFLLRE QHHEFVIRQGR RQVIQRTDTL HIGYGFNIES
251 QNRHGSTLH SKTDLRL LCH *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2179>:

```
m667.seq (PARTIAL)
1   ATGCGGCTTT TCCCCGGCTT GTGCGGACAG GTAATCCGC ATCCGTTTGA
51  TTTCATTTC GTATTCGTCC GCATCCAGCC TGCCGCTGAC CAGACAGAAA
101 CGCAGGTACA TCAGATAAGT GTTTGCCGCG TCGGTTTCGC AATAATTGCG
151 GATTTCCCTC AGCCTGCCCC TATGGAATGC CTCCCAAACC TTGCTGCCGT
201 CCATACCAG CTGCCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAGC
251 GGCACGTTTG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTGCGCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GGC GTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGATCGA AACCGCGGCC
451 GTTCCAAC TG ACCAGTTGCG GCGTATGTTT TTCAATCAAT TCGAAAAATT
501 TAGCAATGAC CACTTCCTCG CCGTCATCCA TCTCGCCGAT GGTGCCGACA
551 TGTACTTTAT CCTGCCCCCA ACGCATGCGC CACGAAATCG CCACAACCTG
601 ATGAAGATGA TGCTGCATAA AATCGCCGCC CGTCTGAGCA CGGCGTTTGT
651 GCTGGGCAAT CAGCACCCT TG...
```

This corresponds to the amino acid sequence <SEQ ID 2180; ORF 667>:

```
m667.pep (partial)
1   MRLFPGLCGQ VIPHPDFHF VFVRIQPAAD QTETQVHQIS VCRVGFALIA
51  DFLQPARMEC LPNLAHVHTQ LARKTAQFRH IVQRHVCPRL VKREQIHQIA
101 VALVITADV VPLEIAAAVE IAVAHPIAR GVDVYQGA V MQYGQIETAA
151 VPTDQLRRMF FNQFEKFSND HFLAVIHLAD GADMYFILPP THAARNRHN L
201 MKMMLHKIAA RLSTAFVLGN QHHL...
```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m667/g667 75.0% identity in 224 aa overlap

```

          10      20      30      40      50      60
m667.pep  MRLFPGLCGQVIPHPDFHFVFVRIQPAADQTETQVHQISVCRVGFALIAADFLQPARMEC
          ||:  | |::  | ||:||||: | |||||:| | : : ||||| | | |
```

1071

```

g667      MRFVFC LGGEIVSDPCDFHLV FVRVESAADQTETQIHQIRIHGIGFAIIADFLQRRARVER
           10      20      30      40      50      60

           70      80      90      100     110     120
m667.pep  LPNLA AVHTQLARKTAQFRHIVQRHVCPRLVKREIQIHQIAVALVITADVVPLEIAAAVAE
           ::::::::::::::::::::: ||||| ::::::::::::::::::::: ||::|
g667      FPFHAAVHTQLARKAAQFRHIVQRHIRPRLVKREIQIHQIAVALVITADVVPLEIAAAVAE
           70      80      90      100     110     120

           130     140     150     160     170     180
m667.pep  IAVAHIPIARGVD VAVYQGAVM QYQGIETAAVPTDQLRRMFFNQFEKFSNDHFLAVIHLAD
           |||:||||| ::::::::::::::::::::: ||||| ::::::::::::::::::::: ||::|
g667      IAVARIPIARGVD VAVYQGAVM QYQGVETA AVPADQLRRMFFNQFEKLGNDHFFAIVHLAD
           130     140     150     160     170     180

           190     200     210     220
m667.pep  GADMYFILPPTHAAARNRHNLMKMLHKIAARLSTAFVLGNQHHL
           ||| :|||:|:| |||||::| ||||| | :|||:| :|||:
g667      GADMNLVLEPPAHTAGNRHNLM EVVLHKIAAGLCAAFLLREQHHFVIRQGRRQVIQRTDTL
           190     200     210     220     230     240

g667      HIGYGFNIESQNRHIGSTLHSKTDLRLLLCHX
           250     260     270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2181>:

```

a667.seq
1  ATGCGGTTTG TCTTCTGTTT GGGCGGAGAG ATAGTTTCTG ATCCGCTTGA
51  TTTCCATTTC GTATTCGTCT GCGTCGAATC TGCCGCTGAC CAGACAGAAA
101 CGCAGATACA TCAGATAGGT ATTTACCGCA TCGGTTTCGC AATAATTGCG
151 GATTTCCTTC AGCCTGCCCG CGTGGAACGC CTCCACACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTCGCCAT ATCGTCCAAC
251 GGCACATTTC CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 ATGACGTTTG TGGTAGCGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTGCGCCGA ATCGCCGTCG CCCATATCCC AATAGCGCGC GGCGTTGATG
401 CCGTGTAGCA GCGAACGGTA ATGCAGAACG GGCAGGTCGA AACCGCGGCC
451 GTTCCAAC TG ACCAGTTGCG GCGTATGTTT TTCAATCAAC TCGAAAAATT
501 TGGCGATAAC CACTTCCTCG CCGTCATCCA TCTCGCCGAT TGTACCGACA
551 TGGACTTTAT CCTGCCCCCA ACGCATGCAG CACGAAATCG CCACAATCTG
601 ATGAAGATGA TGCTGCATAA AATCCCCACC CGTCTGAGCA CGGCGTTTTT
651 GCTGGGCAAA CAGCACC ACT TCATCGTCGG GCAGCGAGGA CGGCAAGTCA
701 TACAGCGTAC GGATACACTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTG GTCATGACAG CACCTTGAT TTA AAA.CAG ACTTGCGCCT
801 ATTGTGTCAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2182; ORF 667.a>:

```

a667.pep
1  MRFVFC LGGE IVSDPLDFHF VFVCVESAAD QTETQIHQIG IYRIGFAIIA
51  DFLQPARVER LPHLA AVHTQ LARKTAQFRH IVQRHIRPRL VKREIQIHQIA
101 MTLVVAADV VPLEIAAAVAE IAVAHIPIAR GVDV*QRTV MQNRQVETAA
151 VPTDQLRRMF FNQLEKFGDN HFLAVIHLAD CTDMDFILPP THAARNRHNL
201 MKMMLHKIPT RLSTAFLLGK QHFFIVGQRG RQVIQRTDTL HIGYGFNIES
251 QNRGH DSTLY LKXDLRL LCH *

```

m667/a667 79.0% identity in 224 aa overlap

```

           10      20      30      40      50      60
m667.pep  MRLFPGLCGQVIPHPFDHFV FVRIQPAADQTETQVHQISVCRVGF AIIADFLQPARMEC
           ||: | |::| :||| ||| :| |||||:|::| :|:| |||||:|:|
a667      MRFVFC LGGEIVSDPLDFHFV FVCVESAADQTETQIHQIGIYRIGFAIIADFLQPARVER
           10      20      30      40      50      60

           70      80      90      100     110     120
m667.pep  LPNLA AVHTQLARKTAQFRHIVQRHVCPRLVKREIQIHQIAVALVITADVVPLEIAAAVAE
           ||: ||||| |||||:| |||||:|:|:|:|:|:|:|:|:|:|:|:|
a667      LPHLA AVHTQLARKTAQFRHIVQRHIRPRLVKREIQIHQIAMTLVVAADVVPLEIAAAVAE

```

		70	80	90	100	110	120
		130	140	150	160	170	180
m667.pep		IAVAHIPIARGVD	AVYQGAVM	QYQGIETA	AAVPTD	QLRRMFFN	QFEKFSNDHFLAVIHLAD
a667							
		130	140	150	160	170	180
		IAVAHIPIARGVD	AVXQRTVM	QNRQVETA	AAVPTD	QLRRMFFN	QLEKFGDNHFLAVIHLAD
		130	140	150	160	170	180
		190	200	210	220		
m667.pep		GADMYFILPPT	HAARNRHNLM	KMMLHKIAA	RLSTAFVL	GNQHHL	
a667		:					
		190	200	210	220	230	240
		CTDMDFILPPT	HAARNRHNLM	KMMLHKI	PTRLSTAF	LLGKQHHF	IVGQRGRQVIQRTDTL
		190	200	210	220	230	240
a667		HIGYGFNIESQ	NRGHDSTLY	LKXDLRL	LCHX		
		250	260	270			

```
g669.seq
  1  ATGCGCGCGCA TCGTTAAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
    51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCTTTGGGC
   101  GGAACGCTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGGATC
   151  GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAACTCTC
   201  CAACAGGCAA AGCGGCAGAC AGCCGGTTTG CACCAAACCG CCAACACGG
   251  CAAGCCTTAA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTCAATGCC
   301  GACATCTTAC GGATACTGTA A
```

g669.pep  
1 MRRIVKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRLRRQHG  
51 EGMGFDFKQI FRHVQSSNRQ SGRQPVCTKP PNTASLQTAL SRPAVEFGYNA  
101 DIKRIL\*

```
m669.seq
1  ATGCGCCGCA TCATTAAAA ACACCAGCCC ATAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA ATAGTCATCG CGCGTTTGTG TTCTTGGGG
101 GGAACGCTCC CCATCATCAT GACAGACGCC TTGGCGGCGA ACACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACAGC TTCAATCTCT
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAACCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTCAATGCC
301 GACATCCAAC GGATACTGTA A
```

```
m669.pep
1  MRRIKKHPQ INAPHIVLEI RIMKLHRAFV FLGRKRPHHH DSSLRRQHG
51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQ TAL SRPAVFGYNA
101 DIKRIL*
```

**m669/g669 96.2% identity in 106 aa overlap**

	10	20	30	40	50	60
m669.pep	MRRIIKKHQPINAPHIVLEIRIMKLRHAFVFLGRKRPHHHDSLLRQHGIEGMGDFDKQI					
	:     :     :     :     :     :     :     :     :     :     :     :					
g669	MRRIVKKHQPVNAPHIVLEIRIMKLRHAFVFLGRKRPHHHDRSLRQHGIEGMGDFDKQI					
	10	20	30	40	50	60
	70	80	90	100		

1073

```

m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
g669        FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
1   ATGCGCCGCA TCATTAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAACGTCC  CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGAATC
151 GAAGGGATGG GTTTCGATT  CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pep
1   MRRIKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

m669/a669 98.1% identity in 106 aa overlap

```

              10      20      30      40      50      60
m669.pep    MRRIKKHQPINAPHIVLEIRIMKLHRAFVFLGRKRPHHHDSLRRQHGI EGMGFDFKQI
             |||||:|||||
a669        MRRIKKHQPVNAPHIVLEIRIMKLHRAFVFLGRKRPHHHDRSLRRQHGI EGMGFDFKQI
              10      20      30      40      50      60

              70      80      90      100
m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
a669        FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
1   ATGACTTGTT GCAGGAAGTCT CTTGGCGCGT TCGTGTTCG GGTGGTGAA
51  AAACGCTTCC GCGGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAAGT CGGCTCGTCA AACAGCATCA
251 CGCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCACTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTC GCATTTGCC
401 CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTCAAGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pep
1   MTCCRNLAR SCFGLVKNAS GVSSSRICPL STKITSATS RANPISWVTH
51  IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NSITRGSIAS PRAIATRCWC
101 PPESWEGKAS FLCASEPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNVTRC
151 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
1   ATGACTTGTT GCAGGAAGTCT CTTGGCGCGT TCGTGTTCG GGTGGTAAA
51  AAACGCTTCG GCGGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTCGTCA AACACATTA

```

1074

```

251 CGCGCGGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGTAATGT TTTCAACAC GGTGAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2192; ORF 670>:

```

m670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMFSNTVRC
151 G*

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m670/g670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep    MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
              |||||
g670         MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
              10      20      30      40      50      60

              70      80      90     100     110     120
m670.pep    FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCWPPESWEGKASFLCASPTRSK
              |||||
g670         FITFNTSPTISGSSAEVGSSNSITRGSIASPRAIATRCWPPESWEGKASFLCASPTRSK
              70      80      90     100     110     120

              130     140     150
m670.pep    SSIAFFSACS AFCPLTFIGARVMFSNTVRCGX
              |||||
g670         SSIAFFSACS AFCPLTFIGARVMLSNTVRCGX
              130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2193>:

```

a670.seq
  1 ATGACCTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTCG GGTGCGTAA
 51 AAACGCTTCC GCGGTTTCGT CTTGAGGAT TTGCCCTTA TCACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTCGTG GGTACGCAC
151 ATCATGGTCA TACCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCGGACCAT TCGGGGTCGA GTGCGGAGGT CGGTTCGTCA AACACATTA
251 CGCGCGGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGTTCCATCG CTTTTTCTC TGCCTGTTCC GCATTTTGAC
401 CTTTAACCTT CATCGGTGCG AGGTAATGT TTTCAACAC GGTGAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2194; ORF 670.a>:

```

a670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51 IMVIPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AF*PLTFIGA RVMFSNTVRC
151 G*

```

m670/a670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep    MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
              |||||
a670         MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIMVIPLSAKS
              10      20      30      40      50      60

```

	70	80	90	100	110	120
m670.pep	FITFNTSPTISGSSSAEVGSSNNITRGSIAKPRAIATRCWPPEWEGKASFLCASPTRSK					
a670	FITFNTSPTISGSSSAEVGSSNNITRGSIAKPRAIATRCWPPEWEGKASFLCASPTRSK					
	70	80	90	100	110	120
	130	140	150			
m670.pep	SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX					
a670	SSIAFFSACSAFXPLTFIGARVMFSNTVRCGX					
	130	140	150			

g671.seq

1	ATGATCAGCA	GGGTACAAT	CAAAACGCCT	TTCAATGCAC	CGAATACACC
51	GCCCAAAATG	CGGTGGCAA	AGCCCGAGACC	GACCGCCGAA	ACTGCGCCGG
101	TCAGCAGCGA	ACGGAGCATT	TTCTGGATCA	GACAGGCCAAT	GACGACAACAGG
151	GAAATGAATG	ACAGAgccaa	TGCAAAACAgg	cggggTTGGA	ACGaggCAAA
201	GGCGAGGTcg	gcgaaggGTG	CGGCaaAGAG	TTTggcaaaa	AAGAagggAAA
251	ccaccCATGC	cACCATcgaa	ccTGTTCGC	CAATCACGCC	GCGCATCGTG
301	GAAATGACGA	TGCAGGCGGC	GATCAGCGcg	gAGGCGAGGA	GGTCGGCAAT
351	GGGAGGCTA	TTCAATCGTT	ACGTGGCGCG	CGATGCCGTG	CACGCGCAGT
401	TTGTTCAAA	CGCGTTCGGC	ATCCCTTGCG	TTTTTATAGT	TGCTTGA

g671.pep

1	MISRVTIKTP	FNAPNTPPKM	RLAKRPRTAE	TAPVSSERSI	FWIRQAMTNR
51	EMNDRANANR	RGWNEAKARS	AKGAAKSLAK	KKETTHATIE	PASAITPRIV
101	EMTMQAAMTA	EARRSAMGRL	FIRYLAGDAV	HAQFVQIAFG	IPCVFIVA*

m671.seq

```
1 ATGACCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACGCC
51 GCCCAAAATG CGGT'TGGCAA AGCCCAAACC GACCGCGGAA ACTGCGCTGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAACG ACAGAGCCAA TGCAAAACGG CGGGGT'TGGA ACGAGGCAAA
201 GGCGAGGTCG GCGAAGGAGG CGGCAAAGAG TTTGGCGAAA AAGAAGGAAA
251 CCACCATATC CGCATTGAG CCTGCCTCCG CAATCACGCC GCGCATCGCG
301 GATGACACGA TGCAGGCGCG GATGACGGCG GAGACAGGGA GGT'CGGCAAT
351 GGGGAGGCTA TTCATT'CGT ACCTGACGGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA
```

```
m671.pep
1  MTSRVTIKTP FNAPNTPPKM RLAKPKPTAE TALVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKEAAKSLAK KKETTHAAIE PASAITPRIA
101 DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*
```

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m671.pep	MTSRVTIKTPFNAPNTPPKMLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR					
g671	MISRVTIKTPFNAPNTPPKMLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDRANANR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m671.pep	RGWNEAKARSAKEAAKSLAKKKETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGR.					

```

g671      |||||:|||||:|
          RGWNEAKARS AKGAASLAKKKETTHATIEPASAITPRIVETMQAAMTAEARRSAMGRL
              70           80           90           100           110           120

                130           140           149
m671.pep   FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
          |||||:|:|||||
g671       FIRYLAGDAVHAQFVQIAFGIPCVFIVAX
              130           140

```

a671.seq

a671.pap

m671/a671 93.9% identity in 148 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2201>:

g672.seq

1	ATGAGGAAAA	TCCGCACCAA	AATCTGCGGC	ATCACCACAC	CGGAAGACGC
51	ACTGTATGCC	GCCCACGCCG	GCGCAGACGC	ATTGGGACTG	GTTTTTTACC
101	CCCAAAGCCC	CCGCGCTATC	GACATCATT	AAGCACAATA	AATCGCGGCC
151	GCACTGCCCG	CGTTTGTACG	CGTGTGCGCC	CTTTTCGTCA	ACGAAAGCGC
201	GCAAAACATC	CGCCGCATCC	TTGCCGAAGT	CCGATACAC	ATCATCCAAT
251	TCCACGGCGA	CGAAGACGAT	GCATTCTGCC	GGCAGTTCGA	CCGCCCTTAT
301	ATTAAAGCCA	TTCTGTTCAT	GACGGCATCA	GACATCCGAA	ACGCCGCCAC
351	CGCGTTCCCC	AACGCTCAGG	CAGTCTGTTT	CGATGCCTAT	CACCCCTTCGG
401	AATACGGCGG	CACCGGACAC	CGCTTCGact	Ggagctggt	ggcggAATAT
451	TCGGGCAAGC	CGTGGGTGCT	TGCCGGCGGG	CTGACCCgtt	AAAACGTCGG
501	CGAAGCCGTC	CGCATCACCG	GAGCGGAAGC	GGTCGACGTA	TCCGGCGGCG
551	TGGAAGCGTC	TAAAGGCAAA	AAAGACCCCG	CCAAAGTCGC	CGCCTTTATC
601	GCAACCGCCA	ACCGCTATC	CGGTTAA		



This corresponds to the amino acid sequence <SEQ ID 2202; ORF 672.ng>:

```

g672.pep
  1 MRKIRTKICG ITPEDALYA AHAGADALGL VFYPQSPRAI DIIKAQKIAA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFDRPY
101 IKAIRVQTAS DIRNAATRF NAQALLFDAY HPSEYGGTGH RFDWTLAEY
151 SGKPWVLGG LTPENVGEAV RITGAEAVDV SGGVEASKGK KDKAKVAEFI
201 ATANRLSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

```

m672.seq
  1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
 51 AGCTGCCGCC GCAGCGGCAG GTGCGGATGC CGTCGGGCTG GTCTTTTTC
101 AAGGCAGCAG CCGGGCCGTC GATATTGCC GCGCCAAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCTG CGTTGTCTGC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCTAT
301 ATCAAAGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGAAAC CGCTTCGACT GGACGCTGCT GGCGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCCGTC CGCATCACC GAGCGGAATC GGTGATGTA TCCGGCGGTG
551 TGGAGCGTC TAAAGGCAAA AAAGATGCCG CCAAAGTCGC CGCCTTTATC
601 GCAACCGCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

```

m672.pep
  1 MRKIRTKICG ITPEDAAAA AAAGADAVGL VFFQGSSRAV DIARAKKITA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAATRF DAQALLFDAY HPSEYGGTGN RFDWTLAEY
151 SGKPWVLGG LTPENVGEAV RITGAESVDV SGGVEASKGK KDAAKVAEFI
201 ATANRLSR*

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m672/g672 91.3% identity in 208 aa overlap

m672.pep	10	20	30	40	50	60
	MRKIRTKICGITTPEDAAAAAAGADAVGLVFFQGSSRAVDIARAKKITAALPPFVSVVA					
g672	MRKIRTKICGITTPEDALYA AHAGADALGLVFYPQSPRAIDIIKAQKIAAALPPFVSVVA					
	10	20	30	40	50	60
m672.pep	70	80	90	100	110	120
	LFVNESAQNI RRILAEVPIH IIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAATRF					
g672	LFVNESAQNI RRILAEVPIH IIQFHGDEDDAFCRQFDRPYIKAIRVQTASDIRNAATRF					
	70	80	90	100	110	120
m672.pep	130	140	150	160	170	180
	DAQALLFDAYHPSEYGGTGNRFDWTLAEYSGKPWVLGGGLTPENVGEAVRITGAESVDV					
g672	NAQALLFDAYHPSEYGGTGH RFDWTLAEYSGKPWVLGGGLTPENVGEAVRITGAEVDV					
	130	140	150	160	170	180
m672.pep	190	200	209			
	SGGVEASKGKKDAAKVAEFIATANRLSRX					
g672	SGGVEASKGKKDPAKVAAFIATANRLSRX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

a672.seq

a 672 . pep

```

1 MRKIRTKICG ITTPEDALYA AHAGADALGL VFYQSPRAV DIKAQKITA
51 ALPPFVSUVA LFVNESAQNI RRILAEVPIH IIQFHGDEDD AFRQRFHRPY
101 IKAIRVQTAS DIRNAADRFP DAQALLFDAY HPSEYGGTGH RFDWTLLAEY
151 SGKPWVLWAG LTPENVDEAI RITGAEADV SGGEVASKGK KDPAKVAAFI
201 ATANRLSR*

```

		10	20	30	40	50	60
m672.pep		MRKIRTKICGITTPE	DAAAAAAAGADAVGLVFFQGS	RAVDIARAKKITAALPPFVSVVA			
a672		MRKIRTKICGITTPE	DALYAAHAGADALGLVFYPQSPRAVDI	IKAKKITAALPPFVSVVA			
		10	20	30	40	50	60
		70	80	90	100	110	120
m672.pep		LFVNESAQNIRRILA	EVPIHI IQFHGDEDDAF	CRQFHRPYIKAIRVQTAS	DIRNAATRFP		
a672		LFVNESAQNIRRILA	EVPIHI IQFHGDEDDAF	CRQFHRPYIKAIRVQTAS	DIRNAADRFP		
		70	80	90	100	110	120
		130	140	150	160	170	180
m672.pep		DAQALLFDAYHPSEYGGT	GNRFDWTL LAEYSGKPWVL	AGGLTPENVGEAVRITGA	ESVDV		
a672		DAQALLFDAYHPSEYGGT	GHRFDWTL LAEYSGKPWVL	AGGLTPENVDEAIRITGA	EAVDV		
		130	140	150	160	170	180
		190	200	209			
m672.pep		SGGVEASKGKKDAAKVAAFI	ATANRLSRX				
a672		SGGVEASKGKKDPAKVAAFI	ATANRLSRX				
		190	200				

g673.seq

1	ATGGATATTG	AAACCTTCCT	TGCAGGGGAA	CGCGCCGCCG	GCGGATACCG
51	TTGCGGCTTC	GTGGCGATTG	TCGGTCGTCC	GAACGTGGGC	AAATCAACGC
101	TGATGAACCA	TCTCATCGGT	CAGAAAAATCA	GTATTACGAC	CAAAAAGGCG
151	CAGACGACGA	GCAACCGCGT	AACGGGGATT	TATACCGAGC	ATACCGCGCA
201	GTTCTGTGTT	GTCGATACGC	CGGGCTTTCA	AACCGACAC	GCACACGCGC
251	TCAACGACAG	GCTGAATCAA	AATGTTACCG	AGGCGCTCGG	CGGTGTGGAT
301	GTCTGGGTTT	TCGTCGTGGA	GGCGTATCGC	CTTACCGATG	CCGACCGCGT
351	CGTGTGTGAA	CAACTGTCCCA	AGCACATCGC	GGTCATTTTA	GTGATCAACA
401	AAATCGACAA	GGACAAGGCG	AAAGACCGTT	ACGCGTGGGA	GCGGTTTGTT
451	GCCCAAGTGC	GCGCGCGAAT	TGAATTTGCG	GCGGCGGAGG	CGGTCAGTGC
501	GAAACACGGT	TTGCGGATTG	CCAACCTGGT	GGAGCTGCTC	AAGCCGTATC
551	TGCCCCAAAG	CGTACCGATG	TATCCCGAAG	ACATGGTTAC	GGACAAATCG
601	GCGCGTTTTT	TGGCGATGGA	AATCGTGCCT	GAAAACTCT	TCCGCTATTT

1079

```

651 GGGCGAGGAG CTGCCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTTGGT CGACAAAGAA
751 AGCCAAAAGG CGATTTTGAT CGGTAAAGGC GGGGAGCGTT TGAAAAAAT
801 TTCCACCGAA GCGCGGCTGG ATATGGAAAA ACTGTTTGAT AACAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
901 TTCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

```

g673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR LTDADRVVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
151 AQVRAEFEDA AAEVSAKHG LRIANLLELL KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD NKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

```

m673.seq
1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CCGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GGCGATGCGC TTTACCGATG CCGACCGCGT
351 CGTGTGTAAG CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGCTTTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTGCG GCGGCGGAGG CGGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCCT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CAATTTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

```

m673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEDA AAEVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

          10      20      30      40      50      60
m673.pep MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
          |||
g673      MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
          10      20      30      40      50      60

          70      80      90     100     110     120
m673.pep YDDTAQFVFVDTPGFQTDH RNALNDRLNQ NVTEALGGVDVVVFVVEAMRFTDADRVVLK
          |||

```

1080

```

g673      YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRLTDADRVVLK
           70      80      90      100     110     120

           130     140     150     160     170     180
m673.pep  QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           130     140     150     160     170     180

           190     200     210     220     230     240
m673.pep  KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           190     200     210     220     230     240

           250     260     270     280     290     300
m673.pep  IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVSGWADDIR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVSGWADDIR
           250     260     270     280     290     300

m673.pep  FLRELGLX
           |||||
g673      FLRELGLX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2211>:

```

a673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCGCCCG ACGGATACCG
51  TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAATCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTTGTGTTT GTCGATACGC CCGGTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACCG TTTGAATCAA AACGTTACCG AGGCACTCGG CGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA AGCGATGCGT TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
401 AAATCGATAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTGTT
451 GCCCAGGTGC GCGCCGAATT TGAATTGCG GCGGCGGAGG CGGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TAGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CGATTTTAAT CGGCAAAGGC GGGAGCGGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2212; ORF 673.a>:

```

a673.pep
1  MDIETFLAGE RAADGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51  QTTRNRVTGI YTDDTAQFVF VDPGFQTDH RNALNDRLNQ NVTEALGGVD
101  VVVVFVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151  AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYLPESVEM YPEDMVTDKS
201  ARFLAMEIVR EKLFRYLGE ELPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251  SQKAILIGKG GERLKKISTE ARLDMEKLFDT KVFVKVWVK VSGWADDIR
301  FLRELGL*

```

m673/a673 99.7% identity in 307 aa overlap

```

           10      20      30      40      50      60
m673.pep  MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a673      MDIETFLAGERAADGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           10      20      30      40      50      60

```

1081

	70	80	90	100	110	120
m673.pep	YTDDTAQFVFVDTPGFQTDHRNALNDRNLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
a673	YTDDTAQFVFVDTPGFQTDHRNALNDRNLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m673.pep	QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
a673	QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m673.pep	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR					
a673	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m673.pep	IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVSGWADDIR					
a673	IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVSGWADDIR					
	250	260	270	280	290	300
m673.pep	FLRELGLX					
a673	FLRELGLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2213>:

```

g674.seq
1  ATGAAACAG CCCGCCGCGG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAACATCC
101 GCGAAATGTC CGACTTTGCC AAAGCGGACG AAGAATTGTT CAACAACTC
151 TTCTTCGGCA CACAAACCAA TGCAGCGGAC TACATCCAAA AAATCCGCC
201 GCTGCTCGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTTTCCGCTA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2214; ORF 674.ng>:

```

g674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL
51  FFGTQTNAAD YIQKIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2215>:

```

m674.seq
1  ATGAAACAG CCCGCCGCGG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAACATCC
101 GCGAAATGTC CGACTTTGCC AAGCGAGACG AAGAATTGTT CAACAACTT
151 TTCTTCGGCA CGCAAACCAA TGCAGCAGAG TATATCCGAC AAATCCGCC
201 GCTACTTGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2216; ORF 674>:

```

m674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL

```

1082

51 FFGTQTNAEE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP  
 101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R\*

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m674/g674 97.9% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAEE					
g674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLDRDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	:					
g674	YIQKIRPLDRDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
g674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2217>:

a674.seq  
 1 ATGAAAACAG CCCGCCGCGG TTCCCGCGAG CTGCGGTAC AAGCCGTTTA  
 51 CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAGATTGCT AAAACATCC  
 101 GCGAAATGCC CGACTTTGCC AAGGCAGACG AAGAATTGTT CAACAAACTT  
 151 TTCTTCGGCA CGCAAACCAA TGCGGCAGAG TACATCCGAC AAATCCGCCC  
 201 CCTGCTCGAC CGCGACGAAA AAGACCTCAA CCCATCGAA CGCGCCGTCC  
 251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAC GCCCTACCCC  
 301 GTCATCATCA ACGAAGCCAT CGAAGTAACC AAAACCTTCG GCGGCACGGA  
 351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC  
 401 GTCCCGACGA GCCCAAACGC CGTTGA

This corresponds to the amino acid sequence <SEQ ID 2218; ORF 674.a>:

a674.pep	1	MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMPDFA KADEELFNKL				
	51	FFGTQTNAEE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP				
	101	VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*				
m674/a674	99.3% identity in 141 aa overlap					
	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAEE					
a674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMPDFAKADEELFNKLFFGTQTNAEE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLDRDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
a674	YIRQIRPLDRDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
a674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

g675.seq

```
1 ATGAACACCA TCGCCCCaa cctcgacgGC AAACACCTCC GCATCGGCAT
51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAa catcaccgtc
151 gccaccgtac CCGGCGCGCT TGAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTCCGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
301 GGCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
351 CACCGAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTTCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

g675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSQM LKVCCTRLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVANESGAGI
101 GRVALDYNIP IANAVLTEN DAQAIERIGE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2221>:

m675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTTCCGAA AAGTTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTGAG CTGGTTTCCA ACGAATCCGG AGCAGGCGTC
301 AGCCGCGTCG CACTCGACTA CAATATCCCG ATTGCCAATG CCGTCCTAAC
351 CACCGAAAAC GACGCGCAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCCGTC GAATGCGCCA ACCTCGTCAA CCTGCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2222; ORF 675>:

m675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCTRLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV
101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m675/g675 96.8% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEM LKVCCTRLQELGVADENITVATVPGALEIP					
g675	MNTIAPNLDGKHLRIGIVQARFTNEIGSQMLKVCCTRLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
g675	IALMNFASSEKFDALIAIGVVIRGETYHFELVANESGAGIGRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEX					
g675	DAQAIERIGEKASDAAKVAVECANLVNLLLEEQFEDEX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2223>:

a675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201 CTCTTCTGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTTATCCGTG
251 GCGAAACCTA CCATTTGAG CTGGTTTCCA ACGAATCCGG AGCAGGGGTC
301 AGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAATG CCGTCCTGAC
351 CACGGAAC GACGCACAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTCCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2224; ORF 675.a>:

a675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCTRLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV

```



1085

101 SRVALDYNIP IANAVLT TEN DAQAIERIEE KASDAAKVAV ECANLVNLLL  
 151 EEQFEDEE\*

m675/a675 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCRTLQELGVADENITVATVPGALEIP					
a675	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVS NESGAGVSRVALDYNIP IANAVLT TEN					
a675	IALMNFASSEKFDALIAIGVVIRGETYHFELVS NESGAGVSRVALDYNIP IANAVLT TEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
a675	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

g677.seq  
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTtg  
 51 ggAAACGGTG CGCTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT  
 101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGGC CTTCGGCGGT  
 151 GTTCAAAACC ACTTCGTCGC CTTGCGCGCG TTTAATCAGG CAACGCGCCA  
 201 ACGGCGAAAT CCAAGAAATT TTGTTTTCG CCGTATCGAT TTCATCGACG  
 251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCGCGCA ACAGACCGAC  
 301 GGTGCGCCCG AAAAATACTT GGTGCGTCGC TTCGCGCAAT TCGGGATCGA  
 351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAACGGAT GCGGCGGTGCG  
 401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCGGT TTTGCTGCG  
 451 GTCGCGGTTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT  
 501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG  
 551 GCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

g677.pep  
 1 MPQILVRIFL IRYSEFIWETV RLCRFRRHSR SVDFDVFDRK DFNFLTAFR  
 51 VQNHVAFAR FNQATRRRN PRNFVLRGID FIDADDFDGL LAPVAAQQT  
 101 GRAEKYLVR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA  
 151 VAVACRPVDD LDDFGAFFID QLIKLVFQCL PSGGRNVVFG FGTHIVCG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

m677.seq  
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTtg  
 51 GGAAACGGCG CGCTTTTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT  
 101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGCC CTTCGGCGGT  
 151 GTTCAAAACC ACTTCGTCGC CTTGCGCGCG TTTAATCAGA CAACGAGCCA  
 201 GCGGCGAAAT CCAAGAAATT TTGTTTTCG CCGTATCGAT TTCATCGATG  
 251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGTCGCGCA ACAGTCCGAC  
 301 CGTCGCGCCG AAAAACACTT GGTGCGTCGC TTCGCGCAAT TCGGGATCGA  
 351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAACGGAT GCGGCGGTGCG  
 401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCGGT TTTGCTGCG  
 451 GTCGCGGTTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT  
 501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG  
 551 GCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

m677.pep  
 1 MPQILVRIFL IRYSEFIWETA RLCRFRRHSR SVDFDVFDRK DFNFLTPFR

1086

51 VQNHFAVAFAR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVVAQQSD  
 101 RRAEKHLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA  
 151 VAVACRPVDD LDDFGAFFVD QLIKLVFQCL PSGGRNVVFG FGTHIVCG\*

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m677/g677 94.9% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVDRKDFNFLT	PFRRVQNHFAVAFAR				
g677	MPQILVRIFLIRYSFIWETVRLCRFRHRSVDFDVDRKDFNFLT	AFRRVQNHFAVAFAR				
	10	20	30	40	50	60
	70	80	90	100	110	120
m677.pep	FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG					
g677	FNQATRQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTDRRAEKYLVGRFAQFGIDDDG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m677.pep	SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL					
g677	SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFIDQLIKLVFQCL					
	130	140	150	160	170	180
	190	199				
m677.pep	PSGGRNVVFGFGTHIVCGX					
g677	PSGGRNVVFGFGTHIVCGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2229>:

a677.seq  
 1 ATGCCGAGCAG TTTTGGTGCG GATTTTCCTC ATTCCGGTATT CCTTTATTTG  
 51 GGAAACGGCG CGTTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT  
 101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCAGCGC CTTCGGGCGT  
 151 GTTTAAACCC ACTTCGTCGC CTTACGCGCG TTTAATCAGA CAACGAGCCA  
 201 GCGGCGAAAT CCAAGAAATT TTGTTTTCGC CGGTATCGAT TTCATCGATG  
 251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCCGCGCA ACAGACCGAC  
 301 GGTCGCGCCG AAAAACACTT GGTCGGTCGC TTCGCGCAAT TCGGGATCAA  
 351 CGACGACGGC GGCTTCCAAA CGCTTGGTCA GGAAACGGAT GCGGCGGTGCG  
 401 ATTTGCGGCA TACGGCGGTT GCGGTAAAGG TAGTCGCGCT TTTCGCTGCG  
 451 GTCGCGGTTG CCTGCGCGCC AGTTGACGAT TTGGACGATT TCGGGGCGTT  
 501 CTTTATTAAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG  
 551 GCGTAATGT AGTTTGTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2230; ORF 677.a>:

a677.pep  
 1 MPQILVRIFL IRYFSIWETA RLCRFRHRSR SVDFDVDRK DFNFLTFFRR  
 51 V\*NHFVAFTR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVAAQQT  
 101 GRAEKHLVGR FAQFGINDDG GFQTLGQETD AAVDFAHTAF AVKVVAVFAA  
 151 VAVACRPVDD LDDFGAFFIN QLIKLVFQCL PSGGRNVVFG FGTHIVCG\*

m677/a677 93.4% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVDRKDFNFLT	PFRRVQNHFAVAFAR				
a677	MPQILVRIFLIRYSFIWETARLCRFRHRSVDFDVDRKDFNFLT	PFRRVXNHFAVAFTR				
	10	20	30	40	50	60
	70	80	90	100	110	120

1087

```

m677.pep  FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG
          |||||||||||||||||||||||||||||||||||||||||||||
a677      FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGINDDG
          70      80      90      100     110     120

          130     140     150     160     170     180
m677.pep  SLQTFGQETDAAVDEAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL
          ::|||:|||||||||||||||||||||||||||||||||||||
a677      GFQTLGQETDAAVDEAHTAFVAVKIVAVFAAVAVACRPVDDLDDFGAFFINQLIKLVFQCL
          130     140     150     160     170     180

          190     199
m677.pep  PSGGRNVVFGFGTHIVCGX
          ||||||||||||||||||
a677      PSGGRNVVFGFGTHIVCGX
          190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2231>:

```

g678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GCCTcgcCGG TCATCGCCGC
51  CTGCATCGTC ATTCCACGA TGCGCGGCGT GATTGCGGAA GCAGgttcGA
101 TGGTGGCATG ggtggTTTcc tTCTTTTttg ccAAACTCTt tGCCGCACcc
151 ttcgcccACC TCGCCTTTGc ctCGTTCCAA ccccgccTGT TTGCAttggc
201 tCTGTcATTC ATTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTcGCT GCTGACCGGC GCAGTTTCGG CGGTcGGTCT GGGCTTTGCC
301 AACCGcATT TGGCGGcGTG ATTCGGTGCA TTGAAAGCGG TTTTGATTGT
351 TACCCTGCTG ATCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCAACA GTCCTATACC GTACCGTTTT TCGTATCGCT TTCCGAAGCG
451 GTGTAAACC atacggaCAA CGCaccgaa tCCctcgacg acgactaa

```

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

```

g678.pep
1  MNSLPIADLL ASAVIAACIV ISTMRGVIAE AGSMVAWVVS FFFAKLFAAP
51  FADLAFASFO PRLFALALSF ISLEVIACLI QKMLRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGV LIVTLL IMLASKTDLP DTEEWQSYT VPFFVSLSEA
151 VLNHTDNAPE SLDDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2233>:

```

m678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GTCTCCGCCG TCATCGCCGC
51  CTGCATCGTG CTATCCGCGA TGCGCGGCGT GATTGCGGAG GCAGGCTCAA
101 TGGCGGCATG GGTGGTTTCC TTCTTTTTCG CCAAACCTCTT TGCCGCCTCC
151 TTCGCCGACC TCGCCTTTGC CTCGTTCCAA CCCCcGCTGT TTGCATTGGC
201 TCTGTcGTTc ATTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTcGCT GCTGACcAGC GCAGTTTCGG CGGTcGGTTT GGGCTTTGCC
301 AACCGcATT TGGCGGcCGT ATTCGGTGCA TTGAAAGCGG TTTTGATTGT
351 TACCCTGCTG GTCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

```

m678.pep
1  MNSLPIADLL VSAVIAACIV LSAMRGVIAE AGSMAAWVVS FFFAKLFAAS
51  FADLAFASFO PRLFALALSF ISLEVIACLI QKMLRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGV LIVTLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m678/g678 89.7% identity in 165 aa overlap

1088

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ					
	:     :     :     :     :     :     :					
g678	MNSLPIADLLASAVIAACIVISTMRGVIAEAGSMVAWVVSFFFAKLFAAPFADLAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	:     :     :     :     :     :     :					
g678	PRLFALALSFISLFVIACLIQKMLRSLTGAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	:     :     :     :     :     :     :     :					
g678	IMLASKTDLPDTEEWQSYTVFFVSLSEAVLNHTDNAPESLDDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2235>:

```

a678.seq
1  ATGAATAACC TCCCGTTGC CGACCTCCTC GTCTCCGCCA TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TGC CGCGCGT GATTGCGGAG GCTGGCTCAA
101 TGGCGGCATG GGTGGTTGCC TTTTTCG CCAAACCTCT TGCCGCACCC
151 TCGCGGACA TCGCCTTGC ATCGTTCCAA CCCC GCCTGT TTGCATTGGC
201 TCTGTCGTTT ATTTCCCTAT TCGTCATTGC CTGTCTGATC CAGAAAATAC
251 TCCGCTCGCT GCTGACCGGG GCAGTTTCGG CCGTCGGTTT GGGCTTTGCC
301 AACC GCATTT TGGGCGGCGT ATTCGGTGCA TTGAAAGGCA TTTTGATTAT
351 TACCTGCTG GTCATGCTCG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2236; ORF 678.a>:

```

a678.pep
1  MNNLPVADLL VSAIIAACIV LSAMRGVIAE AGSMAAWVVA FFFAKLFAAP
51  FADIAFASFQ PRLFALALSF ISLFVIACLI QKILRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGILITLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

m678/a678 93.9% identity in 165 aa overlap

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ					
	:     :     :     :     :     :     :					
a678	MNNLPVADLLVSAIIAACIVLSAMRGVIAEAGSMAAWVVAFFFAKLFAAPFADIAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	:     :     :     :     :     :     :					
a678	PRLFALALSFISLFVIACLIQKILRSLTGAVSAVGLGFANRILGGVFGALKGILITLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	:     :     :     :     :     :     :					
a678	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2237>:

```

g680.seq
1  ATGACGAAGG GCAGTTCCGC GATGTCCAGC CCACGCGCGG CGATATCGGT
51  GCGCAGCAGG ACGCGCAGGC TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCTGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGTTG

```

1089

```

151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTtttgCA
201 AAAGACGATA ACTTGGTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251 GGTTGCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTG
301 GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTG
451 TCGATAAAC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501 TTCGGCTTTG TTTAACTGA TGTTTTCTG TTTACATGG TCGAGCAGCC
551 GTCCGACGGT GGCAGCACT ATTTCCGAGC CGGCACGCAG GTCGGCGGTT
601 TGTTTGTTCA TGTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651 GTTTTTAATg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

g680.pep

```

1 MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
51 RRTSSRVTRS TLCLVLQKTI TWFICRSTIS RSSRLRFWKV STAMMCCSTL
101 ALVVFWAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SINPISNMRS ASSRTTISAL FKLMMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSMLTPPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

m680.seq

```

1 ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
51 GGCACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CCGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTTTTCGA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGTTTTGGCG GGCAGACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTG
451 TCGATAAAC CCATATCCAG CATACGGTCG GCTTCGTCCA AAACGACGAT
501 TTCGACTTTG TTCAAATGGA TGTTTTCTG TTTACGTGG TCGAGCAGCC
551 GTCCGACGGT GGCAGCAGC ATTTCCGAGC CGGCACGCAG GTCGGCGGTC
601 TGTTTGTTCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTTGATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

m680.pep

```

1 MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51 RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVFWAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPENK TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m680/g680 90.9% identity in 220 aa overlap

	10	20	30	40	50	60
m680.pep	MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS					
g680	MTKGSSAMSSPRAAISVATRTRRLPSLKALSVSSLLCWERSPCACADRLRRTSSRVTRS					
	10	20	30	40	50	60
m680.pep	70	80	90	100	110	120
	TLCLVLQNTMTWFIKSTISRSSRLRFKXVSTAMMCCSTLALVVFWAATSTVSGAFMKSC					
g680	TLCLVLQKTITWFIKSTISRSSRLRFKXVSTAMMCCSTLALVVFWAATSTVSGAFMKSC					
	70	80	90	100	110	120
m680.pep	130	140	150	160	170	180
	ASLRIGAEKVAEKSRVWRWRGSICMILRMSSSIKPISSIRSASSKTTISTLFKWMFFCFTW					

```

g680      |||||
          ASLRIGAEKVAEKSRVWRWGSICMLRMSSINPISNMRSASSRTTISALFKLMFFCFTW
          130      140      150      160      170      180

          190      200      210      220
m680.pep  SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX
          |||||
g680      SSSRPTVATTISQPARRSAVCLSLMTPPKRTVCRSGRFLMX
          190      200      210      220

```

a680.seq

1	ATGACGAAGG	GCAGTTCGGC	AATATCCAGC	CCCCGCGCGG	CGATATCGGT
51	GGCGACGAGG	ACGCGCAGGT	TGCCGCTCTT	GAAGGCGTTG	AGTGTTTTGA
101	CGCGCGCTTG	TTGGGAACGG	TGCGCGTGTA	TGCGCTGTGC	GGACAGGTTG
151	CGGCGCACCA	GTTGCGCGCT	TACGCGGTGC	ACGCTTTTGT	TGGTTTGTGA
201	GAACACGATG	ACCTGGTTCA	TATGCAAATC	GACAATCAGC	CGTTCGAGCA
251	GGTTGCGCTT	CTGAATGGTA	TCGACGCGCA	TGATGTGCTG	CTCGACGTTG
301	GCGTTTGGTG	TGCTTGGCGC	GGCGACTTCG	ACGGTTTCGG	GCGCGTTTAT
351	GAAGTCTTGC	GCCAGTTTGC	GTATCGGGGC	GGAGAAGGTG	GCGGAAAAGA
401	GCAGGGTTTG	CGGTGGGCGG	GGCAGCATCT	GCATGATTTT	GCGGATGTGC
451	TCGATAAAAC	CCATATCCAG	CATACGGTCG	CGTTCGTCCA	AAACGACGAT
501	TTCGACTTTG	TTCAAATGGA	TGTTTTTCTG	TTTCAGTGGG	TGCAGACGCC
551	GTCCGACGGT	GGCGACGACG	ATTTCGCAGC	CGGCACGCAG	GTCGGCGGTC
601	TGTTTGTCCA	TATTCATACC	GCCGAACAAG	ACGGTGTGGC	GCAGCGGCAG
651	GTTTTTGATG	TAG			

a680.pep

1	MTKGSSAIISS	PRAAISVATR	TRRLPSLKLW	SVSSRLCWER	SPCIACADRL
51	RTRTSSRVTRS	TLCLVLQNTM	TWFIKCTSTI	RSRSLRWF*V	STAMMC CSTL
101	<u>ALVVSCAATS</u>	TVSGAFMKSC	ASLRIGAEKV	AEKSRVWVRW	GSICMILRMS
151	SIKPISSIRS	ASSKTTISTL	FKWMEFCFTW	SSSRPTVATT	ISQFARRSAV
201	CLSIFFPPNK	TVWTRSGRFL	*		

	10	20	30	40	50	60
m680.pep	MTKGSSAMSSPRAAMS VATRTRRLPSLKALSVSSRLCWERSPC IACADRLRRTSSRVTRS					
a680	:     :     :     :     :     :     :     :					
	10	20	30	40	50	60
<hr/>						
	70	80	90	100	110	120
m680.pep	TLCLVLQNTMTWFICKSTISRSSLRF XMVSTAMCCSTLALVVFCAATSTVSGAFMKSC					
a680	:     :     :     :     :     :     :     :					
	TLCLVLQNTMTWFICKSTISRSSLRF XMVSTAMCCSTLALVVSCAATSTVSGAFMKSC					
	70	80	90	100	110	120
<hr/>						
	130	140	150	160	170	180
m680.pep	ASLRIGAEKVAEKS RVWWRGSICMILRMSSIKPISSIRSASSKTITSTLFKWMFFCFTW					
a680	:     :     :     :     :     :     :     :					
	ASLRIGAEKVAEKS RVWWRGSICMILRMSSIKPISSIRSASSKTITSTLFKWMFFCFTW					
	130	140	150	160	170	180
<hr/>						
	190	200	210	220		
m680.pep	SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX					
a680	:     :     :     :     :     :     :     :					
	SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX					
	190	200	210	220		

g681.seq  
1 ATGACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCGG AAGAGGCCAA  
51 GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGcgacga

1091

```

101  tgatgtTTTC GTCTGCTACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151  TTGAGCATTT GGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201  GATGCGGAGG TGTTTGCCgt cgaggttgGG GCGCATGGTG TTCATTGGGT
251  GTCCTTTGGT ATTCGGGGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301  CGGCTGCCAG TCGGCAACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351  ACGCGCTGCC TTCGGGTTGG GAAAGCAGTG CGGCGGTTTC AGGGTTGGTT
401  TTGGTGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCGG GGTCTCGGT
451  GTATTCGTCG GTTTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501  CAAAAACGGG GGCTTCGCGG TAAAGGAAGC CGACGGGCCG GTTTTGTTTG
551  GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601  TGCAAATGCG TTCATTGCGG GAATACGTTG GGGGGGGGGA AACTTGCGGA
651  TTTTACCACG ATTCGCCGCT TGTCGGCAGA CGGCGGCGGT TTGGTGGTAC
701  AATGTGCGCC GTTTGCAGCC TTAAGGTGTT TCTGTATTTT TGGAGTATGG
751  AAACGCATTC GGGCTGTTTT TTGCGGAAGA CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

```

g681.pep
1  MTTDMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVGNLEEC AVFGKLPRAA FGLGKQCGGF RVGFGDVGEA DDAEVVGVVG
151 VEVGFVAAEE TPAAVVFKNG GFAVKEADGP VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTL GGGKLADFTT IPALSADGGG LVVQCAPFAA LRCFCIFGVW
251 KRIRAVFCGR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

```

m681.seq
1  ATGACGACGC CGATGGCAAT CAGTGCCTCA AACTTTTCGG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GCGCATGGTG TTCATTGGGT
251 GTCCTTTGGT ATTCGGAGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301 CGGCTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351 ATGCGCTGCC TTCGGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGCGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCGG GATCGTCGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCCG GTTTTGTTTG
551 GCGACGGTGT TGGTGGCGAT ACAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTACGG GAATACGTTG GGGG.AAAAC TTACGGATT
651 TACCACGATT CGTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTTTG AGTATGGAAA
751 CGCATTCGGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

```

m681.pep
1  MTTDMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVGDGLEC AVFGKLPCAA FGLGEQCGGF RVGFGDVGEA DDAEVVRIVG
151 VEVGLVAAEE TPAAVVFKNG GFAVEEADGP VLFGDGVGGD TAVECRGKCL
201 CKCVHYGNTL GXKLTDFTTI RALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGR *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

m681/g681

```

          10      20      30      40      50      60
m681.pep  MTTDMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
          |||
g681      MTTDMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPISLV
          10      20      30      40      50      60

```

1092

```

      70      80      90      100      110      120
m681.pep  KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRKLVSVLRLPVG DGLECAVFGKLPCAA
          |||||
g681      KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRKLVSVLRLPVG NGLECAVFGKLPRAA
          70      80      90      100      110      120

      130      140      150      160      170      180
m681.pep  FGLGEQCGGFRVGFVDVGEADDAEVVRIVGVFVGLVAAEETPAAVVFKN GGFAVEEADGP
          |||:|||||
g681      FGLGKQCGGFRVGFVDVGEADDAEVVGVGVFVGLVAAEETPAAVVFKN GGFVAVKEADGP
          130      140      150      160      170      180

      190      200      210      220      230      239
m681.pep  VLFGDGVGGDTAVECRGKCLCKCVHYGNTLGX-KLTDFTTIRALSADGGGLV VQCAPFAA
          |||||:|||||
g681      VLFGDGVGGDAAVECRGKCLCKCVHCGNTLGGGKLADFTTIPALSADGGGLV VQCAPFAA
          190      200      210      220      230      240

      240      250      260
m681.pep  LRCFCIFGVWKRIRAVFCGRRX
          |||||
g681      LRCFCIFGVWKRIRAVFCGRRX
          250      260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2247>:

```

a681.seq
1  ATAACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCAG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTC GTCTGCCACG CCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTG CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GCGCATGGTG TTCATTGAGT
251 GTCCTTTGGT ATTCGGAGGT TTCGGAATGC CGTCTGAAGG GTCAGTCCTT
301 AGGTTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCT GCCAATTCCC
351 ACGCGCTGCC TTCAGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGTGATAT CCGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCTGCGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCTG GTTTTGTTTG
551 GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTGCGG GAATACGTT. GGGGGAAC TTGCGGATT
651 TACCACGATT CTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGAAA
751 CGCATTCCGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2248; ORF 681.a>:

```

a681.pep
1  ITTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSISLPISLV KRACTMPMRR CLPSRLGAMV FIECPLVFGG FGMPSEGSVL
101 RLPVGDGLEC AVFCQFPRAA FRLGEQCGGF RVFGDIGEA DDAEVVRVVG
151 VVGLVAAEE TPAAVVFKN GFAVEEADGL VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTX GGLADFTTI LALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGRR *

```

m681/a681 90.8% identity in 260 aa overlap

```

      10      20      30      40      50      60
m681.pep  MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
          :|||||
a681      ITTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
          10      20      30      40      50      60

      70      80      90      100      110      120
m681.pep  KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRKLVSVLRLPVG DGLECAVFGKLPCAA
          |||||
a681      KRACTMPMRRCLPSRLGAMVFIGCPLVFGGFGMPSEGSVLRLPVG DGLECAVFCQFPRAA
          70      80      90      100      110      120

```



1093

	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGF	GDVGEADDAEVVR	IVGVFVGLVAAEET	PAAVVFKNGGF	AVEEADGP	
a681	FRLGEQCGGFRVGF	DIGEADDAEVVR	VGVFVGLVAAEET	PAAVVFKNGGF	AVEEADGL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVE	CRGKCLCKCVHY	NTLGXKLTDFTT	IRALSADGGGLV	VQCAPFAAL	
a681	VLFGDGVGGDAAVE	CRGKCLCKVHCG	NTXGGKLADFTT	ILALSADGGGLV	VQCAPFAAL	
	190	200	210	220	230	240
	250	260				
m681.pep	RCFCIFGVWKRIR	AVFCGRRX				
a681	RCFCIFGVWKRIR	AVFCGRRX				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

g682.seq

```

1  ATGCGCGATT TCGCCGATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCCTGAGC CCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTATATTTGT GTGAATGATG AAATAAAAAT GCCGTCTGAA CCCGATTGGA
251 TTCAGACGGC ATTTTGTATG GCAGGATTTA TTCGCTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

g682.pep

```

1  MRDFAVWVPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWQTAFCM AGFIRFPTDR
101 PILTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

m682.seq

```

1  ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTC
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGGTTTCC AACTGACCGA
301 CCCATTCCGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

m682.pep

```

1  MRDETVWVS YGKWRKNWDIR YCLLHLIHL STRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY... EMAMPSEP DWIQTAFCA YGFIRFPTDR
101 PIRTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

m682/g682

[illegible]

a682.seq

```
1 ATGCGCGATT TTACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51 GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 ATAT.....
251 .....TATA TTCGTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCCGAC AGGCGTTGTT CGGATTTGCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA
```

```
a682.pep
1 MRDFTVWVSY GKWRKNWDIR YCLLHLIHLN STRLRKCGRI LSGICEPFCL
51 ITPDLTMHYC PILILIEY.. ..... ..YIRFPTDR
101 PILTRPTGVV RISPRTGFY PTRSLPKSKK AYK*
```

		10	20	30	40	50	60
m682.pep		MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEFFCLITPDLTMHYC					
a682		MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEFFCLITPDLTMHYC					
		10	20	30	40	50	60
		70	80	90	100	110	120
m682.pep		PILILIDYEMAMPSEPDWIQTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFRYPTRS					
		:	:	:	:	:	:
a682		PILILIEY-----YIRFPTDRPILTRPTGVVRISPRTGFRYPTRS					
			70	80	90	100	
		130					
m682.pep		LPKSKKAYGX					
a682		LPKSKKAYGX					
		110					

g683.seq

1	ATGATTAAGG	AAACCCTAAT	CGGCCCAATC	TTCCTATCTT	TCGTTTTACT
51	CCCTATTTTG	ATACCCGCCT	GCAGCACACC	GGACAAGTCT	GCCCAGTGGG
101	AAAATATCGG	CAACAATCTA	AACGGCAATA	TTCATACATA	TATTAATATA
151	GACAGTGTGA	GAATAAACGG	AATCTGTATG	ATTTTCCAAG	ATAAAAAAGT
201	TGTTACCAAT	CTGAACAAG	AACGTTTTCG	CAACACCCCC	GCATACAAGA
251	CTGCCATTGC	CGAGTGGGAA	ATCCACTGCA	ACAACAACAC	ATACCGGTTA
301	AGTTTCGCTAC	AGTTATTGTA	TACAAAAAAC	ACGGAAATTT	CCACACAATA
351	CTACACAGCC	TCTTCCCTCC	GCCCGATGAG	CATCCGTGCC	GGGACATTA

1095

401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683>:

g683.pep

```

1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMISILS GTLTEKQYET VCGKKL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

m683.seq..

```

1 ATGATTAAGG AAACCTAAT GCGCCCAATC TTCCTATCTT TCGTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201 TGTTACCAAT CTAAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAA ACTCTG A
```

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

m683.pep..

```

1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
101 SSLQLFDTKN TEISTQNYTA SSLRPMISILS GTLTEKQYET VCGKKL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

m683/g683 99.3% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPIFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
g683	MIKETLMRPIFLSFVLLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
g683	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMISILSGTLTEKQYETVCGKKLX					
g683	SSLRPMISILSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

a683.seq

```

1 ATGATTAAGG AAACCTAAT GCGCCCAATC TTCCTATCTT TCGTTTATT
51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCNAG ATAAAAAAGT
201 TGTTACCAAT CTAAAACAAG AACGTTTTCG CNACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AATTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAA ACTCTG A
```

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

a683.pep

```

1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
51 DSVRKNGNLM IFXDKKVVVN LKQERFAXTP AYKTAIAEWE IHCNNKTYRL
```

101 SSLQLFDTKN TEISTQXYTA SSLRPMISLS GTLTEKQYET VCGKKL\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 683 shows 97.9% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. meningitidis*:

m683/a683 97.9% identity in 146 aa overlap

```

      10      20      30      40      50      60
m683.pep  MIKETLMRPIFLSFVLFPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM
a683      |||||
      10      20      30      40      50      60
m683.pep  IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA
a683      |||||
      70      80      90      100     110     120
m683.pep  IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA
a683      |||||
      70      80      90      100     110     120
m683.pep  IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQXYTA
a683      |||||
      130     140
m683.pep  SSLRPMISLSGTLTEKQYETVCGKKLX
a683      |||||
      130     140
m683.pep  SSLRPMISLSGTLTEKQYETVCGKKLX
a683      |||||
      130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2261>

```

g684.seq
1  ATGCGCCTTT TCCCATCGC CGCCGCCCTG ACGCTTGCCG CCTGCGGTAC
51  TGTGCAAAGC ACACAATATT TCGTGTGCC CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGCGGCGGAA ACCGCCGTCG AAGTCCGTCT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCATCAACAC
201 CGCACAAAAC CATGTTTGGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGGACA GCACACGCAC CTTTGTTCCT
301 GCCTCAGCA GCGGCAGTAC CGACAAATGG ACGGTCTATA TCGACGCATT
351 CCAAGGCAGC TACACGGGCA AAACCCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CCATGACCGC CGCACTCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG GTCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2262; ORF 684>:

```

g684.pep
1  MRLFPIAAL TLAACGTVQS TQYFVLPDSR YIRPATQGGG TAVEVRLAEP
51  LKRGGVLYQT DRYRLNTAQN HWADTLDDM LEAALSNAFN RLDSTRIFVP
101 ASRSGSTDKW TVYIDAFQGS YTGKTLISGY AVLPGDGNRP FHIETEQQGD
151 GYAAMTAAL QGLKQAAQOM VE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2263>:

```

m684.seq
1  ATGCGCCTTT TCCGATTGC CGCCGCCCTG TCGCTTGCCG CCTGCGGTAC
51  TGTGCAAAGC ACACAATATT TCGTGTGCC CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGCGGCGGAA ACTGCCGTCG AAGTCCGTCT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCCTCAACAC
201 CGCACAAAAC CAGTCTGGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGGACA GCACACGCAT CTTTGTTCCT
301 GCCTCAGCA GCGGCAGTAC CGAAAAATGG ACGGTCTATA TCGACGCATT
351 CCAAGGCAGC TACACGGGCA AAACCCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CGATGACCGC CGCACTCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG GTCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2264; ORF 684>:

```

m684.pep
1  MRLFPIAAL SLAACGTVQS TQYFVLPDSR YIRPATQGGG TAVEVRLAEP
51  LKRGGVLYQT DRYRLNTAQN HWADTLDDM LEAALSNAFN RLDSTRIFVP
101 ASRSGSTERW TVYIDAFQGS YTGKTLISGY AVLPGDGNRP FHIETEQQGD

```

### Homology with a predicted ORF from *N. gonorrhoeae*

m684/g684 97.7% identity in 172 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2265>

This corresponds to the amino acid sequence <SEQ ID 2266; ORF 684.a>:

Homology with a predicted ORF from *N. meningitidis*

ORF 684 shows 99.4% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. meningitidis*

m684/a684 99.4% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFP	IAAALS	LAACGT	VQSTQY	FVLPDS	RYIRPATQ
a684	MRLFP	IAAALT	LAACGT	VQSTQY	FVLPDS	RYIRPATQ
	GGETA	VEVRLA	EPLKRG	GLVYQT		
	10	20	30	40	50	60
m684.pep	DPYRL	NTAQN	HVWADT	LDMDL	EAALS	NAFNRLD
a684	DPYRL	NTAQN	HVWADT	LDMDL	EAALS	NAFNRLD
	STRIF	VPASR	SGSTE	KWTV	YIDA	FGGS
	70	80	90	100	110	120
	130	140	150	160	170	

```

m684.pep      YTGKTLISGYAVLPDGTNRPFHIETEQQQGDGYAAMTAALEOGLKQAAQMVEX
              |||||||||||||||||||||||||||||||||||||||||||||||||||
a684          YTGKTLISGYAVLPDGTNRPFHIETEQQQGDGYAAMTAALEOGLKQAAQMVEX
              130      140      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2267>

```

g685.seq
1   TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TGC GCGCTGG TTTCTGCAGG
51  TTGTTTGCCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACAC
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCCT GCCGGCCGCC
151 TGTTGCGCCG AACCTGCCGC CGAAAAAACT GTATccgCCG CATCCCAAGC
201 CGCATCCACA CCTGTCGCCA CGCTGACCGT GCCGACCGCG CGGGCGCATG
251 CCGTTGTGCC GAAGAATCCC GAACGcgTcg ccgtgtAcga CtggCGCGCG
301 TtggATACGC TGACCGAGCC GGGCGTGAAT GTGGGCGCAA CCACCGCGCC
351 GGTGCGCGTG GACTATTGTC AGCCTGCATT TGACAAGGCG GCACCGGTGG
401 GGACGCTGTT TGAGCCCGAT TGC GAATCCC TGCACCGCCA CAATCCGCAG
451 TTTGTCAATTA CCGCGGGGCC GGTGCGGAA CCGTATGAAC AGTTGGCGAA
501 AAACGCGACC ACCATAGATT TGACGGTGGG CAACGGCAAT ATCCGCACCA
551 GCGCGAGAA GCAGATGGAG ACCCTGTCGC GGATTTTCGG TAAGGAAGCG
601 CGCGTGGCGG AATTGAATGC GCAGATTGAC GCGCTGTTCC CCCAAAAGCG
651 CGAAGCCGCC AAAGGCAAAG GACGCGGGCT GGTGCTGTCG GTTACAGGCA
701 ACAAGGTGTC CGCCTTCGGC ACGCAATCGC GGTGGCAAG TTGGATACAC
751 GCGGACATCG GCCTGCCGCC CGTGGACGAA TCTTACGCA ACGAAGGGCA
801 CCGGCAGCCC GTTTCCTTCG AATACATCAA AGAGAAAAAC CCCGGCTGGA
851 TTTTCATCAT CGACCGCACC GCCGCCATCG GGCAGGAAG GCCGGCTGCC
901 GTGGAAGTGT TGGATAACGC GCTGGTATGC GGCACGAACG CTTGGAAGCG
951 CAAGCAAATC ATCGTCATGC CTGCCGCGAA CTACATTGTC GCGGCGGCG
1001 CGCGGCAGTT GATACAGGCG GCGGAACAGT TGAAGCGGCG GTTTGAAAAG
1051 GCAGAACCCG TTGCGGCGCA GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2268; ORF 685>:

```

g685.pep
1   LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLPAA
51  CSPEPAEAKT VSAASQAAS PVATLTVPPTA RGDVAVPKNP ERVAVYDWAA
101 LDTLTEPGVN VGATTAAPVRV DYLPQAFDKA ATVGTLFEPD CESLHRHNPQ
151 FVITGGPGAE AYEQLAKNAT TIDLTVDNNGN IRTSGEKQME TLSRIFGKEA
201 RVAELNAQID ALFAQKREAA KGKGRGLVLS VTGNKVSFAFQ TQSRLASWIH
251 GDIGLPPVDE SLRNEGHGQP VSFEYIKEKN PGWIFIIDRT AAIQGEPPAA
301 VEVLDNALVC GTNAWKRRQI IVMPAANYIV AGGARQLIQA AEQLKAAFEK
351 AEPVAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2269>:

```

m685.seq
1   TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TGC GCGCTGG TTTCTGCAGG
51  TTGTTTGCCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACAC
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
151 TGTTGCGCCG AACCTGCCGC CGAAAAAACT GTATCCGCGG CATCCGCATC
201 TGCCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG TGCGCGTGGG
351 TTATTTGCAG CCTGCATTG ACAAGGCGGC AACGGTGGGG ACGCTGTTCC
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCATTACC
451 GCGCGGCGCG GCGCGGAAGC GTATGAACAG TTAGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GGCAGAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGGCGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCCGC CAAACGCGCG AAGCCGCCAA
651 AGGCAAGGA CGCGGGCTGG TGCTGTCGGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG
851 ACCGTACCGC CGCATCGGG CAGGAAGGCG CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGAAGCGCA AGCAAATCAT
951 CGTCATGCTT GCCCGCAACT ACATTGTGCG GGGCGGCGCG CGGCAGTTGA
1001 TTCAGGCGCG GGAGCAGTTG AAGCGGCGGT TAAAAAGGC AGAACCCTT
1051 GCGGCGGGGA AAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2270; ORF 685>:

m685.pep

```

1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51  CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLO PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGEAEYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGKG RGLVLSVTGN KVSAGTQSR LASWIHGDIG
251 LPPVDESLRN EGHGQPVSEF YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGA RQLIQAAEQL KAAFKKAEPV
351 AAGKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from *N. gonorrhoeae*:

m685/g685 94.4% identity in 356 aa overlap

```

m685.pep      10      20      30      40      50      60
LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
g685          10      20      30      40      50      60
LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLPAACSPEPAAEKT

m685.pep      70      80      90      100     110
VSAASASA----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRV
g685          70      80      90      100     110     120
VSAASQAASTPVATLTVPTARGDAVVPKNPERVAVYDWAALDTLTPGVNVGATTAPVRV

m685.pep     120     130     140     150     160     170
DYQLQPAFDKAATVGTILFEPDYEALHRYNPQLVITGGPGAEEYQLAKNATTIDLTVDNGN
g685         120     130     140     150     160     170     180
DYQLQPAFDKAATVGTILFEPDCESLHRHNPQFVITGGPGAEEYQLAKNATTIDLTVDNGN

m685.pep     180     190     200     210     220     230
IRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAGF
g685         180     190     200     210     220     230     240
IRTSGEKQMETLSRIFGKEARVAELNAQIDALFAQKREAAKGKGRGLVLSVTGNKVSAGF

m685.pep     240     250     260     270     280     290
TQSLASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAA
g685         240     250     260     270     280     290     300
TQSLASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAA

m685.pep     300     310     320     330     340     350
VEVLDNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPVAAAGKKX
g685         300     310     320     330     340     350
VEVLDNALVCGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFEKAEPVAAQX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2271>

```

a685.seq
1  TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TGCGGCGTGG TTTCTGCAGG
51  TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
151 TGTCGCGCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACA CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GTGTGAATGT GGGCGCAACC ACCGCGCCGG TGCGCGTGGA
351 TTATTTCAGC CCTGCATTG ACAAGCGCGC AACGGTGGGG ACGCTGTTCTG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCAATTACC
451 GGGCGGCGCG GCGCGGAAGC GTATGAACAG TTGGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GGCGAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGCGCGAA
601 TTGAAGCGCG AGATTGACGC GCTGTTCCGC CAAACGCGCG AAGCCGCCAA
651 AGGCAAAGGA CGCGGCTGG TGCTGTCGGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG

```

1100

```

851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGAGCGCA AGCAAATCAT
951 CGTCATGCCT GCCGCGAACT ACATTGTCGC GGGCGGCTCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGAGCGCT TTGAAAAGGC AGAACCCGTT
1051 GCGGCGGGGA AAGAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2272; ORF 685.a>:

```

a685.pep
1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51  CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLO PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GPGAEAYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGGK RGLVLSVTGN KVSAGFTQSR LASWIHGDIG
251 LPPVDESLRN EGHGQPVSE YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGS RQLIQAAEQL KEAFEKAEPV
351 AAGKE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 685 shows 98.9% identity over a 355 aa overlap with a predicted ORF (ORF 685) from *N. meningitidis*:

```

m685/a685    98.9% identity in 355 aa overlap

      10      20      30      40      50      60
m685.pep    LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPPEAAEKT
a685         LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPPEAAEKT
      10      20      30      40      50      60

      70      80      90     100     110     120
m685.pep    VSAASASAATLTVPARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLO
a685         VSAASASAATLTVPARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLO
      70      80      90     100     110     120

      130     140     150     160     170     180
m685.pep    PAFDKAATVGTLEFEPDYEALHRYNPQLVITGGPGAAYEQLAKNATTIDLTVDNGNIRTS
a685         PAFDKAATVGTLEFEPDYEALHRYNPQLVITGGPGAAYEQLAKNATTIDLTVDNGNIRTS
      130     140     150     160     170     180

      190     200     210     220     230     240
m685.pep    GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGGKRGVLVSVGNKVSAGFTQSR
a685         GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGGKRGVLVSVGNKVSAGFTQSR
      190     200     210     220     230     240

      250     260     270     280     290     300
m685.pep    LASWIHGDIGLPPVDESLRNEGHGQPVSEYIYEKNPDWIFIIDRTAAIGQEGPAAVEVL
a685         LASWIHGDIGLPPVDESLRNEGHGQPVSEYIYEKNPDWIFIIDRTAAIGQEGPAAVEVL
      250     260     270     280     290     300

      310     320     330     340     350
m685.pep    DNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEFVAAGKKX
a685         DNALVRGTNAWKRKQIIVMPAANYIVAGGSRLIQAAEQLKEAFEKAEPVAAGKEX
      310     320     330     340     350

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2273>

```

g686.seq (partial)
1  ..AATTCTCCT GCCGCGCCGA TGATGTTTT GACGATATCT CGAGTGCCGT
51  TGAAGGCTTC ggcgGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TGCCTCAGCA TAGCGCCGGC
151 ATTGTGGAAG CCGTCGGCAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
201 GGTGAGGCG GATATTTTGG CCAACGCCCT TTATGTCGTA GCTGTATATA
251 TCCCTCGGCG CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGT CGTATCCGTC CCAATGGATG CGGTAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCGT CAGAATCGGA ATGTGA

```



This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686>:

g686.pep (partial)  
 1 ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSILRQHSAG  
 51 IVETVGKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFSG GIAAALWPFVI  
 101 AVGGMVVFVS PMDAVKAESV NGTTGFVRIG M\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

m686.seq..  
 1 ATGATGTTGA AAAAATTCGT ACTCGGCGGT ATTGCCGCAT TGGTTTGGC  
 51 GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT  
 101 TCTCCTGCAG CGCCGATGAT GTTTTAAACG ATATCTGCAG TGCCGTTGAA  
 151 GGCTTCGGCG GCATTGCCCG ATCTGTCCAG CTCGGGGCTG TATCGGGTGG  
 201 CGCGTTTGAA TCCGTGCGCT ACTCCTTGCG TCAGCATACT ACCGGCATTG  
 251 TGGAAACGGT CGGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGTT  
 301 GAGGCGGATA TTTTGGGCAA CGCCTTTTAT GTCGTAGCTG TATATATCCC  
 351 TCGCGCCTTT GGGAGCGGGA TAGCCGCCGC CCTGTGGCCC GTCATAGCCG  
 401 TCGGCGGGAT GGTGTTTCGTA TCCGTCCCAA TGGATCCGGT AAAGGCTAAA  
 451 TCCGTCAACG GGACTACCGG CTTCATCAGA ATCGGAATGT GA

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

m686.pep  
 1 MLKKFVLGG IAALVLAACG GSEGGSGAXX XXNFSCSADD VFNDICSAVE  
 51 GFGGIARSVQ LGAVSGGAFE SVAYSLRQHT TGIVETVGKP LSGAAVVGQV  
 101 EADILGNAFY VVAVYIPRAF GSGIAAALWP VIAVGGMVFV SVPMDAVKAK  
 151 SVNGTTGFIR IGM\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

g686.pep				10	20	30
				NFSCRADDVFDDICSAVEGF	GGGIARSVQLG	
m686	LKKFVLGGIAALVLAACG	GSEGGSGAXX	XXNFSCSADDVFNDICSAVEGF	GGGIARSVQLG		
	10	20	30	40	50	60
g686.pep		40	50	60	70	80
		AVSGGAFESVAYSLRQHSAG	IVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFSG			
m686		AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFSG				
		70	80	90	100	110
g686.pep		100	110	120	130	
		GIAAALWPFVIAVGGMVFVS	VPMDAVKAESVNGTTGFVRIGMX			
m686		GIAAALWPFVIAVGGMVFVS	VPMDAVKAESVNGTTGFIRIGMX			
		130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

a686.seq (partial)  
 1 ..AATTCTCCT GCCGCGCCGA TGATGTTTT GACGATATCT GCAGTGCCGT  
 51 TGAAGCTTC GCGGCGATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG  
 101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TCGCTCAGCA TACTACCGGT  
 151 ATTGTGGAAA CGGTCGACAA GCCGTTGTCC GGTGCTGCGG TTGTGCGTCA  
 201 GGTGAGGCG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA  
 251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA  
 301 GCCGTCGGCG GGATGGTGT CGTATCCGTC CCAATGGATG CGGTAAAGGC  
 351 TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

a686.pep (partial)

### Homology with a predicted ORF from *N. meningitidis*

ORF 686 shows 96.2% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N meningitidis*:

```

      10          20          30          40          50          60
m686.pep LKKFVLGGIAALVLAACGSGEGSGAXXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG
      ||| ||||| :||||| :||||| :||||| :||||| :|||||
a686      NFSCRADDFDDICSAVESFGGIARSVQLG
                        10          20          30

      70          80          90          100         110         120
m686.pep AVSGGAFESVAYSRLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAPYVVAVYIPRAFGS
      ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
a686      AVSGGAFESVAYSRLRQHTTGIVETVDKPLSGAAVVGQVEADILGNAPYVVAVYIPRAFGS
                40          50          60          70          80          90

      130         140         150         160
m686.pep GIAAALWPVIAVGGMVFSVPMDAVKAKSVNGTTGFIIRIGMX
      ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
a686      GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFIIRIGMX
                100         110         120         130

```

g687.sag

```
1 ATGAAATCCA GACACCTCGC CCTCGCCCTC GGCGTTGCCG CCTGTTCGCG
51 CTTTGCCGCG TCGGACAGCA AAGTCCAAC CAGCGTCCCC GCGGCAGCGG
101 CGCCTGCCGC TTGCGACGCC GCGCCCCCGG CAGGACTGTT CGAAGGGCAA
151 AACTACACCG TCCTTGGCAA CCGGATTCCC CAACAGCAGG CAGGCAAGGT
201 TGAAGTGCTT GAGTTTTTCG GCTATTTTTG TC CGCATCTGCG GCGCCGCTcg
251 AACTCGTTTT GAGCAACAAC GCGCAAGTCTT TTAAGACGCA TATGTACCTG
301 CGTACCGACA ACCTGCTCTG GCAGAAGAAG ATGCTGCCGC TGCGACGCct
351 cGCCGCCGCG CTGCATATGG CTGCCGCCGA AAGCAAAGAT GTGGCGCAc
401 GCCATATTTT CGATGCGGAT GTCAACCAAA AATCAAGCT GCAAGCGCGG
451 GAAGTCTCTCA AAAAAATGGCT GGGCGAACAA ACcgcttTfG ACGGCAAAAA
501 AGTCTTGTCG GCCTACGAAT CCCCCGAAAG TCAGGCGCGG GCcggcAAAA
551 TCAGGAGGAG GACCCGAACC TTCAAATCG ACGGTACGCC CACGGTATGA
601 GTCGGCGGCA AATATAAAGT CGAATTGGCC GACTGGGAGT CCGGTATGAA
651 CACCATCGAC CTTTGGCGG ACAAAGTACG TGAAGAACAA AAAGCCGCGC
701 AGTAG
```

g687.pep

1	<u>MKS</u> RHLAL <u>AL</u>	<u>GVA</u> ALFAL <u>AA</u>	CDSKVQTSVP	ADSAPAASAA	AAPAGLVEQG
51	NYTVLANP <u>IP</u>	QOQAGKVEVL	EFFGYFC <u>PH</u>	ARLEPVLSKH	AKSFKDMMYL
101	RTEHV <u>VW</u> QKE	MLPLARLAA <u>A</u>	VDMAAAESKD	VANS <u>HI</u> FDAM	VNQKTKLOEP
151	EVLLKKWLEQ	TA <u>FD</u> GKKVL <u>A</u>	AYESPESQAR	AGKMQL <u>ET</u>	FQIDGPTTVI
201	VGGKYKVEFA	DWESGKV <u>LD</u>	LLADKKVRE <u>Q</u>	KAAQ*	

```
m687.seq
1  ATGAATATCCA GACACCTTGC CCTCgGCGTT GCCGCCCTGT TCGCCCTTGC
51  CGCGTTCGCAC AGCAAAGTCC AAACCAGCGT CCCCGCCGAC AGCCGCCCTG
101 CGGCTTCGGC AGCCGCCGCC CGCGCAGGGC TGGTTCGAAG GCAAACACTA
151 ACCGTCCTTG CCAACCCGAT TCCCAACGCA CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCCACT CTCGAACCTG
251 TTTTAAGCAA AGCAGCCAAG TCTTTTAAAG ACGATATGTA TCCGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTGGCAC GCTCGCCGCG
351 CGCGCTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAATACTA AGCTGCAAAA TCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAAGTCTT
```

```

501 TGCCGCTAC GAGTCCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGTAAATATA AAGTTGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA AAAAAAGCC GCGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2282; ORF 687>:

```

m687.pep
1  MKSRHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWQKEML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QKIKLQNPV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFO IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 687 shows 97.0% identity over a 234 aa overlap with a predicted ORF (ORF 687) from *N. gonorrhoeae*:

```

m687/g687  97.0% identity in 234 aa overlap

              10      20      30      40      50
m687.pep    MKSRHLAL--GVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
              |||||
g687         MKSRHLALALGVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
              10      20      30      40      50      60

              60      70      80      90      100     110
m687.pep    QQQAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTHEHVWQKEMLTLARLAAA
              |||||
g687         QQQAGKVEVLEFFGYFCPHCARLEPVLSKHAKSFKDDMYLRTHEHVWQKEMLPLARLAAA
              70      80      90      100     110     120

              120     130     140     150     160     170
m687.pep    VDMAAADSKDVANSHIFDAMVNQKIKLQNPVLEVLKKWLGEQTAFDGKKVLAAYESPESQAR
              |||||
g687         VDMAAADSKDVANSHIFDAMVNQKIKLQNPVLEVLKKWLGEQTAFDGKKVLAAYESPESQAR
              130     140     150     160     170     180

              180     190     200     210     220     230
m687.pep    ADKMQELTETFTQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
              |
g687         AGKMQELTETFTQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2283>

```

a687.seq
1  ATGAAATCCA AACACCTCGC CCTCGGCGTT GCCGCCCTGT TCGCACTTGC
51  CGCGTGCGAC AGCAAAGTCC AAACCAAGCGT CCCCGCCGAC AGCGCGCCTG
101 CCGCTTCGGC AGCCGCCGCC CCGCAGGGC TGGTCGAAGG GCAAACTAT
151 ACTGTCCTTG CCAACCCGAT TCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTCGAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTCGCAC GCCTCGCCGC
351 CGCCGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAGA GCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAACGCC TTTGACGGCA AAAAAGTCCT
501 TGCCGCTTAC GAATCTCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGCAAAATATA AAGTCGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA AAAAAAGCC GCGCACTAA

```

This corresponds to the amino acid sequence <SEQ ID 2284; ORF 687.a>:

```

a687.pep
1  MKSKHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWQKEML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QKIKLQPEV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFO IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 687 shows 98.7% identity over a 232 aa overlap with a predicted ORF (ORF 687) from *N meningitidis*:

m687/a687 98.7% identity in 232 aa overlap

m687.pep	10	20	30	40	50	60
	MKSRLHLAGVAALFALAACDSKVQTSVPADSAPASAAAAPAGLVEGQNYTVLANPIPQQ					
a687	MKSRLHLAGVAALFALAACDSKVQTSVPADSAPASAAAAPAGLVEGQNYTVLANPIPQQ					
	10	20	30	40	50	60
m687.pep	70	80	90	100	110	120
	QAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTEHVWQKEMTLARLAAAVD					
a687	QAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTEHVWQKEMTLARLAAAVD					
	70	80	90	100	110	120
m687.pep	130	140	150	160	170	180
	MAAADSKDVANSHIFDAMVNQIKLQNPVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
a687	MAAADSKDVANSHIFDAMVNQIKLQNPVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
	130	140	150	160	170	180
m687.pep	190	200	210	220	230	
	KMQLTETTFQIDGTPVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX					
a687	KMQLTETTFQIDGTPVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAHX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2285>

g688.seq

1	GTGCTACACT	AGACATCCCG	ATTGACACAG	AAAGGTTCTC	CCGTGAACAA
51	AACCCCTCATC	CTCGCCCTTT	CCGCCCTGTT	CAGCCTGACC	CGGTGCAGCG
101	TCGAACGCGT	CTCGCTGTTT	CCCTCCTACA	AACTCAAAAT	CATCCAAGGC
151	AACGAACGCG	AACCGCGCGC	CGTTGCCGCC	CTCGCCCCG	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCTTTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAACCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGCCCTCC	AAAATGCCGC	CGAAGCCCTC	CGCGCGAAAC
401	AAAACGCAGA	CAAACAATAA			

This corresponds to the amino acid sequence <SEQ ID 2286; ORF 688>:

g688.pep

1	VLH*TSRFAQ	KGSPVNKTLI	LALSALFSLT	ACSVERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DALQNAEAL	RAKQNAADKQ*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2287>:

m688.seq

1	GTGTTACACT	ACCCATCCCG	ATTGACACAG	AAAGGCATTT	CCGTGAACAA
51	AACCCCTCATC	CTCGCCCTTT	CCGCCCTCCT	CGGCCTTGCC	CGGTGCAGTG
101	CCGAACGCGT	TTCCTGTTC	CCCTCGTACA	AACTCAAAAT	CATACAGGGC
151	AACGAACGCG	AACCGCGCGC	CGTTGCCGCC	CTCGCCCCG	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCTTTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAATCTGAC	CGTCTATTTT	GAAAACGGCG	TACTCGTCCG
351	CACCGAAGGC	GACGCTCTGC	AAAACGCTGC	CGAAGCCCTC	AAAGACCGCC
401	AAAACACAGA	CAAAACATAA			

This corresponds to the amino acid sequence <SEQ ID 2288; ORF 688>:

m688.pep

1	VLHYPSRFAQ	KGISVNKTLI	LALSALLGLA	ACSAERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DVLQNAEAL	KDRQNTDKP*	

1105

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. gonorrhoeae*:

```
m688/g688    90.6% identity in 138 aa overlap

              10      20      30      40      50      60
m688.pep     VLHYPSRFAQKGISVNKTLILALSALLGLAACSARVSLFPPSYKLKIIQGNELEPRVAA
              ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688          VLHXTSRFAQKGSPVNKTLILALSALFSLTACSVVERVSLFPPSYKLKIIQGNELEPRVAA
              10      20      30      40      50      60

              70      80      90     100     110     120
m688.pep     LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688          LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
              70      80      90     100     110     120

              130     140
m688.pep     DVLQNAAEALKDRQNTDKPX
              :||| :|||
g688          DALQNAAEALRAKQNAKQX
              130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2289>

```
a688.seq
1  GTGTTACACT ACCCATCCCG ATTTGCACAG AAAGGCATTT CCGTGAACAA
51 AACCCCTCATC CTCGCCCTTT CCGCCCTCCT CGGCCTTGCC GCGTGCAGCG
101 TCGAACGCGT TTCACTGTTC CCTCGTACA AACTCAAAAT CATACAGGGC
151 AACGAACTCG AACCTCGCGC CGTCGCCTCC CTCCGCCCCG GTATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCATTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCCGCAA CGGCATCATC
301 AAAGACCGAA GCAATCTGAC CGTCTATTTT GAAACGGCG TGCTCGTCCG
351 CACCGAAGGC AACGCCCTGC AAAATGCCGC CGAAGCCCTC CGCGTAAAC
401 AAAACGCAGA CAAACAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2290; ORF 688.a>:

```
a688.pep
1  VLHYPSRFAQ KGISVNKTLI LALSALLGLA ACSVERVSLF PSYKLKIIQG
51 NELEPRAVAS LRPGMTKDQV LLLLGSPILR DAFHTDRWDY TFNTSRNGII
101 KDRSNLT VYF ENGVLVRTEG NALQNAAEAL RVKQNAKQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

```
m688/a688    93.5% identity in 138 aa overlap

              10      20      30      40      50      60
m688.pep     VLHYPSRFAQKGISVNKTLILALSALLGLAACSARVSLFPPSYKLKIIQGNELEPRVAA
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688          VLHYPSRFAQKGISVNKTLILALSALLGLAACSARVSLFPPSYKLKIIQGNELEPRVAA
              10      20      30      40      50      60

              70      80      90     100     110     120
m688.pep     LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688          LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
              70      80      90     100     110     120

              130     140
m688.pep     DVLQNAAEALKDRQNTDKPX
              :||| :|||
a688          NALQNAAEALRVKQNAKQX
              130     140
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2291>

g689.seq (partial)

```

1  ..TCTCCGCCCC TTCCTCCGAT GAGCGGAAAA CTGATGGCGG TTTTGATGGC
51  GGTACTGGTC GCGCTGATGC CGTTTTCCAT CGATGCCCTAC CTGCCCGCGA
101 TTCCCGAAAT GCGCAGCCG CTGAACGCGG ATATCCACCG TATCGAATAG
151 AGTCTGAGTT TGTATTGTT CGGCACGGCG TTCGGGCAAG TGGCCGGCGG
201 CGCGGTGTCC GACATCAAAG GCGCAAACC CGTCGCCCTG ACCGGTTTGA
251 TTGTATATTG CCTTGCCGTT GCCGCCATCG TATTTGCTTC GAGTACCGAA
301 CAGCTCCTTA ACCTGCGTGC GGTACAGGCG TTCGGCGCAG GCATGGCTGT
351 AGTCATCGTC ggtgcgatgg tgcgcgatTA TTATTCGGGA CGCAAAGCCG
401 cgcAGATGTT TGCCCTTATC GGCATCATT TGATGGTTGT GCCGCTGGCC
451 GCACCATGG TCGGCGCATT GTTGCAAGGA TTGGGCGGAT GGCGGGCGAT
501 TTTCTGTTTC ttggcGgcgt ATTCGCCGGT GCTGCCCGGT TTGGTACAGT
551 ATTTCTTGCC CAATCCCGCC GTCGGCGGCA AAATCGGCAG GGATGTGTTT
601 GGGCTGGTGG CGGGGCGGTT CAAGCGCGTA TTGAAAACCC GTGCCGCGAT
651 GGGTtatCTG TTTTTTCAGG CATTACAGTT CGGTTTCGATG TTCGCTTTT
701 TGACCGAATC TTCCTTCGTG TACCGGCAGC TCTACCACGT TACGCCGCAC
751 CGGTACGCAT GGGTGTGTC ACTCAACATC ATCAGCATGA TGTTTTTTCA
801 CGCGTTTACC GCGTGGCGGC TTAACACCGG CGCGCATCCG CAAAGCATCC
851 TGCTGCGGGG GATTGTCGTC CAATTGCGC CCAACCCGTC CCAACTCGCC
901 GCCGTGCTGT TTTTCGGGTT GCCCCCGTTT TGGCTGCCGG TCGCGTGCCT
951 GATGTTTTTC GTCCGTACGC AGGGCCTGGT CGGTGCGGAC ACGCAGGCAT
1001 GCTTTATGTC TTATTTCAA GAAGAGGGCG GCAGCGCGAA CGCCGTGTCC
1051 GGTGTATTCC GGTCTTAAT CGGCGCGGCG GTGGTCATGG CGGCAACCGT
1101 GATGGCGGCA ACCATGACCG CGTCCGCCTC TTGCGGCATT GCGCTTTTGT
1151 GGCTCTGCTC GCACAAGGCG TGGAAAGGAA ACGAAAAAAA GCGAATACTT

```

This corresponds to the amino acid sequence <SEQ ID 2292; ORF 689 >:

g689.pep (partial)

```

1  ..SPPLPMSGK LMAVLMAVLV ALMPFSIDAY LPAIFEMAQP LNADIHRIE*
51  SLSLFMFGTA FQVAGGAVS DIKGRKPVAL TGLIVYCLAV AAIVFASSTE
101 QLLNLRAVQA FGAGMAVVIV GAMVRDYYSG RKAQMFAI GIIIMVUPLA
151 APMVGALLQG LGGWRAIFVF LAAYSPLVPG LVQYFLPNPA VGGKIGRDVF
201 GLVAGRFKRV LKTRAAMGYL FFQAFSFGSM FAFLTSSSFV YRQLYHVTTPH
251 RYAWVFALNI ITMFFSRVT AWRLKTGAHP QSILLRGIVV QFAANPSOLA
301 AVLFFGLPEF WLPVACVMFS VGTQGLVGAD TQACFMSYFK EEGGSANAVS
351 GVFRSLIGAG VVMAATVMAA TMTASASCGI ALLWLCSHKA WKENEKKRIL

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2293>:

m689.seq

```

1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51  GTTGCCGCCCT GTTGTGCCG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTGTGTTGC GAATCCGACG AGAATTTATG
151 CCTTCTGCCC ATTATCCTGA AATGAGCGAA AAAGTATGCG CGGTTTTGAT
201 GCGGATGCTG GTTACGCTGA TGCCGTTTTT CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAA TCGCTGAACG CGGATGTTCA CCGCATCGAA
301 CAGAGTTTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGCTCGG
351 CCGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCC CTGACCGGTT
401 TGATTGTATA TTGCCTTGCC GTTGCCGCCA TCGTATTTGT TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTCCGGT CGGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGCGCGA TTATTATTCC GGACGCAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTGTCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTTGTT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTGTTGTAC
701 AGTATTTCCT GCCCAAGCCC GCCGTGCGCG CCAAAATCGG ACGGGACGTG
751 TTCGGGCTGG TGGCGGGGCG GTTCAAGCGC GTATTGAAAA CCCGTGCTGC
801 GATGGGTTAT CTGTTTTTTC AGGCATTGAG CTTGCGTTCC ATGTTCCGCT
851 TCTGACCGA ATCTTCTTC GTGTACCAGC AGCTCTACCG TGTACGCCCT
901 CATCAATACG CTTGGGCGTT TGCATCAAC ATCATCACGA TGATGTTTTT
951 CAACCGCGTT ACCCGGTGGC GGCTCAAAAC CGGCGTGCAT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCAACCT GTCCAACTC
1051 GCCGCCGTGC TGTTTTTCGG GTTGCCCCCG TTTTGGCTGC TGGTCCGCTG
1101 CGTGATGTTT TCCGTCCGTA CGCAGGGCTT GGTGGGTGCA AACACGCAGG
1151 CGTGTTTTAT GTCCTATTTT AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTTGAC GACGGTTCCG CAACCGTGAT GCGGCAACG ATGACCGCGT
1301 CCACCTCTTG CGGCATTGCG CTTCTGTGCG TCTGCTCGCA TCGTGCCTGG

```

m689.pap

— 325 —

### Homology with a predicted ORF from *N. gonorrhoeae*

*N. gonorrhoeae*:

m689.pcp

**g689**

m689.pap

m689.pcp

m689.pap

m689.pcp

m689.pap

m689.pap

m689.pap

LWLCSHKAWKENEKKRIL  
390 400

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2295>

```
a689..seq
1   TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51  GTTGCCGCCT GTTTGTGCCG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTTATG
151 CCTTCTGCCG ATTATCCTGA AATGAGCGAA AACTGATGG CGGTTTTGAT
201 GCGGATGCTG GTTACGCTGA TGCCGTTTTT CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAG TCGCTGAACG CGGATGTCCA CCGCATCGAA
301 CAGAGCCTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGGTCGG
351 CCGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCG CTGACCGGAC
401 TGGCCGCTCA CTGCCCTTGC GTTGGCCGCA TCGTATTTGC TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGACG GCATTGCGTG CGGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGGCGCA TTATTATTCC GGACGCAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGACG GGCTTGGGTG GCTGGCAGGC
651 GATTTTGTGT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTGTTGGTAC
701 AGTATTTCTT GCCCAAGCCC GCCGTGCGCG GCAAATCGG CAGGGATGTG
751 TCGGGCTGGG TGGCTGGGCG GTTCAAACGC GTATTGAAAA CCCGTGCCGC
801 GATGGGTAT CTGTTTTTTC AGGCATTGAG CTTGCGTTTCG ATGTTCCGCT
851 TTCTGACCGA ATCTTCTTTC GTGTACCAGC AGCTCTACCA CGTTACGCCG
901 CACCAGTACG CTTGGGCGTT TGCACCTCAC ATCATCACA TGATGTTTTT
951 CAACCGTATT ACCGCGTGGC GGCTCAAAAC CGGCGTGCGT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACCT GTCCCAACTC
1051 GCCGCCGTGC TGTTTTTCGG GTTGCCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTGCGTGCA AACACGCAGG
1151 CGTGTTTAT GTCTATTTC AAAGAAGAGG GCGGCAGCGC AACGCCGTA
1201 TTGGGTGTAT TCCAATCTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTGCAC GACGGTTCGG CAACCGTGAT GCGGCAACC ATGACCGCGT
1301 CTACCTCTTG CGGCATTGCG CTTTGTGGC TCTGCTCGCA TCGTCCGTGG
1351 AAAGAAACG GCAAAGCGA ATACCTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2296; ORF 689.a>:

```
a689.pep
1   LLIHIVPVR PVLPGLLPP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTLMPFSIDA YLPAIPEMAQ SLNADVHRIE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLAVYCLA VAAIVPASSA
151 EQLNLNRVVQ AFGAGMTVVI VGAMVRDYSY GRKAAQMFAL IGIILMVVPL
201 VAPMVGALLQ GLGGWQAI FV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251 FGLVAGREFKR VLKTRAAMGY LFFQAFSFGS MFAFLTESSV VYQQLYHVT
301 HQYAWAFALN IITMMFFNRI TAWRLKTGVH PQSILLWGIV VQFAANLSQL
351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NQACFMSYF KEEGGSANAV
401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTAATSCGIA LLWLCSHRAW
451 KENGQSEYL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 689 shows 99.1% identity over a 459 aa overlap with a predicted ORF (ORF 689) from *N. meningitidis*:

m689/a689 99.1% identity in 459 aa overlap

	10	20	30	40	50	60
m689.pep	LLIHIVPVRPVLPGLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE					
a689	LLIHIVPVRPVLPGLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE					
	10	20	30	40	50	60
m689.pep	KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV					
a689	KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV					
	70	80	90	100	110	120
m689.pep	SDIKGRKPVALTGLIVYCLAVAAIVFSSAEQLNLNRVVQAFGAGMTVVIVGAMVRDYS					
a689	SDIKGRKPVALTGLAVYCLAVAAIVFSSAEQLNLNRVVQAFGAGMTVVIVGAMVRDYS					
	130	140	150	160	170	180
m689.pep	GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAI FVFLAAYSLVLLGLVQYFLPKP					
a689	GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAI FVFLAAYSLVLLGLVQYFLPKP					



1109

```

a689      |||||
          GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAFVFLAAYSLVLLGLVQYFLPKP
          190      200      210      220      230      240

          250      260      270      280      290      300
m689.pep  AVGGKIGRDVFGVLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTP
          |||||
a689      AVGGKIGRDVFGVLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYHVT
          250      260      270      280      290      300

          310      320      330      340      350      360
m689.pep  HOYAWAFALNIIITMMFFNRVTAWRLKTGVHPQSILLWGIVVQFAANLSQLAAVLFFGLPP
          |||||
a689      HOYAWAFALNIIITMMFFNRITAWRLKTGVHPQSILLWGIVVQFAANLSQLAAVLFFGLPP
          310      320      330      340      350      360

          370      380      390      400      410      420
m689.pep  FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMATFLH
          |||||
a689      FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMATFLH
          370      380      390      400      410      420

          430      440      450      460
m689.pep  DGSATVMAATMTASTSCGIALLLWLCSHRAWKENGQSEYLY
          |||||
a689      DGSATVMAATMTASTSCGIALLLWLCSHRAWKENGQSEYLY
          430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2297>

```

g690.seq (partial)
1  ATGAAAAACA AAACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
51  GGCCGCGCGT TCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTTC GTCTTCCGCG TCATCGGCTT CTTCCCAAAC CGATTGCAA
151 CCGCCGCGAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
201 GTGAAATTGC ACCGGCTGC ACCCGCCGC CCGCATTGGC GATCTCATAC
251 AGCAAATCGC CGAACACATC GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 AACGAACGCG AAACCCGTTT CGGCTTACCC GCGCGCGGCT ATGACAACAT
351 ACAGCGGctG CTgtttCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAAC GCGCACCATC
451 AGccgGCAGG CACAAGATGC CATAATGGAA CAGGAACGCC gcctccGaGa
501 agCGACGCTG ATGCTGACAC AGGGCAGTCA AAAAAACCCG GGAAGAGCG
551 AGGAACCGAA ACAGCGCAGT TATTTGAAG TTTCCGCAAC ATctgCctaT
601 TTgaaccggc ACRAcaacGG ACTTggcgGC AATTTCCAAT ACATCGGCCA
651 ATTGCCCGGC TATCTGAAAA TGCACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCACG CGTATTGTCT TTTACGAAAA
801 AAATATCTAT...

```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690>:

```

g690.pep (partial)
1  MNKNTSSLPL WLAAIMLAAR SPSKEDKKE NGASRASSSA SSASSQTDLQ
51  PAASAPDNVK QAESAPL*NC TGLHPAAGIG DLIQQIAEHI DSDCLFALSH
101 NELETREGLP GGGYDNIQRL LFPDIRPEDP DYHQIMLAI EDLRYGTRTI
151 SRQAQDAIME QERRLREATL MLTQGSQKTR GQGEPEPKRAR YFEVSATSAY
201 LNRHNNGLGG NFQYIGQLPG YLKMHGEMLE NQSLFRLSNR ERNPDKPFID
251 IHFDENGKIT RIVVYEKNII ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2299>:

```

m690.seq..
1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
51  GACCCGCTGT TCTCCGAGCA AAGACGATAA AACCAAAGAA GTCGGTGATC
101 CCGCTGCTTC GTCCCTCCGCG TCATCAGCTC CTTCCCAAAC CGATTGCAA
151 CCGACCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCGCC
201 GTCAAATTGC ACCAGCCTGC ACCCGCCAC CCGCATTGAC GATCTCATGC
251 AGCAAATCGC CGAACACATT GACTCGGACT GTCTGTTTGC CCTTTCCCAT
301 CACGAACGCG AAACCCGTTT CGGCTTACCC GACGGTGGCT ATGACAACAT
351 ACAGCGGCTG CTGTTTCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT ACTGGCAATT GAAGACTTGC GTTACGGAAA GCGCAGGATC
451 AGCCGGCAGG CACAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
501 AGCGACGCTG TTGCTGATAC AGGGCAGTCA AGAAACCCG GGAAGAGCG

```

1110

```

551 AGGAGCCGAA ACGCACGCGT TATTTTGAAG TTTCGGCAAC CCCTGCCTAT
601 TCGAGCCGGC ACAACAACGG ACTTGGCGGC AATTTCCAAT ACATCAGCCA
651 ATTGCCCGGC TATCTGAAAA TACACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTGTAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCAGC CGTATTGTCG TTTACGAAAA
801 AAACATCTAC TTCATCCAA ACACGGGCGC AATATAA

```

This corresponds to the amino acid sequence <SEQ ID 2300; ORF 690>:

```

m690.pep
1  MKNKTSLLL WLTAIMLTAC SPSKDDKKE VGASAASSA SSAPSQTDLO
51  PTASAPDNVK QAESAPPSNC TSLHPATGID DLMQIAEHI DSDCLFALSH
101 HELETRFGLP DGGYDNIQRL LFPDIRPEDP DYHQKIILAI EDLRYGKRTI-
151 SRQAQNALME QERRLREATL LLIQGSQETR QGGEKPKRTR YFEVSATPAY
201 SSRHNNLGGG NFQYISQLPG YLKIHGEMLE NQSLFRLSNR ERNPKDPFLD
251 IHFDENGKIT RIVVYEKNIY FNPNTGRI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 690 shows 89.3% identity over a 408 aa overlap with a predicted ORF (ORF 690) from *N. gonorrhoeae*:

```

m690/g690 89.3% identity in 408 aa overlap

      10      20      30      40      50      60
m690.pep MKNKTSLLLWLTAIMLTACSPSKDDKKEVGASAASSSASSAPSQTDLOPTASAPDNVK
g690      ||||| |||:||||:| |||:|||| ||||| |||||:|||||
      10      20      30      40      50      60
m690.pep MKNKTSLLPLWLAAILAARSFSPKEDKTKENGASAASSSASSQTDLPASAPDNVK
g690      ||||| |||:||||:| |||:|||| ||||| |||||:|||||

      70      80      90      100     110     120
m690.pep QAESAPPSNCTSLHPATGIDDLMQIAEHI DSDCLFALSHHELETRFGLPDGGYDNIQRL
g690      ||||| |||:||||:| |||:|||| ||||| |||||:|||||
      70      80      90      100     110     120
m690.pep QAESAPLNCTGLHHPAAGIGDLIQIAEHI DSDCLFALSHNELETRFGLPGGGYDNIQRL
g690      ||||| |||:||||:| |||:|||| ||||| |||||:|||||

      130     140     150     160     170     180
m690.pep LFPDIRPEDPDYHQKIILAI EDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQETR
g690      ||||| |||:||||:| |||:|||| ||||| |||||:|||||
      130     140     150     160     170     180
m690.pep LFPDIRPEDPDYHQKIILAI EDLRYGTRTISRQAQDAIMEQERRLREATLMLTQGSQKTR
g690      ||||| |||:||||:| |||:|||| ||||| |||||:|||||

      190     200     210     220     230     240
m690.pep QGGEKPKRTRYFEVSATPAYSSRHNNLGGNFQYISQLPGYLKIHGEMLENQSLFRLSNR
g690      ||||| |||:||||:| |||:|||| ||||| |||||:|||||
      190     200     210     220     230     240
m690.pep QGGEKPKRTRYFEVSATPAYSSRHNNLGGNFQYISQLPGYLKMHGEMLENQSLFRLSNR
g690      ||||| |||:||||:| |||:|||| ||||| |||||:|||||

      250     260     270     279
m690.pep ERNPKDPFLDIHFDENGKITRIVVYEKNIYFNPNTGRIX
g690      ||||| |||:||||:| |||:|||| ||||| |||||:|||||
      250     260     270
m690.pep ERNPKDPFLDIHFDENGKITRIVVYEKNIY
g690      ||||| |||:||||:| |||:|||| ||||| |||||:|||||

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2301>

```

a690.seq
1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTGCCG CAATGATGCT
51  GACCGCGTGT TCCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCCCTC GTCCACGGCA TCCGCCGCTT CGTCTTCCGC GCCCCAAACC
151 GATTTGCAAC CGGCCGCATC CGCCCTGAT AACGTCAAGC AGGCAGAAAG
201 CGTGCCGCCG TCAAATTGCA CCGACCTGCA CCGGCCACC GGCATTGACG
251 ATCTCATGCA GCAATCGCC GAACACATTG ACTCGGACTG TCTGTTTGCC
301 CTTTCCCATC ACGAAGTGA AACCCTTTC GGCTTACCCG GCGGCGGCTA
351 TGACAACATA CAGCGGCTGC TGTTCCTCGA CATCCGCCCT GAAGATCCCG
401 ACTACCATCA GAAATCATA CTGGCAATTG AAGACTTGCG TTACGGAAG
451 CGCACGATCA GCCGCGAGGC ACAAGATGCC TTGATGGAAC AGGAACGCCG
501 CCTCCGAGAA GCGACGCTGT TGCTGATACA GGGCAGTCAA GAAACCCGCG
551 GACAAGCGGA GGAGCCGAAA CGCACGCTT ATTTTGAAGT TTCGGCAACC
601 CCTGCCTATT CGAGCCGGA CAACAACGGA CTTGGCGGCA ATTTCCAATA
651 CATCGGCCAA TTGCCCGCT ATCTGAAAT ACACGGAGAA ATGCTTGAAA

```

1111

701 ACCAATCACT CTTCCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG  
 751 TTTTTAGACA TCCATTTTGA CGAAAATGGC AAAATCACGC GTATTGTCGT  
 801 TTACGAAAAA AACATCTACT TCAATCCAAA CTTGGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep  
 1 MKNKTSLLLL WLAAMMLTAC SPSKEDKKE NGASAASSTA SAASSAPQT  
 51 DLQPAASAPD NVKQAESVPP SNCTDLHPAT GIDDLMQQIA EHIDSDCLFA  
 101 LSHHELETRF GLPGGGYDNI QRLFPDIRP EDFDYHOKII LAIEDLRYGK  
 151 RTISRQAQDA LMEQERRLRE ATLLLIQGSQ ETRGQGEEP K RTRYFEVSAT  
 201 PAYSSRHNN LGGNFQYIGQ LPGYLKIHGE MLENQSLFRL SNRERNPKP  
 251 FLDIHFDENG KITRIVVYEK NIYFNPNLGR R\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

m690.pep	10	20	30	40	50
	MKNKTSLLLLWLTAIMLTACSPSKDDKTKEVGASAASSASSAPS---	CTDLQPTASAPD			
a690	MKNKTSLLLLWLAAMMLTACSPSKEDKTKENGASAASTASAASSAPQTDLQPAASAPD				
	10	20	30	40	50
					60
m690.pep	60	70	80	90	100
	NVKQAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNI				
a690	NVKQAESVPPSNCTDLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPGGGYDNI				
	70	80	90	100	110
					120
m690.pep	120	130	140	150	160
	QRLFPDIRPEDPDYHOKIILAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQ				
a690	QRLFPDIRPEDPDYHOKIILAIEDLRYGKRTISRQAQDALMEQERRLREATLLLIQGSQ				
	130	140	150	160	170
					180
m690.pep	180	190	200	210	220
	ETRGQGEEP K RTRYFEVSATPAYSSRHNNLGGNFQYISQLPGYLKIHGEMLNQLFRL				
a690	ETRGQGEEP K RTRYFEVSATPAYSSRHNNLGGNFQYIGQLPGYLKIHGEMLNQLFRL				
	190	200	210	220	230
					240
m690.pep	240	250	260	270	279
	SNRERNPKPFLDIHFDENGKITRIVVYEKNIYFNPNTGRIX				
a690	SNRERNPKPFLDIHFDENGKITRIVVYEKNIYFNPNLGRRX				
	250	260	270	280	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq  
 1 GTGCCGCTGC CTGCTCCCTG CCGTTTTGCC AAACCTGCCG CCTCTTTTT  
 51 AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA  
 101 TCCCCCGGAA CGATTTTCAA CCGAAGTCGC ACATACGCCG GCTCGGGCTG  
 151 ACACAGGGTC AGCACAAATGA GCTGCGTAAA ATCCGCGCCG CCTTCAAAAT  
 201 GCGGGGCGAC AGGGCGCGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC  
 251 GCCGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCGGAACGAG  
 301 GCGGCGGATT ATGTCGAAAG CCGCTACCAC TCCAGCATGG ATTTTGGCGT  
 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC  
 401 AGCAGCAAT GTGGCTTTCT TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >:

g691.pep  
 1 VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL  
 51 TQGHNELRK IRAAFKMGAD RARLKMVHSE HSRRRSVVEI ISSDVFNRE  
 101 ARDYVESRYH SSMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2305>:

```
m691.seq
1  GTGCCACTGC CTGCTCCCTG CCGTTTTGCC AACCTGCCG CCTCTTTTT
51  AAGTATGGCT TTGCTTTCCT GTCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG ACTCGGGCTG
151 ACCCAAAGTC AGCACAATGA GCTGCGTAAA ATCCGCACCG CCTTCAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGTTAT GCATTCCGAA CACAGCCGCC
251 GCGGTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAT GTGGCTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2306; ORF 691>:

```
m691.pep
1  VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
51  TQSQHNELRK IRTAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. gonorrhoeae*:

```
m691/g691  97.2% identity in 144 aa overlap

          10      20      30      40      50      60
m691.pep  VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFO PNCDIRRLGLTQSQHNELRK
          |||
g691       VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFO PNCDIRRLGLTQSQHNELRK
          10      20      30      40      50      60

          70      80      90      100     110     120
m691.pep  IRTAFKMAGDRARLKMVHSEHSRRRSVVEIISDVFNRNNEARDYVESRYLSGMDFAVDEL
          |||
g691       IRAAFKMAGDRARLKMVHSEHSRRRSVVEIISDVFNRNNEARDYVESRYHSSMDFAVDEL
          70      80      90      100     110     120

          130     140
m691.pep  EIQRFFHILTPQQQMWLSCLKX
          |||
g691       EIQRFFHILTPQQQMWLSCLKX
          130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2307>

```
a691.seq
1  GTGCCACTGC NTGCTCCCTG CCGTTTTGCC AACCTGCCG CCTCTTTTT
51  AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCTGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGACTG
151 ACACAGGTC AGCACAATGA ACTGCGTAAA ATCCGCGCCG CCTTCAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGTTAT GCATTCCGAA CACAGCCGCC
251 GTCGGTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAT GTGGCTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2308; ORF 691.a>:

```
a691.pep
1  VPLXAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPLNDFQ PNCDIRRLGL
51  TQSQHNELRK IRAAFKMAGD RARLKMVHSE HSRRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

**m691/a691** 97.2% identity in 144 aa overlap

	10	20	30	40	50	60
m691.pep	VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIIPNDFQPNCDIRRLGLTQSQHNELRK					
a691	VPLXAPCRFAKPAASFLSMALLSCQLSHAATAYIIPNDFQPNCDIRRLGLTQSQHNELRK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m691.pep	IRTAFFKMAGDRARLKVHMHSEHSRRRSVVEIISDDVFNRNNEARDYVESRYLSGMDFAVDEL					
a691	IRAAFFKMAGDRARLKVHMHSEHSRRRSVVEIISDDVFNRNNEARDYVESRYLSGMDFAVDEL					
	70	80	90	100	110	120
	130	140				
m691.pep	EIQHRFFHILTPQQQQMWLSSCLKX					
a691	EIQHRFFHILTPQQQQMWLSSCLKX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2309>

```

g992.seq
1      GTATCGCACA  CACGCTGTCTG  CTGTTCCGGA  TCGAtacGCC  GGATTTGCGG
51     GAATGGCAGG  GAATGCGCGA  TTTAAAGGCA  AAAATGCCGT  CTGAACACGG
101    ATGCGGTTCA  CAGGGCATCA  TTTATACGA  CTGCCTTATT  TGGCTGCGCG
151    TTCATTCCAT  GCGGCAGGGT  ATTTGTAGCC  CTCGAAGCGT  TTGTGCGCGT
201    AGGCTTTGAA  CGCTCGGGAG  TTATAGCCCT  CGGTTACGCT  TTTAAGCCAT
251    TGGCTGCTTT  TGTGCGCGGT  TTGgacGGCA  GACCAAGTTA  CATAAGGCAA
301    GCTCGGCTCT  TGGAAcAGGG  CTTCGGTcAG  CTTcATGCCG  CTGCTTATGG
351    CGTAgTTGCC  GTTGcAGCAG  GCAAaATCCA  CGTCGGGCGG  CTGCGCGGGC
401    AGTTTGTGGG  CTTCAAGCTC  GACGATTTTG  ATGTTTTTCA  GGGTTTTCCG
451    TCGTGTGGCT  TTGGATGCGG  TCAGCGGATT  GATGCCGTCT  TTGAGTTTGA
501    TCAACCCcAG  TCGGTTcAGC  ATCACCAGGT  CGCGTGCGGA  GTGGGAcggy
551    TcgtTGGGGC  CTTCAAGCAG  CTGCGCGCTT  TTGACTTTCT  CCAGCGATTG
601    CAGTTTGGCC  GGATACAGTC  CCAAGAGCGC  GGTcGGCACT  TGGAAAGGCT
651    CGGTGATGTC  CAGGTTGTGT  TCTTTTTTGA  AATCGCAcAG  ATAGGGTTTG
701    TGTGGGAAGA  CGTTGATGTC  CAACTCGGTC  TCCGCCAATG  CCAGATTcGG
751    GGCACATAG  TcggTAAATT  cgaccaatTT  gacgGTGTag  cTTTTTTTCT
801    CCAGCTCGgc  ttGGATTtGT  TcTTTTGACCA  TATcgcgcgaa  gtcgcccacg
851    gTCGTGCCGA  agacgaATTT  TTTTTTGCgc  GgcgcCGTAT  CGCGCAAGGT
901    CGCGCGGcga  gaggctgcGG  GCGCGCTGTC  TTTTtgaccG  ccgcGAGGCT
951    CGAGGATGAG  CGCGAGtgcg  gcggcggaaa  ggGTTTGAa  GAAAGGTTTT
1001   atATTTCTc  ctga

```

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692>:

g992.pap

1	VSHTRCRCE	SIRRIWRNGR	EWRIKQKCR	LNTDAVQTAS	FYTTALFGCA
51	FIPCGRVFVA	LEAFVRVGF	RVGVIGLGY	FKPLAVFVGG	DFGRFVDIG
101	ARLLGQGGQ	LHAAAYGVVA	VDDGKHVGA	AARQLCGFKL	DDFDVQVFR
151	DVGFGCGQRI	DAVFEDPTQ	FVQHQQGAC	VGRVVRGRGY	AAVDFQQQIR
201	QFARIQSRR	GRHLEGGDV	QVVFVEIVK	IGVLEVDV	QALRQCCQF
251	AHIVGFGDF	DGVAFFLQL	LDLFFDHIA	VAHGRAEEDF	FFRAVIGRR
301	GGGRGCGRA	FLTAAGCEDE	RECGGKGFE	EGEHS*	

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2311>:

m692.seq

1	GTGTTGCACA	CGCTTTTGTCG	CTGTTTCGGAA	TCGATACGCC	GGATTTCGGCG
51	GAATGGCAGG	GAATGGCGGA	TTAAAGACA	AAAATGCCGT	CTGAACACGG
101	ATACAGTTCA	GACGGCATCA	TTTTATACGA	CTGCCTTATT	TGGCTACGCC
151	TTCAATTCAT	CGCGGACGGG	ATTGTGATCC	CTCGAAGCGT	TTGTGTCGGGT
201	AGGCTTTGAA	CGCGTCGGAG	TTATAGGCGT	CGGTTACGCT	TTTAGGCCAT
251	TGGCTGTCTT	TGTCGGCGGT	TTTGACGGCA	GACCAGTTGA	CATAGGCAAA
301	GCTCGGTTCT	TGGACACAGG	CTTCGGTCAG	CTTCATCGCC	CTGCTTATGG
351	CGTAGTTGCC	TTTGACGACG	GC AAAATCCA	CGTCGGCGGC	GCTACGGCGG

1114

```

401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTCCTCGGC
451 GATGTCCGCT TTGGATGCGG TCAACGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTGCGAGC ATCACCAGA CGCGGGCGAA GTTGACGGG
551 TCGTTGGCGG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTCGGCACT TGGAAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTTCGG
751 GCGTACATAG TCGGTAAACT CGACCAGTTT GACGGGTAG CTTTTTTCT
801 CCAGCTCGGC TTGGATTGT TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCCGTGT GCGCGCGGCG
901 AGAAGCGGAT GCGCGGGCG CGCTGTCTTT TTGACCGCCG CAGCGCGCGA
951 GGATGAGCGC GAGTGCGGCG GCGGAAAGGG TTTGAAGAA GGTTCCTCATA
1001 TTTTCTCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2312; ORF 692>:

```

m692.pep
1 VLHTLCRCSE SIRRIIRNGR EWRIKQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFVA LEAFVRVGFE RVGVIGLGYV FKPLAVFVGG FDGRFPVDIGK
101 ARFLEQGFQ LHAAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVFGVLG
151 DVRFQCGQRI DAVFEFDPQ FVEHHQDAGE VGRVVGGRYG AAVDFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AYIVGKLDQF DGVAFFLQLG LDFFDHIAE VADGRAEDDF FFRRAVVG
301 RSGCGGRAV LTAAGGEDER ECGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 692 shows 91.1% identity over a 338 aa overlap with a predicted ORF (ORF 692) from *N. gonorrhoeae*:

m692/g692 91.1% identity in 338 aa overlap

m692.pep	10	20	30	40	50	60
	VLHTLCRCSESIRRIIRNGREWRIKQKCR	LNTDTVQTASFYTTALFGCA	FIPCGRGFVA	LEAFVRVGFE	RVGVIGLGYV	FKPLAVFVGG
g692	10	20	30	40	50	60
	VSHTRCRCSESIRRIWRNGREWRIKQKCR	LNTDAVQTASFYTTALFGCA	FIPCGRVFVA	LEAFVRVGFE	RVGVIGLGYV	FKPLAVFVGG
m692.pep	70	80	90	100	110	120
	LEAFVRVGFERVGVIGLGYVFKPLAVFVGG	FDGRFPVDIGKARFLEQGFQ	LHAAAYGVVA	VDDGKIHVGA	ATRQLRGFKL	DDFDVFGVLG
g692	70	80	90	100	110	120
	LEAFVRVGFERVGVIGLGYVFKPLAVFVGG	FDGRFPVDIGKARLLEQGFQ	LHAAAYGVVA	VDDGKIHVGA	ATRQLRGFKL	DDFDVFGVLG
m692.pep	130	140	150	160	170	180
	VDDGKIHVGAATRQLRGFKLDDFDVFGV	QVLDVRFQCGQRI	DAVFEFDPQ	FVEHHQDAGE		
g692	130	140	150	160	170	180
	VDDGKIHVGAARQLCGFKLDDFDVFGV	QVLDVRFQCGQRI	DAVFEFDPQ	FVQHHQGACE		
m692.pep	190	200	210	220	230	240
	VGRVVGGRYGAAVDFDFQRFQLARVQSQR	GRHLEDFGDVQIVFFFEVVK	IGFVLEDVDV			
g692	190	200	210	220	230	240
	VGRVVGGRYGAAVDFDFQRFQFARIQSQR	RHLEGFDVQVVF	FEIVKIGFVLEDVDV			
m692.pep	250	260	270	280	290	
	QLALSQCQIRAYIVGKLDQFDGVAFFLQLGL	DLFFDHIAE	VADGRAEDDF	FFRRAVVG--		
g692	250	260	270	280	290	300
	QLALRQCQIRAHIVGKFDQFDGVAFFLQLGL	DLFFDHIAE	VAHGRAEDDF	FFRRAVIGRR		
m692.pep	300	310	320	330		
	GGRSGCGGRAVFLTAAGGEDERE	CGGKGFE	EGFHIFS			
g692	300	310	320	330		
	GGRSGCG-RAVFLTAAGCEDERE	CGGKGFE	EGFHIFS			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2313>

```

a692.seq
1 GTGTTGCACA CGCTTTGTGCG CTGTTCCGAA TCGATACGCC GGATTCGGCG

```

1115

```

51 GAATGGCAGG GAATGGCGGA TTAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTCTT TGAACACAGG CTTCCGGTCAG CTTTCATCCC CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGG CTTCAAGCTC GACGATTTG ATGTTTTTCA GGTTTTCGGC
451 AATGTCGCGT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAGA CGCGGGCGAA GTTGGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATTT
601 CAGCTTGCCC GGGTACAGTC CCAAAGCGCG GGTCCGCACT TGAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGCTAAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGCACATAG TCGGTAAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGG TTGGATTGTG TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTT TTTTTCGCC CGCGCGTGTG CGGCGGCGGC
901 AGAAGCGGAT GCGCGGCGCG CGCTATCTTT TTGACCGCCG CAGGCGGCGA
951 GGATGAGCGC GAGTGCGGCG GCGGAAAGGG TTTTGAAGAA GGTTTTCATA
1001 TTTTCTCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

a692.pep

```

1 VLHTLCRCSE SIRRIRNRG EWRKQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFVA LEAFVRVGF RVGVIGLVY FKPLAVFVGG FDGRPVDIGK
101 ARFLEQGFQ LHAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQVFG
151 NVRFQCGQRI DAVFEFDPTQ FVEHHQDAGE VGRVVRGYG AAVFDFFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AHIVGKLDQF DGVAFELQLG LDLFFDHIAE VADGRAEDDF FFRRAVVGGG
301 RSGCGGRAIF LTAAGGEDER ECGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

m692/a692 98.8% identity in 336 aa overlap

m692.pep	10	20	30	40	50	60
	VLHTLCRCSESIRRIRNRGREWRIKQKCR	LNTDTVQTASFYTTALFGCA	FIPCGRGFVA			
a692	10	20	30	40	50	60
	VLHTLCRCSESIRRIRNRGREWRIKQKCR	LNTDTVQTASFYTTALFGCA	FIPCGRGFVA			
m692.pep	70	80	90	100	110	120
	LEAFVRVGFERVGVIGLVYFKPLAVFVGG	FDGRPVDIGKARFLEQGFQ	LHAAYGVVA			
a692	70	80	90	100	110	120
	LEAFVRVGFERVGVIGLVYFKPLAVFVGG	FDGRPVDIGKARFLEQGFQ	LHAAYGVVA			
m692.pep	130	140	150	160	170	180
	VDDGKIHVGAATRQLRGFKLDDFDV	QVLDVRFQCGQRIDAVFE	FDPTQFVEHHQDAGE			
a692	130	140	150	160	170	180
	VDDGKIHVGAATRQLRGFKLDDFDV	QVLDVRFQCGQRIDAVFE	FDPTQFVEHHQDAGE			
m692.pep	190	200	210	220	230	240
	VGRVVRGYGAAVFDFFQRFQLARVQS	QRRGRHLEDFGDVQIVFFFEVVK	IGFVLEDVDV			
a692	190	200	210	220	230	240
	VGRVVRGYGAAVFDFFQRFQLARVQS	QRRGRHLEDFGDVQIVFFFEVVK	IGFVLEDVDV			
m692.pep	250	260	270	280	290	300
	QLALSQCQIRAHIVGKLDQFDGVA	FFLQLGLDLFFDHIAE	VADGRAEDDF	FFRRAVVGGG		
a692	250	260	270	280	290	300
	QLALSQCQIRAHIVGKLDQFDGVA	FFLQLGLDLFFDHIAE	VADGRAEDDF	FFRRAVVGGG		
m692.pep	310	320	330			
	RSGCGGRAIFLTAAGGEDERE	CGGKGFEFGFHIFS				
a692	310	320	330			
	RSGCGGRAIFLTAAGGEDERE	CGGKGFEFGFHIFS				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2315>:

```
g694.sag
1  TCGGCATTTG TGTGCCCCAA ACATCCGATG CCTGCGTTAA CGCCTGCGTC
51  AACGTTTGCA CAAATCGGGT TTGGTTTCGC CCTCGCGGCG CAGCTCCTTG
101 GGCAGGACGA ACACGATGCT TTCTTCCGCG CCCCCCCTT CGCGCACGGT
151 TTTCATGCCCC CATCCGCGTA TGGTTGCCAA TACTTCCCGC ACCAACACCT
201 CGGGCGCGGA CGCGCCTGCC GTTACGCCGA CTTTGCTTTT GCCTTCAAAC
251 CACGTGCGTT GCaggTAGGA CGCGTTGTCC ACCATATACG CATCGATTCC
301 GCGCGATGCC GCCACTTCGC GCAGGCGGTT GCTGTTGGAC GAATTGGGCG
351 AACCGACCAAC AATCACGATG TCGCACTGTT CCGCCAGCTC TTGACGGGCG
401 GTTTCGCGGT TGGTCGTGCG ATAGCAGATG TCTTCTTGT GCGGATTGCG
451 GATATTGGGG AAACGCGCGT TCAGCGCGGC GATGATGTCT TTGGTTTCAT
501 CGACCGAGAG CGTGGTTTGG CTGACATAGG CGAGTTTGTG GGGGTTTCTG
551 ACTTCGAGTT TTGCCACATC TCCGACCGTT TCGACCAAAA GCATTTTGCC
601 CGGTGCAAGC TGCCCCATCG TGCCCTTCGAC CTCGGCGTGC CCCTTATGCC
651 CGATCATGAT GATTTACAG TCTTGGGCAT CCAGTCGGGC GACTTCCTTA
701 TGCATTTTCG TCACGACGCG GCAAGTCGCA TCAAATACCC GGAAACCGCG
751 CTCCGCGCGT TCCTGCTGCA CCGCCTTCGA TACGCCGTGT GCCGAATAAA
801 CCAGTGTGCG GCCCGGCGGC ACTTCCGCGA AGTCTTCGAT AAACACCGCG
851 CTTTTTTCGC GCAGGTTGTC CACGACGAAT TTGTGTGGA CGACTTCGTG
901 GCGCACATAA ACCGGCGCGC CGAATCTTTC CAAAGCACGT TCGACAATAC
951 TGATTGCCCG ATCCACACCG GCGCAGAAGC CGCGCGGATT GGCAAGGATG
1001 ATGGTTTTTC CGTTCATAAG TTTTGCATTC CGTGTTCAGA CGGCATTAC
1051 GTTTTTTTGC TNNATCTTTG CGATGGACGA TATTGTCAAG CACCGCCAAC
1101 ACCGCACCGA CGCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2316; ORF 694>:

```
g694.pep (partial)
1  SAFVLPHKHEM PALTPASTFA QIGFGFALAA QLLGQDEHDA FFRAPPFAHG
51  FMPPSAYGCG YFPHQHFRG RACRYADFAP AFKPRALQVG RVVHHIRIDS
101 ARCRHFAQAV AVGRIGRTDH NHDVALFRQL FDGGLPVGRR IADVFLVRIA
151 DIGETRVQRG DDVFGFIDRE RGLADIGEFV GVSDFEFCHI SDRFDQKHFA
201 RCKLPHRAFD LGVPLMPDHD DFTVLGIQSG DFLMHFRHQR ASRIKYPETA
251 LRRFLHLRLR YAVCRINQCR ARRHFRQVFD KHRAFFAQVV HDEFVVDVDFV
301 AHINRRAEFF QSTFDNTDCP IHTGAEEARI GKDDGFSVHK FCIPCSBGIH
351 VFLLXLCDGR YQAPPTPHR RR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2317>:

```
m694.sag
1  TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
51  GACGGCATTG GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGCAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTGCGCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCGG TTACGCGGAC TTTGTTTTTG CCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCAGCATGT CGCACTGTTT TGCCAACTCT TTGACGCGCG TTTGCCGGTT
451 GGTGCTGCGA TAGCAGATAT CTTCCTTGTC CGGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTGCG GGTTTCTGA CTTCGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTITGCCC GCGCAAGCT
651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CCTTATGCCG GATCATGATG
701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACGACGGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCGGCGGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTTGTCC ACGACGAATT TGTTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACCTTCC AAAGCACGTT CGACAATACT GATT GCCCGA
1001 TCCACACCAAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTC GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGCCAAC ACCGCCAACA CCGCACCAGC
1151 CGAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2318; ORF 694>:

```
m694.pep
1  LVASGSTRQK CRLKPVQTAFL VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDHVALF CQLFDGGLPV
```



```

151 GRIADIPLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPKR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRVAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVNN DFVAHINRRA ELQSTFDNT DCPIHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from *N. gonorrhoeae*:

```

m694/g694      86.8% identity in 372 aa overlap

      10      20      30      40      50
m694.pep    LVSASGRQKCR LKPQTA FVLPHK S-----TPASTFAQIGFGFALAAQLFGQDEHNAFFR
g694              :|||||  '|||||:|||||:|||||:|||||:|||||
              SAFVLPKHMPALTPASTFAQIGFGFALAAQLLGQDEHDAFFR
                  10      20      30      40

      60      70      80      90     100     110
m694.pep    TLAFAVGFPSPAYGCGYFPHQHFGGRGRACRYADFVFKPCALQVACIIHHIRIDSARC
g694          :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
          APFFAHGFMPPSAYGCGYFPHQHFGGRGRACRYADFAFAFKPRALQVGRVVHHIRIDSARC
              50      60      70      80      90     100

      120     130     140     150     160     170
m694.pep    RHFAQAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRRIADIFLVRIADIGETRVQRGDDV
g694          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
          RHFAQAVAVGRIGRTDHNHDVALFRQLFDGGLPVGRRRIADVFLVRIADIGETRVQRGDDV
              110     120     130     140     150     160

      180     190     200     210     220     230
m694.pep    FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPKRSFDLDVPLMPDHDDFT
g694          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
          FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPKRSFDLDVPLMPDHDDFT
              170     180     190     200     210     220

      240     250     260     270     280     290
m694.pep    VLGIQSGDFLMHFRHQASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHR
g694          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
          VLGIQSGDFLMHFRHQASRIKYPETALRRFLHRLRYAVCRINQCRARRHFRQVFNKHR
              230     240     250     260     270     280

      300     310     320     330     340     350
m694.pep    TFFTQVVHDEFVNNDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGI
g694          :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
          AFFAQVVHDEFVNNDFVAHINRRAELFQSTFDNTDCPIHTGAEARIGKDDGFSVHKFCI
              290     300     310     320     330     340

      360     370     380
m694.pep    SFS DGINIFLLGFYGGRCCTPPTPHRRRX
g694          :||:|||||:|||||:|||||:|||||
          PCS DGIHVLXLC DGRYCOAPPTPHRRRX
              350     360     370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2319>:

```

a694.nseq
1  TTGGTTTC CG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
51 GACGGCATT GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTGCAC
101 AAATCGGGT TGGTTTCGCC CTCGCGCGC AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTTCGCAC CCTCGCCTT CCGTACGGT TCGTGCCCC
201 ATCCGCGTAT GGTGCGCAGT ACTTCCGCA CCAACACTT CCGCGCGGAC
251 GCGCCTGCCG TTACGCGGAC TTGTTT TTTG CCCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACG ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCA
401 ATCACGATGT CGCACTGTTT TGCCAACTCT TTGACGGCGG TTTGCGGTT
451 GGTGCTCGCA TAGCAGATAT CTCTCTTG TGCGATTGCG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTGAGGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GCGCAAGCT
651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CCTTATGCC GATCATGATG

```

1118

```

701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGCCGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGTTGTGCC ACGACGAATT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACTCTTCC AAAGCACGTT CGACAATACT GATTGCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTT GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTATC GGTGGACGAT GTTGCCAAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2320; ORF 694.a>:

```

a694.pep
1  LVSASGTRQK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDVALF CQLFDGGLPV
151 GRRADIPLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPKR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVND FVAHINRRRA ELFQSTFDNT DCPHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPT PHRRRX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 694 shows 100% identity over a 385 aa overlap with a predicted ORF (ORF 694) from *N. meningitidis*:

m694/a694 100.0% identity in 385 aa overlap

m694.pep	10	20	30	40	50	60
a694	10	20	30	40	50	60
m694.pep	70	80	90	100	110	120
a694	70	80	90	100	110	120
m694.pep	130	140	150	160	170	180
a694	130	140	150	160	170	180
m694.pep	190	200	210	220	230	240
a694	190	200	210	220	230	240
m694.pep	250	260	270	280	290	300
a694	250	260	270	280	290	300
m694.pep	310	320	330	340	350	360
a694	310	320	330	340	350	360
m694.pep	370	380				
a694	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

```
g695.seq
1   TTGCTCTCAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTTGTATGC GCCGCCCAGT
101 GTCAAAATTC TCAAAGATT CAATCAAAAC CTGCCGAACG ATACGCGGAT
151 GTCCCCATC ACCCTGCCCG TCGGCGACGG TTTGACCCGT CTTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTTGGCTG TCTGTGTCTG
251 CCTCCTGTGC TTCCGTTTCA CCCGTTCCGG AGGGCAGCCG AACCGAAATG
301 CCGACACAGG AAAATGCTTC AGACGGCATT CCTATCCCG TTCCACTCT
351 GCAAGACCGT TTGGACTATC TGGAAAGCAA AATCGTCCGG CTGTGCAACG
401 AAGTGGAAT GTTAAACGGG AAAGTCAAAG CATTTGGAGCA TACGAAAAATA
451 CACCCCTCCG GCAGGACATA CGTCCAAAAA CTCGACGACC GCAAATTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACCGTCG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAAACATA TCAAAACGGC
601 AGGTTTCTG CCGCAGCCGC CTTGTTGAAG GGGCGGACG CGCGAGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCGAA GTCATATTCA AAATCGGCCA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCGCCGCA
901 GCCGTACGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695 >:

```
g695.pep
1   LPQTRPARRH HRHRQYFVER KGDARSGF*C AAQONSQRF QSKPAERYAD
51  CPHPARRRRR FDPASEKIMK TKLPLFIWL SVSASCASVL PVPESRTEM
101 PTQENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151 HPSGRTYVQK LDDRKLKEHY LNTEGGSASA HTVETAQONLY NQALKHYQNG
201 RFSAAAALLK GADGGDGGSI AQRSMYLLLO SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQQKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

```
m695.seq
1   TTGCTCTCAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCGGCATCC TCAAAGATTT CAATCAAAAC CTGCCGAACG ACCCGCGCAT
151 CGTCCCATC ACCCTGCCCG TCGGCGACGG CTTGACCCGT CTTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTAT CATTTGGCTG TCTGTGTCCG
251 CCTCCTGTGC TTCCGTTTCA CCCGTTCCGG CAGGCAGCCA AACCGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGGACTATC TGGAAAGCAA AATCGTCCGG CTGTGCAACG
401 AAGTGGAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAACA
451 CATCTTCCG GCAGGCATA CGTCCAAAAA CTCGACGACC GCAAGTTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTGC
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAAACATA TAAAGCGGC
601 AAGTTTCTG CCGCTGCCTC CTTGTTGAAA GGGCGGGACG GAGGCGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGCAA CTGCGAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTCA AAATCGGCCA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCGCCGCA
901 GCCGTGCGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

```
m695.pep
1   LPQTRPSRRH HRHRQYFAER KGDARSGFRC AAQRRHPQRF QSKPAERPAP
51  RPHHPARRRR LDPASEKIMK IKLPLFIWL SVSASCASVS PVPAGSQTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHAKT
151 HSSGRAYVQK LDDRKLKEHY LNTEGGSASA HTVETAQONLY NQALKHYKSG
201 KFSAAASLLK GADGGDGGSI AQRSMYLLLO SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE AMFKIGECQY RLQQKDIARA TWRSLIQTYP GSPAARKRAA
301 AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:

1120

m695/g695 90.8% identity in 305 aa overlap

```

      10      20      30      40      50      60
m695.pep  LPQTRPSRRHRHRQYFAERKGDARSGFRCAAQRRHPQRQFQSKPAERPAHRPHHPARRRR
g695      LPQTRPARRHRHRQYFVERKGDARSGFXCAAQCCNSQRQFQSKPAERYADCPHHPARRRR
      10      20      30      40      50      60

      70      80      90      100     110     120
m695.pep  LDPASEKIMKIKLPLFIWLVSASCSVSPVPAGSQTEMSTRENASDGIYPVPVPTLQDR
g695      FDPASEKIMKTKLPLFIWLVSASCSVLPVPEGSRTMPTQENASDGIYPVPVPTLQDR
      70      80      90      100     110     120

      130     140     150     160     170     180
m695.pep  LDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTEGGSASA
g695      LDYLEGKIVRLSNEVEMLNGKVKALEHTKIHPSGRTYVQKLDLDRKLKEHYLNTEGGSASA
      130     140     150     160     170     180

      190     200     210     220     230     240
m695.pep  HTVETAQNLNQALKHYKSGKFSAAASLLKGADGGDGGGSAQRSMYLLQLSRARMGNCS
g695      HTVETAQNLNQALKHYQNGRFSAAALLLKGADGGDGGGSAQRSMYLLQLSRARMGNCS
      190     200     210     220     230     240

      250     260     270     280     290     300
m695.pep  VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAARKRAA
g695      VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRSLIQTYPGSPAARKRAA
      250     260     270     280     290     300

m695.pep  AVRKRKX
g695      AVRKRKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2325>:

```

a695.seq
1  TTGCCTCAAG CTTGTCCGGC AAGGCGGCAT CATTGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCAGC
101 GTCGGCATCC TCAAAGATTT TAATCAAAAC CTGCCGAACG ATACGCGGAT
151 TGTCCTCCATC ACCCTGCCC GTCGGCAGCG TTTGACCCCTG CTTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTGGCTG TCCGTATCCG
251 CCGCCTGTTT TCCCCTGTT TCCCGCAATA TTCAGGATAT GCGGCTCGAA
301 CCGCAGGCAG AGGCAGGTAG TTCGGACGCT ATCCCTATC CCGTTCCAC
351 TCTGCAAGAC CGTTTGATT ATCTGGAAG CACACTCGTC CGCCTGTCGA
401 ACGAAGTGA AACCTTAAAC GGCAAAGTCA AAGCACTGGA GCATGCGAAA
451 ACACACCCCT CCAGCAGGGC ATACGTCCAA AACTCGAGC ACCGCAAGTT
501 GAAAGAGCAT TACCTCAATA CCGAAGGCG CAGCGCATCC GCACATACCG
551 TCGAAACCGC ACAAACCTC TACAATCAG CACTCAAACA CTATAAAGC
601 GGCAGGTTT CTGCCGCTGC CTCCTGTTG AAAGGCGCG ACGGAGGCGA
651 CGGCGGCAGC ATCGCGCAAC GCAGTATGTA CCTGTTGCTG CAAAGCAGGG
701 CGCGTATGG CAACTGCGAA TCCGTATCG AAATCGGAG GCGTTACGCC
751 AACCGTTTCA AAGACAGCCC AACCGCGCCT GAAGCCATGT TCAAAATCGG
801 CGAATGCCAA TACAGGCTTC AGCAAAAAGA CATTGCAAGG GCGACTTGGC
851 GCAGCCTGAT ACAGACCTAT CCCGGCAGCC CGGCGGCAAA ACGCGCCGCC
901 GCAGCCGTGC GAAACGATA G

```

This corresponds to the amino acid sequence <SEQ ID 2326; ORF 695.a>:

```

a695.pep
1  LPQACPARRH HCHRQYFVER KGDARSGFRC AAQRRHPQRF *SKPAERYAD
51  CPHHPARRRR FDPASEKIMK TKLPLFIWL SVSAACSSPV SRNIQDMRLE
101 PQAEAGSSDA IPYPVPTLQD RLDYLEGLTV RLSNEVETLN GKVKALEHAK
151 THPSSRAYVQ KLDDRKLKEH YLNTEGGSAS AHTVETAQNL YNQALKHYKS
201 GRFSAASLL KGADGGDGGG IAQRSMYLLL QSRARMGNCE SVIEIGGRYA
251 NRFKDSPTAP EAMFKIGECQ YRLQKDIAR ATWRSLIQTY PGSPAARKRAA
301 AAVRKRK*

```

Computer analysis of this amino acid sequence gave the following results:

m695/a695 88.3% identity in 308 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2329>:  
a696.seq

1122

```

1   TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTCATT TTGTCTGCCG CTCCTGAGT CGCGTCGGCA
101 GCTTTGTTC AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTC ATCAGCCGCA GCATCTTTGA
201 CTTGGCTCTT CGCTTCTTC ACGGCAGAAG CGGCAGACTC GGCGGCAGAA
251 GCCGCAGTGT CTTTAACATC GGAACAACG GCTTGAACCG CTCCTTAAC
301 CTCCTGTTG GCTTCTTGC AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2330; ORF 696.a>:

```

a696.pep
1   LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSEFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFLN
101 LLFGLRTSC QGSRHHCGNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 696 shows 100.0% identity over a 120 aa overlap with a predicted ORF (ORF 696.a) from *N. meningitidis*:

```

m696/a696    100.0% identity in 120 aa overlap

          10      20      30      40      50      60
m696.pep    LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSYSFLGTCLC
          |||
a696         LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSYSFLGTCLC
          10      20      30      40      50      60

          70      80      90      100     110     120
m696.pep    ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNGLNRFLNLLFGFLRTSCQGSRRHHCGNQ
          |||
a696         ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNGLNRFLNLLFGFLRTSCQGSRRHHCGNQ
          70      80      90      100     110     120

m696.pep    X
            |
a696         X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2331>:

```

g700.seq
1   ATGAGCAGCC TGATGACGTT GTTTTCGGTA TTGGTACCGA TGTTGCCCGG
51  ATTTTTTATC CGTGTTCCTCA AGCCTTACCT GCCCGCTTCG GACAAGGTGC
101 TGTCGGTTTT GGTGTATGCC GTGCTGCTGC TGATCGGCGT ATCGTTGTTCG
151 CGCGTGGAGG ATTTGGGTTC GCGGTTGGGC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TAGGGGCGAA CCTGCTTGCC TTGGCAGTGT
251 TGGGAAAGTT GTCCCGTGG CGGATAGGGG GAAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GAGGCAGCTC GGATGCGTAC TGCTCGGTTT
351 TGTGTCCGGC AAATTGATGT GCGATATTG GATGCCGTCT GAAAACGCGG
401 GTATGTACTG CCTGATGCTG CTGGTGTTC TCATCGGCGT ACAGCTCAA
451 AGTAGCGGCG TATCGTTGCG GCAGGTTTTG CTTAACCGGC GGGGCATCCG
501 GCTGTCCGTT TGGTTTATAT TGTCTCTCT TTCAGGCGGG CTGCTGTTT
551 CCGCATCGGC AGATGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATCCCT CTCGGGTTTG GTAATGACG AGGCTTACGG
651 GGCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTGGCA CGAGAGCTGT
701 TTGCACTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTCC GGATGCGGCG
751 GTGGGGGTGC GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTAATTCA
801 GGGTGC GGCGG GGTTTGGAAG TCGTGCCGCT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTC CACGCTGGG
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2332; ORF 700>:

```

g700.pep
1   MSSIMTLFSV LVPMFAGFFI RVPKPYLPAS DKVLSVLVYA VLLIGVSL
51  RVEDLGSRLG DMALTVLWLF VCTVGANLLA LAVLGKLSPW RIGGKKGVS
101 VGVSGSVRQL GCVLLGFVSG KLMCDIWMPS ENAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL LNRGRILSV WFILSSLSGG LLFAASADGV SWTKGLAMAS

```

1123

201 GFGWYLSLGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA  
 251 VGVGGATSMD FTLPVIQAG GLEVVPVAVS FGVVVNIAAP FLMVVVFSTLG  
 301 \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2333>:

m700.seq  
 1 ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG  
 51 ATTTTTTATC CGTGTGCCCA AGCCTTACCT GCCCGCTTGG GATAAGGTGC  
 101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCG  
 151 CGCGTGGAGG ATTTGGGTTT GCGGTTGGAC GATATGGCGT TGACGGTTCT  
 201 GTGGCTGTTT GTTGTACGG TCGGGGCGAA CCTGCTTGTCT TTGGCAGTGT  
 251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAAGGGAA GGCGCTTTCG  
 301 GTCGGCGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT  
 351 TGCATTCCGC AACTGATGC GCGATATTG GATGCCGTCT GAAAGCGCGG  
 401 GCATGTATTG TCTGATGCTG CTGGTGTTC TCATCGGCGT ACAGCTCAAA  
 451 AGCAGCGGCG TATCGTTGCG GCAGGTTTGG GTCAACCGCA GGGGTATTTCG  
 501 GTTGTGCGTC TGGTTTATGC TTTCACTCTT TCGGGGCGGG CTGCTGTTTG  
 551 CCGCATCGAC AGACGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC  
 601 GGCTTCGGTT GGTATCCCT CTGGGTTTG GTCATGACCG AGGCTTACGG  
 651 CGCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTTGGA CGAGAGCTGT  
 701 TTGCACTGGC ATTTATCCCG CTGCTGATGA AGCGTTTTC AGATGCGGCG  
 751 GTGGGGGTG GCGGTGCGAC CAGTATGGAT TTTACATTGC CCGTGATTCA  
 801 GGGTGCGGGC GGTGGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG  
 851 TGGTCAATAT CGCCGCCCG TTTCTGATGG TGGTGTTCG CTCTTGGGT  
 901 TGA

This corresponds to the amino acid sequence <SEQ ID 2334; ORF 700>:

m700.pep  
 1 MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLIGVSL  
 51 RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLFPP RIKGKGKGV  
 101 VGVSGSVGQL GCVLLGFAFG KLMRDIWMP ESAGMYCLML LVFLIGVQLK  
 151 SSGVSLRQVL VNRRGIRLSV WEMLSSLSGG LLFAASTDGV SWTKGLAMAS  
 201 GFGWYLSLGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA  
 251 VGVGGATSMD FTLPVIQAG GLEVVPVAVS FGVVVNIAAP FLMVVFSALG  
 301 \*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

ORF 700 shows 94.7% identity over a 300 aa overlap with a predicted ORF (ORF700.ng) from *N. gonorrhoeae*:

m700/g700

m700.pep	10	20	30	40	50	60
	MDSLMTLLSVLIPMFAGFFIRV	PKPYLPALDKVLSVLVYAV	LLIGVSLRVEDLGSRLD			
g700	10	20	30	40	50	60
	MSSLMTLFSVLVPMFAGFFIRV	PKPYLPASDKVLSVLVYAV	LLIGVSLRVEDLGSRLG			
m700.pep	70	80	90	100	110	120
	DMALTVLWLFVCTVGANLLA	LAVLGKLFPPRIKGKGKGV	SVGVSGSVGQLGCVLLGFAFG			
g700	70	80	90	100	110	120
	DMALTVLWLFVCTVGANLLA	LAVLGKLSFWRIGKGKGV	SVGVSGSVRQLGCVLLGFVSG			
m700.pep	130	140	150	160	170	180
	KLMRDIWMPSESAGMYCLML	LVFLIGVQLKSSGVSLRQVL	VNRRGIRLSVWFMSSLSGG			
g700	130	140	150	160	170	180
	KLMCDIWMPSENAGMYCLML	LVFLIGVQLKSSGVSLRQVL	LNRRGIRLSVWFMSSLSGG			
m700.pep	190	200	210	220	230	240
	LLFAASTDGVSWTKGLAMAS	GFGWYLSLGLVMTEAYGAVW	GSIMLLNDLARELFALAFIP			
g700	190	200	210	220	230	240
	LLFAASADGVSWTKGLAMAS	GFGWYLSLGLVMTEAYGAVW	GSIMLLNDLARELFALAFIP			

1124

	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFLTPVIQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
g700	LLMKRFPDAAVGVGGATSMDFLTPVIQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
	250	260	270	280	290	300
m700.pep	X					
g700	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2335>:

```

a700.seq
1  ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTGCCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC
101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTGTGCG
151 CGCGTGGAGG ATTTGGGTTC GCGGTTGGAC GATATGCGGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAGGGGAA GGGCGTTTCG
301 GTCGGTGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
351 TGCATCCGGC AAACGTATGC GCGATATTG GATGCCGTCT GAAAACGCGG
401 GTATGTATTG TCTGATGCTG CTGGTGCTCN TCATCGGCGT ACAGCTCAAA
451 AGCAGCGGCG TATCGTTGCG GCAGGTTTGT GTCAACCGCA GGGGTATTTCG
501 GTTGTGCGTC TGGTTTATGC TTTCATCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGACGGTGTG TCGTGGGTGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTGATGACCG AGGCTTACGG
651 CGCGGTATGG GGCAGTATCG CGCTTTTGAA CGATTGGCA CGAGAGCTGT
701 TCGCGCTGGC ATTTATCCG CTGCTGATGA AGCGTTTTC CGATGCGGCA
751 GTGGGGGTGCG GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTGATTTCG
801 GGGTGCGGGC GGCTTGAAG CCGTACCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCTCCG TTTCTGATGG TGGTGTTCG CGCTTTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2336; ORF 700.a>:

```

a700.pep
1  MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLIGVSL
51  RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLFPPW RIKGKGKGV
101 VGVSGSVGQL GCVLLGFASG KLMRDIWMP ENAGMYCLML LVLXIGVQLK
151 SSGVSLRQVL VNRGIRLSV WFMLSSLSGG LLFAASADGV SWVKGLAMAS
201 GFGWYSLSGL VMTEAYGAVW GSIALNDLA RELFALAFIP LLMKRFPDAA
251 VGVGGATSMDF LTPVIRGAG GLEAVPVAVS FGVVVNIAAP FLMVVFSALG
301 *

```

m700/a700 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVVPKPYLPALDKVLSVLVYAVLLIGVSLSRVEDLGSRLD					
a700	MDSLMTLLSVLIPMFAGFFIRVVPKPYLPALDKVLSVLVYAVLLIGVSLSRVEDLGSRLD					
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLFPPWRIKGKGKGVSVGVSGSVGQLGCVLLGFAG					
a700	DMALTVLWLFVCTVGANLLALAVLGKLFPPWRIKGKGKGVSVGVSGSVGQLGCVLLGFASG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRGIRLSVWFMLSSLSGG					
a700	KLMRDIWMPSENAGMYCLMLLVXIGVQLKSSGVSLRQVLVNRGIRLSVWFMLSSLSGG					
	130	140	150	160	170	180
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRGIRLSVWFMLSSLSGG					
a700	KLMRDIWMPSENAGMYCLMLLVXIGVQLKSSGVSLRQVLVNRGIRLSVWFMLSSLSGG					
	130	140	150	160	170	180



1125

	190	200	210	220	230	240
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYLSGLVMT	EAYGAVWGSIMLLNDLARELFALAFIP				
a700	LLFAASADGVSWVKGLAMASGFGWYLSGLVMT	EAYGAVWGSIALLLNDLARELFALAFIP				
	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFTL	PVIQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG				
a700	LLMKRFPDAAVGVGGATSMDFTL	PVIRGAGGLEAVPVAVSFGVVVNIAAPFLMVVFSALG				
	250	260	270	280	290	300

m700.pep	X
a700	X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2337>:

g701.seq

```

1  ATGTCCTGGC ACATATTCCA AGTGCAGGG ATACCGACCG CTTCGATGGC
51  ACAATCTACG CCGTCTTCGC CGACGATGGC GAAAACCTGT TTGGAGACGT
101 CGCCGGAAGC GGGGCTGATG GTATGGGTCG CGCCCAACTC TTTCGCCGGT
151 TTCAAACGGT TTTCGTCCAT ATCGCACACG ATAATGGCGG CAGGGCTATA
201 CAGTTGGGCG GTCAACAAGG CGGACATACC GACAGGGCCG GCACCTGCGA
251 TGAATACGGT ATCGCCGGGT TTCACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTCG GTAAAGCGTC GCTCAACAGC AGGGCGATTT CTTCGTTGAC
351 GTTGTCGTGC GGCGGCACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2338; ORF 701>:

g701.pep

```

1  MSWHIFQVAG IPTASMAQST PSSPTMAKTC LETSPEAGLM VVWAPNSFAG
51  FKRFSISQHT IMAAGLYSWA VNKADIPTGP APAMNTVSPG FTSPYCTPIS
101 WAVGKASLNS RAISLTLSC GGTRLLSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2339>:

m701.seq

```

1  ATGTCCTGGC ACATATTCCA TGTAGCAGGG ATACCGACCG CTTCGATGGC
51  GCAATCCACG CCGTCTTCGC CGACGATGGC AAAGACTTGT TTGGATACTT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTCG CACCCAATTC TTTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACG ATGATGGCGG CGGGACTGTA
201 CAGTTGGGCG GTCAACAGGG CGGACATACC GACAGGGCCT GCCCCAGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGATTT CTTCGTTGAC
351 ATTATCGGGC AGCGGAACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2340; ORF 701>:

m701.pep

```

1  MSWHIFHVAG IPTASMAQST PSSPTMAKTC LDTSPHAGLM VVWAPNSFAS
51  FKRFSISQHT MMAAGLYSWA VNRADIPTGP APAMNTVSPG LTSPYCTPIS
101 WAVGKASLNN RAISLTLSC SGTLLLSA*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with menB

ORF 701 shows 92.2% identity over a 128 aa overlap with a predicted ORF (ORF701.ng) from *N. gonorrhoeae*:

m701/g701

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTC	LDTSPHAGLMVVWAPNSFAS	FKRFSISQHT			
g701	MSWHIFQVAGIPTASMAQSTPSSPTMAKTC	LETSPEAGLMVVWAPNSFAG	FKRFSISQHT			

1126

	10	20	30	40	50	60
m701.pep	70	80	90	100	110	120
	MMAAGLYSWAVNRADIP TGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	:     :     :     :     :     :					
g701	70	80	90	100	110	120
	IMAAGLYSWAVNKADIPTGPAPAMNTVSPGFTSPYCTPISWAVGKASLNSRAISSLTLSG					
	:     :     :     :     :     :					
m701.pep	129					
	SGTRLLSAX					
	:					
g701	129					
	GGTRLLSAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2341>:

```
a701.seq
1  ATGTCTTGCG ACATATTCCA AGTTGCAGGG ATACCGACGG CTCGATCGC
51  GCAGTCCACG CCGTCTTCGC CGACGATAGC GGCAACTTGC TTGCTTACAT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTG CGCCCACTC TTTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACA ATGATGGCGG CGGGGCTGTA
201 CAGTTGGGCG GTCGGCAAGG CGGACATACC GACAGGAGCG GCACCTGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGTGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGACTT CTTCGTTGAC
351 GTTGTGCGGC AGCGGCACGA GGCTGTTGTC GGCATAA
```

This corresponds to the amino acid sequence <SEQ ID 2342; ORF 701.a>:

```
a701.pep
1  MSWHIFQVAG IPTASIAQST PSSPTIAATC LLTSPEAGLM VWVAPNSFAS
51  FKRFSISQT MMAAGLYSWA VGKADIPTGA APAMNTVSPG LTSPYCTPIS
101 CAVGKASLNN RATSSLTLSG SGTRLLSA*
```

m701/a701 92.2% identity in 128 aa overlap

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASF					
	:     :     :     :     :     :					
a701	MSWHIFQVAGIPTASIAQSTPSSPTIAATCLLTSPEAGLMVWVAPNSFASF					
	:     :     :     :     :     :					
	10	20	30	40	50	60
m701.pep	70	80	90	100	110	120
	MMAAGLYSWAVNRADIP TGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	:     :     :     :     :     :					
a701	70	80	90	100	110	120
	MMAAGLYSWAVGKADIPTGAAPAMNTVSPGLTSPYCTPISCAVGKASLNNRATSSLTLSG					
	:     :     :     :     :     :					
	129					
m701.pep	SGTRLLSAX					
	:					
a701	SGTRLLSAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2343>:

```
g702.seq
1  ATGCCGTGt ccaAAGCCAG TTGGA CTTCG CCCGGAGtgg cAACGCCGGG
51  AATCAGGGGA ATGCCGCTGT TGCGGCCGGC TCTGGCGAGG GATTCTGCA
101 AACCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGGAT TGGTTACCGT ACCTGCGCCG ATGATGGCGT TGGGCATTTT
201 TTTGGCAATC AGGCGGATGG CCTCGAGTCC GACGGGGGTG CGCAAGGTAA
251 TTTGAGGGT GGGGATGCCG CTTTCGACAA GGGCGCGGGA CAAATCGACG
301 GCGGTGCTTA AGTCGTCAAt cgCCATCACA GGCACAACTG CGCCGGCGGT
351 CAGGATTTCG cggggggtca gttga
```

This corresponds to the amino acid sequence <SEQ ID 2344; ORF 702>:

g702.pep

1127

```

1  MPCSKASWTS PGVATPGIRG MPLLRLPALAR DSCCKPGLMAK TAPASSTALS
51  CSGLVTVLPAP MMALGISLAI RRMASSTPTGV RKVISRVGMP PSTRADKST
101 AVLKSSIAIT GTTAPAVRIS RGV3*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2345>:

```

m702.seq
1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAAC TGCGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGGAAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2346; ORF 702>:

```

m702.pep
1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSGLVTVLPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

ORF 702 shows 91.9% identity over a 124 aa overlap with a predicted ORF (ORF702.ng) from *N. gonorrhoeae*:

m702/g702

	10	20	30	40	50	60
m702.pep	MPCSKASWISPGVATPGIRGMPLLWPALARDSCSPGLMAKTAPASSTALSCSGLVTVLPAP					
g702	MPCSKASWTSFGVATPGIRGMPLLRLPALARDSCCKPGLMAKTAPASSTALSCSGLVTVLPAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m702.pep	TMALGTSIAIRRMASRPTGVRVISRVGMPPSTRAWDKSM AVLKSSIAITGTTAPAVKIS					
g702	MMALGISLAI RRMASPTGVRKVISRVGMPPSTRADKSTAVLKSSIAITGTTAPAVRIS					
	70	80	90	100	110	120
	130	140				
m702.pep	RGVSLDISVLRVEWGILLRWDRXL					
g702	RGVSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2347>:

```

a702.seq
1  ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAAC TGCGCCGGCGGT
351 CAAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGGAAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2348; ORF 702.a>:

```

a702.pep
1  MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  CSGLVTVLPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

m702/a702 100.0% identity in 143 aa overlap

10	20	30	40	50	60
----	----	----	----	----	----

1128

```

m702.pep  MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVFAP
          |||
a702      MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVFAP
          10      20      30      40      50      60

          70      80      90      100     110     120
m702.pep  TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
          |||
a702      TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
          70      80      90      100     110     120

          130     140
m702.pep  RGVSLDISVLRVEWGILLRWDRLX
          |||
a702      RGVSLDISVLRVEWGILLRWDRLX
          130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2349>:

```

g703.seq
1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCG CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTTAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAAACG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAGA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAATATGG
351 CTTGAACGGC GAGGCATACG CACTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GTTTACGACA ATATCAGCGG TTTTATAAA
451 GGCACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCGAAAAAA GCGGTTGCCG ATTTGAAGGC GAAAAAAGGT TTTGATGCCG
551 TTTTGAAACA ATACTCGCTC AACGACCGCA CCAAACGGAC CGGCGCGCCG
601 GCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA
701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGcgaggTG
751 AAAGTGCCTT CTTTGTACGA AATGAAAGGA CAGATTGCCG GCAACCTTCA
801 GCGGGAACGG ATTGACCGTG CCGTctgTGc gcTGTtgggT aaggCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2350; ORF 703>:

```

g703.pep
1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51  EDTPQLRQSL LENEVNTTVV AQEVKRLKLD RSAEFKDALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIART QPVSEQEVKA VYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKRTGAP
201 DGVVPLKDLE QGVPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV
251 KVPSFDEMKG QIAGNLQAEI IDRAVCALLG KANIKPAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2351>:

```

m703.seq
1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAAACG AAGTGGTCAA
201 TACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAATATGG
351 CTTGAACGGC GAGGCATACG CATTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAAACA ATATTCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

```

1129

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA  
 751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA  
 801 GCGGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA  
 851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>:

m703.pep

1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA  
 51 EDTPQLRQSL LENEVNTVV AQEVKRLKD RSAEFKNALA KLRAEAKKSG  
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK  
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP  
 201 VGYVPLKDLE QGVPPLYQAI KDLKKGEFTA TPLKNGDFYG VYVNDREV  
 251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK\*

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from *N. gonorrhoeae*:

m703/g703

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
g703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
m703.pep	70	80	90	100	110	120
	LENEVNTVVAAQEVKRLKLDRSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703	LENEVNTVVAAQEVKRLKLDRSAEFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
m703.pep	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
g703	EAYALHIAKTQPVSEQEVKAVYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
	130	140	150	160	170	180
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPLYQAIKDLKKGEFTATPLKNGDFYG					
g703	FDAVLKQYSLNDRTKRTGAPDGYVPLKDLEQGVPPLYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
m703.pep	250	260	270	280	289	
	VYVNDREVVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
g703	VYVNDREVVKVPSFDEMKGQIAGNLQAERIDRAVCALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2353>:

a703.seq

1 ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCTT GTTCCGGCAG  
 51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CCGTCAGAAA ATCGACAGTT  
 101 CCGTCATTGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC  
 151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACGAG AAGTGGTCAA  
 201 CACCGTGGTC GCACAGGAAG TGAAACGCTT GAAACTCGAC CGGTCGGCAG  
 251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC  
 301 GACGACAAGA AACCGTCCTT CAAAACGTT TGGCAGGCGG TAAATATGG  
 351 CTTGAACGGC GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGGTTT  
 401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA  
 451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA  
 501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG  
 551 TCTTGAACA ATATTCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG  
 601 GTCGGATATG TGCCGCTGAA AGATTGGAA CAGGGTGTTT CGCCGCTTTA  
 651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

1130

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA  
 751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA  
 801 GCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA  
 851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2354; ORF 703.a>:

a703.pep  
 1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA  
 51 EDTPQLRQSL LENEVVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG  
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK  
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP  
 201 VGYVPLKDLE QGVPPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSDREV  
 251 KVPSFDEMKG QIAGNLQAEI IDRAVGALLG KANIKPAK\*

m703/a703 100.0% identity in 288 aa overlap

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
a703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60

m703.pep	70	80	90	100	110	120
	LENEVVNTVVAQEVKRLKLDLSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
a703	LENEVVNTVVAQEVKRLKLDLSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120

m703.pep	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
a703	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
	130	140	150	160	170	180

m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPLYQAIKDLKKGEFTATPLKNGDFYG					
a703	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPLYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240

m703.pep	250	260	270	280	289
	VYYVNSDREVKVPSFDEMKGQIAGNLQAEI IDRAVGALLGKANIKPAKX				
a703	VYYVNSDREVKVPSFDEMKGQIAGNLQAEI IDRAVGALLGKANIKPAKX				
	250	260	270	280	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2355>:

a704.seq  
 1 ATGAAAAA CCTGTTTCCA CTGCGGCTG GACGTTCCCG AAAACCTGCA  
 51 TCTGACCGTC CGTTACGAAA ACGAAGACCG CGAAACCTGC TGCGCCGGTT  
 101 GTCAGGCAGT CGCACAAAGC ATTATTGACG CGGGCTTGGG CAGTTATTAC  
 151 AAACAACGCA CCGCCGACGC GCAAAAAACC GAGCTGCCGC CCCAAGAAAT  
 201 CCTCGACCAA ATCCGCCTGT ACGACCTGCC CGAAGTCCAG TCCGACTTTG  
 251 TGGAACCCCA CGGCGGCACG CGCGAGGCGG TTTTAATGCT CGGCGGCATC  
 301 ACCTGCGCCG CCTGCGTCTG GCTGATCGAA CAGCAGCTTT TGCGTACAGA  
 351 CGGCATCGTC CGCATCGACC TCAATTACAG CACGCACCGC TGCCGCGTCG  
 401 TCTGGGACGA CGGCAAAATC CGCCTTTCCG ACATTCTGTT GAAATCAGG  
 451 CAGATAGGCT ACACCGCCGC ACCCTATGAC GCGCAAAAA TCGAAGCCGC  
 501 CAACCAAAAA GAACGCAAAC AATACATCGT CCGCCTCGCC GTTGCCGGGC  
 551 TGGGGATGAT GCAGACGATG ATGTTGCGCG TGCCGACCTA CCTTACGGC  
 601 GCGGACATCG AACCCGATTT CCTGCAAAAT CTCCATTGGG GCGGCTTTT  
 651 AATGGTGCTG CCCGTCGTAT TCTATTGCGC CGTCCCGTTT TATCAAGGCG  
 701 CGCTGCGCGA CTTGAAAAAC CGCCGCGTCG GCATGGATAC GCCGATTACC  
 751 GTCGCCATCA TCATGACCTT TATCGCCGGC GTTTACAGCC TTGCGACAAA

1131

```

801 TCGGGGGCAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTTCC
851 TGCTGGGCGG ACGCTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901 GCCGCCGAGA GGCTGGTGAA GCTGATTCCT GCGTTTGGCC ATCATATGCC
951 CGATTACCCC GATACGCAGG AAACCTGCGA GGCAGCTGTC GTCAAATTGA
1001 AGGCGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCCTTGAC
1051 GGCACGGTGC TGGAAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTCGCCA AAATGCCGTC TGAAAAAGTA ACCGCCGGCA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGCGCG
1201 GGCACGCGAC TGTGCGACAT CGTCCGCTG CTCGACCGCG CCTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCTCG TCTTTCATAT
1301 TCGGCGAACT CCTGCTTGCC GTCCCGTCT TCATCGGCTG GACGCTGTAC
1351 GCCGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCATTAC
1401 CTGCCCTGCG GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGCTTCTA
1451 CCGGTACGCT GGCGCGCGAA GGTATTTTAA TCGGCGGAAA GCAGGCAATC
1501 GAAACCCCTCG CCCAAACCCAC CGACATCATC TTCGACAAA CCGGCACGCT
1551 GACCCAAGGC AAACCCGCGG TCCGCCGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTTCTGCGG GTGGCGCAGG CTTTAGAACA ACAGTCCGAA
1651 CATCCCTTG CCCGCGCCAT CCTCAACTGC CGCATTTTCA ACAGGAGCGT
1701 CCCCGACATC GCTATTAAAC AACGCCTCAA CCGCATCGGC GAAGGCGTGG
1751 GCGCGCAACT GACCGTCAAC GGCGAAACAC AGGTTTGGCG ATTGGGCGAG
1801 GCATCCTATG TCGCCGAAAT TTCAGGTAAG GAACCGCAA CAGAAGGCGG
1851 CGGCAGCGCG GTTTACCTCG GCAGTCAAAG CGGTTTCCAA GCCGTGTTCT
1901 ACCTGCAAGA CCCGCTCAA GACAGCGCGG CGGAGGCGGT GCGGCAAGTG
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGGCGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGCACGCG CCCTGGGTGT CGCGCACTAC CGCGCCCAAG
2051 CCATGCCCGA GGACAAACTG GAATACGTCA AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGGCATC AACGACGCGC CCGTTTTGGC
2151 GACGCAGAC GTATCCGCGG CCGCAGCGG CGGACGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATTGTGTGA TTGAACGAAG ATTGCGTAC CGTCGCCAC
2251 CTGCTCGATC AGGCGCGGCG CACCGCCAT ATTATCCGGC AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATTGCCGT ACCGCTTCCC GTTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTCACAAA CGGGGAAAA TGCAGTCTGA
2451 AAAAATGCCG TCCGAACAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

```

a704.pep
1  MKKTCFHCGL DVPENLHLTV RYENEDRET CAGCQAVAS IIDAGLGSYY
51  KQRTADAQKT ELPPQEILDQ IRLYDLPEVQ SDFVETHGGT REAVLMLGGI
101 TCAACVWLE QQLRDTGIV RIDLNYSTR CRVWDDGKI RLSDILLKIR
151 QIGYTAAPYD AQKIEAANQK ERKQYIVRLA VAGLGMQTM MFALPTYLYG
201 GDIEPDLFI LHWGGFLMVL PVVFCVAVF YQALRLDLN RRVGMDTPIT
251 VAIIMTFIAG VYSLATNAGQ GMYFESIAML LFFLLGGRFM EHIARRKAGD
301 AAERLVKLIP AFCHHMPDYP DTQETCEAAV VKLKAGDIVL VKPGETIPVD
351 GTVLEGSSAV NESMLTGESL PVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALAQKPR TAEALQYAS SFIFGELLTA VPVFIGWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTLARE GILIGKQAI
501 ETLAQTTDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VAQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPQTEGGGSA VYLGSSQSGFQ AVFYLDPLK DSAAEAVRQL
651 AGKNLTLHIL SGDRETAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLMIGDGI NDAPVLAQAD VSAAAAGGTD IARDGADIVL LNEDLRTVAH
751 LLDQARRTRH IIRONLIWAG AYNIIAVFLA VLGYPWPWIA ALGMSFSSLA
801 VLGNALRLHK RGKMQSEKMP SEQ*

```

m704/a704 99.8% identity in 823 aa overlap

```

          10      20      30      40      50      60
m704.pep  MKKTCFHCGLDVPEHLHLTVRYENEDRETCCAGCQAVASIIDAGLGSYYKQRTADAQKT
          |||
a704      MKKTCFHCGLDVPEHLHLTVRYENEDRETCCAGCQAVASIIDAGLGSYYKQRTADAQKT
          10      20      30      40      50      60

          70      80      90     100     110     120
m704.pep  ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLEQQQLRDTGIV
          |||
a704      ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLEQQQLRDTGIV

```

1132

	70	80	90	100	110	120
m704.pep	130	140	150	160	170	180
a704	RIDLNYSTHRCRVVWDDGKIRLS	DILLKIRQIGYTAAPYDAQKIEA	ANQKERKQYIVRLA			
	130	140	150	160	170	180
m704.pep	190	200	210	220	230	240
a704	VAGLGMMQTMFALPTYLYGGDIEP	DFLQILHWGGFLMVL	PVVIFYCAVPFYQ	GALRDLKN		
	190	200	210	220	230	240
m704.pep	250	260	270	280	290	300
a704	RRVGMDTPITVAIIMTFIAGVYSL	ATNAGQGMFYFESI	AMLLFFLLGGRF	MEHIARRKAGD		
	250	260	270	280	290	300
m704.pep	310	320	330	340	350	360
a704	AAERLVKLIPAFCHHMPDYPDTQ	ETCEAAVVKLKAGD	IVLVKPGETIP	PVDGTVLEGSSAV		
	310	320	330	340	350	360
m704.pep	370	380	390	400	410	420
a704	NESMLTGESLPVAKMPSEKVTAG	TINTQSPLIIRTDR	TGGGTRLSHIV	RLLDRALAQKPR		
	370	380	390	400	410	420
m704.pep	430	440	450	460	470	480
a704	TAEAEQYASSFIFGELLAVPVFI	GWTLYADAHTALW	ITVALLVITCP	CALSLATPTAL		
	430	440	450	460	470	480
m704.pep	490	500	510	520	530	540
a704	AASTGTLAREGILIGGKQAIETLA	QTTDIIFDKTGTL	TQGKPAVRRIS	LLRGTD	DEAFVLA	
	490	500	510	520	530	540
m704.pep	550	560	570	580	590	600
a704	VAQALEQQSEHPLARAILNCRISD	GSVPDIAIKQRLN	RIGEGVGAQLT	VNGETQVWALGR		
	550	560	570	580	590	600
m704.pep	610	620	630	640	650	660
a704	ASYVAEISGKEPQTEGGGSAVYL	GSQSGFQAVFYLT	DPLKDSAAEAV	RQLAGKNLT	LHIL	
	610	620	630	640	650	660
m704.pep	670	680	690	700	710	720
a704	SGDRETAVAETARALGVAHYRAQ	AMPEDKLEYVKALQ	KEGKKVLMIGD	GINDAPVLAQAD		
	670	680	690	700	710	720
m704.pep	730	740	750	760	770	780
a704	VSAAGGTDIARDGADIVLLNEDL	RTVAHLLDQARR	RHIIQNLIWAG	AYNIIAVPLA		
	730	740	750	760	770	780
m704.pep	790	800	810	820		
a704	VLGYVQPWIAALGMSFSSLAVL	GNALRLHKRGK	MQSEKMPSEQX			
	790	800	810	820		



This corresponds to the amino acid sequence <SEQ ID 2358; ORF 705>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2359>:

This corresponds to the amino acid sequence <SEQ ID 2360; ORF 705>:

**Computer analysis of this amino acid sequence gave the following results:**

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. gonorrhoeae*:

```

m705/g705      95.0% identity in 238 aa overlap
                10          20          30          40          50          60
m705.pep      VENNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g705          VENNFLASLPFMTETRADMLISAFPMVKAGFTVSLPLAIAASFVIGMIIA VAVALVRIMP
                10          20          30          40          50          60
                70          80          90          100         110         120
m705.pep      AGGIVRKILLKLVEFYISVIRGTPLLVLQLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGAY
                :|| :| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

1134

```

g705      SGGIFQKCLKLVEFYISVVRGTPLLVQLVIVFYGLPSVGIYINPIPAAIIGFSLNVGAY
           70      80      90      100     110     120

           130     140     150     160     170     180
m705.pep  ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||
g705      ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130     140     150     160     170     180

           190     200     210     220     230     239
m705.pep  AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCCKVLFQIARLEKRFDRYVAKX
           |||
g705      AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCCKVLFQIARLEKRFDRYVAKX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2361>:

```

a705.seq
1  GTGTTCAATA ATTCCTTGC TTCGCTGCCG TTTATGACGG AACACGCGC
51  CGATATGATT GTCAGCGCGT TTTGCGCTAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTTGGCGGCA GCTTCTTTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTGG CTTTGGTGCG GATTATGCCC GCCGCGGCA TCGTGCGGAA
201 AATCCTGCTG AAATTGGTGG AATTTTATAT TTCCGTCATT CGCGGTACGC
251 CGCTGTTGGT TCAGCTTGTG ATTGTGTTT ACGGGCTGCC TTCGTCGGC
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGGCGCATAT GCTTCCGAAA CCATACGCGC GGCAATTTG TCCGTACCGA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCCGCA TCGTCGCGCC GCAGGCATTT CGCGTTGCCG TGCCGCCTTT
501 GAGCAACGAG TTTATCGGTT TGTTTAAAAA CACCTCGCTC GCGGCAGTCG
551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGT
651 TTGTAAAGTG CTGTTCTGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2362; ORF 705.a>:

```

a705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51  VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLV IVFYGLPSVG
101 IYIDPIPAAI IGFSNLVGAY ASETIRAAIL SVPKGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTLEF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCCKV LFLIARLEK RFDYVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 705 shows 100.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. meningitidis*:

```

a705/m705  100.0% identity in 238 aa overlap

           10      20      30      40      50      60
a705.pep  VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
           |||
m705      VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
           10      20      30      40      50      60

           70      80      90      100     110     120
a705.pep  AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGAY
           |||
m705      AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGAY
           70      80      90      100     110     120

           130     140     150     160     170     180
a705.pep  ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||
m705      ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130     140     150     160     170     180

           190     200     210     220     230     239
a705.pep  AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCCKVLFQIARLEKRFDRYVAKX
           |||
m705      AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCCKVLFQIARLEKRFDRYVAKX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

g706.seq

```

1 ATGAACCTCT CGCAACGCAA ACGCCTTTCC GgccGCTGGC TCAACTCCTA
51 CGAACGCTac cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCGgaa
101 ccgtCCTGTT CGCCACCGCA CTCGCCCgGc tACTCCACCT CCAacacggc
151 gAATGGATAG GGAtgaCCGT CTTGTCGTC CTCGGCATGC TCCAGTTCCA
201 AGGCcgcgatt tActccaacg cgggtgGAacg taTgctcggt acggtcatcg
251 ggctgGGCGC GGGTTTGGGc gTTTTATGGC TGAACCAGCA TTAtttccac
301 ggcaacCTcc tcttctacct gaccatcggc acggcaagcg cactggccgg
351 ctGGGCGGCG GTCGGCAAAA acggctacgt ccctatgctg GCGGGGctgA
401 CGATGTGCAT gctcatcggc gACAACGGCA GCGAATGGCT CGACAGCGGC
451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCCGCATCG CCATTGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGTATGA CGCGCAACG TTTGGAGCAG AATATGGTCA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCG CCACCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCAC
751 CGCAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAATCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGCGCCCT CATCAACGGC
901 AGACACGCCC GCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

g706.pep

```

1 MNSSQRKRLS GRWLSYERY RHRRLIHAVR LGGTVLFATA LARLLHLQHG
51 EWIGMTVFVV LGMLQFOGAI YSNAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWLD SG
151 LMRAMNVLIG AAIATAAAL LPLKSTLMWR FMLADNLADC SKMIAEISNG
201 RRMTRERLEE NMVKMRQINA RMVKSRSILA ATSGESRISP SMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMROE ISALVILLQR
351 TRRKWLDAHE RQHLRQSLLE TREHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

m706.seq

```

1 ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
51 CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
101 CCGTCCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
151 GAGTGGATAG GGATGACCGT CTTGTCGTC CTCGGCATGC TCCAGTTTCA
201 AGGGGCGATT TACTCCAAGG CGGTGGAACG TATGCTCGGC ACGGTCATCG
251 GGCTGGGCGC GGGTTTGGGc GTTTTATGGC TGAACCAGCA TTATTCCAC
301 GGCACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
351 CTGGGCGGCG GTCGGCAAAA ACGGCTACGT CCCTATGCTG GCAGGGCTGA
401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA
451 CTCATGCGCG CCATGAACGT CCTCATCGGC GCGGCCATCG CCATCGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGCATGA CCGCGAACG CCTCGAGGAG AACATGGCGA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCG CCATCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
751 CGTAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAATCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC
901 AGACACGCCC GCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

m706.pep

```

1 MNTSQNRRLV SRWLSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
51 EWIGMTVFVV LGMLQFOGAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWLD SG
151 LMRAMNVLIG AAIATAAAL LPLKSTLMWR FMLADNLADC SKMIAEISNG
201 RRMTRERLEE NMVKMRQINA RMVKSRSILA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTVALING

```

1136

301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR  
 351 TRRKWLDAHE RQHLRQSLLE TREHG\*

m706/g706 96.5% identity in 375 aa overlap

	10	20	30	40	50	60
m706.pep	MNTSQNRNLVSRWLN	SYERYRRLIHAVRL	GGAFLFATASARLL	LHLQHGEWIGMTVFV		
g706	MNSSQRKRLSGRWLN	SYERYRRLIHAVRL	GCTVLFATALARLL	LHLQHGEWIGMTVFV		
	10	20	30	40	50	60
m706.pep	70	80	90	100	110	120
	LGM	LQFGAIYSKAVERML	GTVIGLGAGLGVLW	LNQHYFHGNLLFYLT	VGTSALAGWAA	
g706	70	80	90	100	110	120
	LGM	LQFGAIYSNAVERML	GTVIGLGAGLGVLW	LNQHYFHGNLLFYLT	TIGTSALAGWAA	
	70	80	90	100	110	120
m706.pep	130	140	150	160	170	180
	VGKNGYV	PMLAGLTMCLIGD	NGSEWLD	SGLMRAMNVLIGA	AIATAAKLLPLK	STLMWR
g706	130	140	150	160	170	180
	VGKNGYV	PMLAGLTMCLIGD	NGSEWLD	SGLMRAMNVLIGA	AIATAAKLLPLK	STLMWR
	130	140	150	160	170	180
m706.pep	190	200	210	220	230	240
	FMLADNL	ADCSKMI	AEISNGRRMTRER	LEENMAKMRQINAR	MVKSRS	HLAATSGESRISP
g706	190	200	210	220	230	240
	FMLADNL	ADCSKMI	AEISNGRRMTRER	LEQNMVQMRQINAR	MVKSRS	HLAATSGESRISP
	190	200	210	220	230	240
m706.pep	250	260	270	280	290	300
	AMMEAMQ	HAHRKIVNTTE	LLTTAAKLQSPK	LGSEIRLLDRHFT	LLQTDLQQT	VALING
g706	250	260	270	280	290	300
	SMMEAMQ	HAHRKIVNTTE	LLTTAAKLQSPK	LGSEIRLLDRHFT	LLQTDLQQT	AAALING
	250	260	270	280	290	300
m706.pep	310	320	330	340	350	360
	RHARRIRIDT	AINPELEALAEHL	HYQWQGF	LWLSTNMRQEISAL	VILLQTRRKWLDA	HE
g706	310	320	330	340	350	360
	RHARRIRIDT	AINPELEALAEHL	HYQWQGF	LWLSTNMRQEISAL	VILLQTRRKWLDA	HE
	310	320	330	340	350	360
m706.pep	370					
	RQHLRQSLLE	TREHG				
g706	370					
	RQHLRQSLLE	TREHG				
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2367>:

a706.seq

1	ATGAACACCT	CGCAACGCAA	CCGCCTCGTC	AGCCGCTGGC	TCAACTCCTA
51	CGAACGCTAC	CGCTACCGCC	GCCTCATCCA	CGCCGTCCGG	CTCGGCGGGG
101	CCGTCCTGTT	CGCCACCGCC	TCCGCCCGGC	TGCTCCACCT	CCAACACGGC
151	GAGTGGATAG	GGATGACCGT	CTTCGTCGTC	CTCGGCATGC	TCCAGTTTCA
201	AGGGGCGATT	TACTCCAAGG	CGGTGGAACG	TATGCTCGGC	ACGGTCATCG
251	GGCTGGGCGC	GGGTTTGGGC	GTTTATATGGC	TGAACCAGCA	TTATTTCCAC
301	GGCAACCTCC	TCTTCTACCT	CACCGTCGGC	ACGGCAAGCG	CACCTGGCCGG
351	CTGGGCGGCG	GTCGGCAAAA	ACGGCTACGT	CCCTATGCTG	GCGGGGCTGA
401	CGATGTGCAT	GCTCATCGGC	GACAACGGCA	GCGAATGGTT	CGACAGCGGC
451	CTGATGCGCG	CGATGAACGT	CCTCATCGGC	GCGGCCATCG	CCATCGCCGC
501	CGCCAACTG	CTGCCGCTGA	AATCCACACT	GATGTGGCGT	TTCATGCTTG
551	CCGACAACCT	GACCGACTGC	AGCAAAATGA	TTGCCGAAAT	CAGCAACGGC
601	AGGCGCATGA	CCCGCAACG	CCTCGAAGAG	AACATGGCGA	AAATGCGCCA
651	AATCAACGCA	CGCATGGTCA	AAAGCCGCAG	CCACCTCGCC	GCCACATCGG
701	GCGAAAGCCG	CATCAGCCCC	GCCATGATGG	AAGCCATGCA	GCACGCCAC
751	CGTAAAATTG	TCAACACCAC	CGAGCTGCTC	CTGACCACCG	CCGCCAAGCT
801	GCAATCTCCC	AAACTCAACG	GCAGCGAAAT	CCGGCTGCTT	GACCGCCACT
851	TCACACTGCT	CCAAACCGAC	CTGCAACAAA	CCGTCGCCCT	TATCAACGGC

1137

901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA  
 951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA  
 1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC  
 1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG  
 1101 CCTGCTTGAA ACACGGGAAC ACAGTTGA

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

a706.pep  
 1 MNTSQNRNLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG  
 51 EWIGMTVFVV LGMLQFQAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH  
 101 GNLLFYLTVG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWFD SG  
 151 LMRAMNV LIG AATAIAAAKL LPLKSTLMWR FMLADNLTDC SKMIAEISNG  
 201 RRMTREERLEE NMAKMRQINA RMVKSRSILA ATSGESRISP AMMEAMQHAH  
 251 RKIVNTTELL LTAAKLQSP KLGSEIRLL DRHFTLLQTD LQQTVALING  
 301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMREQ ISALVILLQR  
 351 TRRWLDAHE RQHLRQSLLE TREHS\*

a706/m706 99.5% identity in 374 aa overlap

a706.pep	10	20	30	40	50	60
	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
m706	10	20	30	40	50	60
	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
a706.pep	70	80	90	100	110	120
	LGMLQFQAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG TASALAGWAA					
m706	70	80	90	100	110	120
	LGMLQFQAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG TASALAGWAA					
a706.pep	130	140	150	160	170	180
	VGKNGYVPM LAGLTMCLIGDNGSEWFD SG LMRAMNV LIG AATAIAAAKL LPLKSTLMWR					
m706	130	140	150	160	170	180
	VGKNGYVPM LAGLTMCLIGDNGSEWLD SG LMRAMNV LIG AATAIAAAKL LPLKSTLMWR					
a706.pep	190	200	210	220	230	240
	FMLADNLTDCSKMIAEISNGRRMTREERLEENMAKMRQINARMVKSRSILAATSGESRISP					
m706	190	200	210	220	230	240
	FMLADNLTDCSKMIAEISNGRRMTREERLEENMAKMRQINARMVKSRSILAATSGESRISP					
a706.pep	250	260	270	280	290	300
	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLGSEIRLLDRHFTLLQTD LQQTVALING					
m706	250	260	270	280	290	300
	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLGSEIRLLDRHFTLLQTD LQQTVALING					
a706.pep	310	320	330	340	350	360
	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMREQ ISALVILLQRTRRWLDAHE					
m706	310	320	330	340	350	360
	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMREQ ISALVILLQRTRRWLDAHE					
a706.pep	370					
	RQHLRQSLLE TREHSX					
m706	370					
	RQHLRQSLLE TREHGX					

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

m707.seq

```

1 ATGGAATTA TTAACGATGC AGAACTTATC CGTTCCATGC AGCGTCAGCA
51 GCACATAGAT GCTGAATTGT TAACTGATGC AAATGTCCGT TTCGAGCAAC
101 CATTGGAGAA GAACAATTAT GTCCTGAGTG AAGATGAAAC ACCGTGTACT
151 CGGGTAAATT ACATTAGTTT AGATGATAAG ACGGTGCGCA AATTTCTTTT
201 TCTTCTTCT GTGCTCATGA AAGAAACAGC TTTTAAACT GGGATGTGTT
251 TAGGTTCCAA TAATTGAGC AGGCTACAAA AAGCCGCGCA ACAGATACTG
301 ATCGTGCGTG GCTACCTCAC TTCCCAAGCT ATTATCCAAC CACAGAATAT
351 GGATTGCGGA ATTCTGAAAT TACGGGTATC AGCAGGCGAA ATAGGGGATA
401 TCCGCTATGA AGAAAAACGG GATGGGAAGT CTGCCGAGGG CAGTATTAGT
451 GCATTCAATA ACAAATTTCC CTTATATAGG AACAAAATTC TCAATCTTCG
501 CGATGTAGAG CAGGGCTTGG AAAACCTGCG TCGTTGCCG AGTGTAAAA
551 CAGATATTCA GATTATACCG TCCGAAGAAG AAGGCAAAAG CGATTACAG
601 ATCAAATGGC AGCAGAATAA ACCCATACGG TTCAGTATCG GTATAGATGA
651 TCGGGGCGGC AAAACGACCG GCAATATCA AGGAAATGTC GCTTTATCGT
701 TCGATAACCC TTTGGGCTTA AGCGATTTGT TTTATGTTTC ATATGGACGC
751 GGTTTGGCGC ACAAACGGA CTTGACTGAT GCCACCGGTA CGGAAACTGA
801 AAGCGGATCC AGAAGTTACA GCGTGCATTA TTCGGTGCCC GTAAAAAAT
851 GGCTGTTTTT TTTAATCAC AATGGACATC GTTACCACGA AGCAACCGAA
901 GGCTATTCCG TCAATTACGA TTACAACGGC AAACAATATC AGAGCAGCCT
951 GGCCGCCGAG CGCATGCTTT GCGTAACAG ACTTCATAAA ACTTCAGTCG
1001 GAATGAAATT ATGGACACGC CAAACCTATA AATACATCGA CGATGCCGAA
1051 ATCGAAGTAC AACGCCGCGC CTCTGCAGGC TGGGAAGCCG AATTGCGCCA
1101 CCGTGCTTAC CTCAACCGTT GGCAGCTTGA CGGCAAGTTG TCTTACAAAC
1151 GCGGGACCGG CATGCCCAA AGTATGCCTG CACCGGAAGA AAACGGCGGC
1201 GATATTCTTC CAGGTACATC TCGTATGAAA ATCATTACTG CCAGTTTGGG
1251 CGCAGCCGCC CCATTATTT TAGGCAACA GCAGTTTTTC TACGCAACCG
1301 CCATTCAAGC TCAATGGAAC AAAACGCCGT TGGTTGCCA AGATAAATTG
1351 TCAATCGGCA GCCGCTACAC CGTTCGCGGA TTTGATGGGG AGCAGAGTCT
1401 TTTCCGAGAG CGAGGTTTCT ACTGGCAGAA TACTTTAACT TGGTATTTTC
1451 ATCCGAACCA TCAGTTCTAT CTCGGTGCAG ACTATGGCCG CGTATCTGGC
1501 GAAAGTGAC AATATGTATC GGGCAAGCAG CTGATGGGTG CAGTGGTCGG
1551 CTTACAGAGA GGGCATAAAG TAGGCGGTAT GTTTGCTTAT GATCTGTTT
1601 CCGGCAAGCC GCTTCATAAA CCCAAAGGCT TTCAGACGAC CAACCCGTT
1651 TACGGCTTCA ACTTGAATTA CAGTTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2370; ORF 707>:

m707.pep

```

1 MEIINDAELI RSMQRQOHID AELLTDANVR FEQPLEKNNY VLSEDETPCT
51 RVNYISLDDK TVRKFSFLPS VLMKETAFTK GMCLGSNNLS RLQKAAQQIL
101 IVRGYLTSA IIQPNMDSG ILKLRVSAGE IGDIREYEEKR DGKSAEGSIS
151 AFNNKFPLYR NKILNLRDVE QGLENLRRLP SVKTDIQUIP SEEEGKSDLQ
201 IKWQNKPIR FSIIGDDAGG KTTGKYQGNV ALSFDNPLGL SDFYVSYGR
251 GLAHKTDLTD ATGTETESGS RSYSVHYSVP VKKWLFSFNH NGHRYHEATE
301 GYSVNYDYNG RQYQSSLAEE RMLWRNRLHK TSVGMKLWTR QTYKYIDDAE
351 IEVQRRRSAG WEAE LRHRAY LNRWQLDGKL SYKRGTMGRQ SMPAPEENG
401 DILPGTSRMK IITASLDAAA PFILGKQOFF YATAIQAWN KTLVAQDKL
451 SIGSRYTVRG FDGEQSLFGE RGFYQNTLT WYFHPNHQFY LGADYGRVSG
501 ESAQYVSGKQ LMGAVVGFRG GHKVGGMFAY DLFAGKPLHK PKGFQTTNTV
551 YGFNLNYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2371>:

a707.seq

```

1 NTGAAAGAAA CAGCTTTTAA AACTGGGATG TGTTTAGGTT CCAATAATTT
51 GAGCAGGCTA CAAAAGCCG CGCAACAGAT ACTGATTGTG CGTGGCTACC
101 TCACTCCCA AGCTATTATC CAACCACAGA ATATGGATTG GGGAAATCTG
151 AAATTACGGG TATCAGCAGG CGAAATAGGN GATATCCGCT ATGAAGAAAA
201 ACGGGATGNG AAGTCTGCCG AGGGCAGTAT TAGTGCAATC AATAACAAAN
251 TTCCCTTATA TAGGAACAAA ATTCTCAATC TTCGCGATGT AGAGCAGGGC
301 TTGGAAAACC TGCGTCGTTT GCCGAGTGTT AAAACAGATA TTCAGATTAT
351 ACCGTCCGAA GAAGAAGGCA AAAGCGATTT ACAGATCAAA TGGCAGCAGA
401 ATAAACCCAT ACGGTTTCACT ATCGGTATAG ATGATGCGGG CGGCAAAACG
451 ACCGGCAAAT ATCAAGGAAA TGTGCTTTA TCGTNCGATA ACCCTTTGGG
501 NTTAAGCGAT TNGTTTTATG TTTTCATATG ACCGCGTTTG GTGCACAAAA
551 CGGACTTGAC TGNTGCCACC GGTACGGAAA CTGAAAGCGG ATCCAGAAGT
601 TACAGCGTGC ATTATTCGGT GNNCGTAAAA AAATGGCTGT TTTCTTTTAA
651 TCACAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT
701 ACGATTACAA CGGCAACAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG

```

```

751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGNCA
1001 NATCCCGTAT GAAAATCATA ACCGCCGGAT TGGATGCAGC GGCCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATTC AAGCTCAATG
1101 GAACAAACG CCTTTGGTTG CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTCG CGGATTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTTCATCCG ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACAATATG
1301 TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCCG AGGAGGGCAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTTGCCGGCA AGCCGCTTCA
1401 TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA
1451 ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```

a707.pep
1  XKETAFTKGM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPQNMDSGIL
51  KLRVSAGEIG DIRYEKRDY KSAEGSISAF NNKXPLYRNK ILNLRDVEQG
101 LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
151 TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSRs
201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDYNKQ YQSSLAERML
251 LWXXXFXXTS VXMKLWTRQT YKYIDDAEIE VQRRSAGWE AELRHAYLX
301 RWQLDGKLSY KRGTMGRQSM PAPEENGSGT IPXSRMKII TAGLDAAPX
351 MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH
451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

a707/m707 95.3% identity in 486 aa overlap

```

a707.pep                                10      20      30
                                XKETAFTKGMCLGSNNLSRLQKAAQQILIVR
m707                                EDETPCTRVNYISLDDKTVRKFSFLPSVLMKETAFKTMCLGSNNLSRLQKAAQQILIVR
                                50      60      70      80      90     100

a707.pep                                40      50      60      70      80      90
                                GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEKRDYKSAEGSISAFNNKXPLYRNKI
m707                                GYLTSQAIQPNMDSGILKLRVSAGEIGDIRYEKRDYKSAEGSISAFNNKXPLYRNKI
                                110     120     130     140     150     160

a707.pep                                100     110     120     130     140     150
                                LNLRDVEQGLLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
m707                                LNLRDVEQGLLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
                                170     180     190     200     210     220

a707.pep                                160     170     180     190     200     210
                                GKYQGNVALSXDNPLGLSDXFYVSYGRGLVHKTDLTXATGTETESGSRsYSVHYSVXVKK
m707                                GKYQGNVALSFDNPLGLSDLFYVSYGRGLAHKTDLTDATGTETESGSRsYSVHYSVPVKK
                                230     240     250     260     270     280

a707.pep                                220     230     240     250     260     270
                                WLFNFHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWXXXFXXTSVXMKLWTRQTY
m707                                WLFNFHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWRNRLHKTsvgmklwtrqty
                                290     300     310     320     330     340

a707.pep                                280     290     300     310     320     330
                                KYIDDAEIEVQRRSAGWEAELRHAYLXRWQLDGKLSYKRGTMGRQSMMPAPEENGSGTII
m707                                KYIDDAEIEVQRRSAGWEAELRHAYLNRWQLDGKLSYKRGTMGRQSMMPAPEENGSDIL
                                350     360     370     380     390     400

```

```

          340      350      360      370      380      390
a707.pep  PXXSRMKIITAGLDAAAPXMLGKQQFFYATAIQAWNKPLVAQDKLSIGSRYTVRGFDG
          | : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
m707      PGTSRMKIITASLDAAAPFILGKQQFFYATAIQAWNKPLVAQDKLSIGSRYTVRGFDG
          410      420      430      440      450      460

          400      410      420      430      440      450
a707.pep  EQSLFGERGFYWNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRRGGHK
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m707      EQSLFGERGFYWNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRRGGHK
          470      480      490      500      510      520

          460      470      480
a707.pep  VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX
          | | | | | | | | | | | | | | | | | | | | | |
m707      VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX
          530      540      550      560

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2373>:

```

g708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCGA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCAACGGC AAGTATTGAA GATGCCTTGA AATCGAACCC
201 TAAAAACGAA CTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC GGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CTGCGGAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGTATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGTGCA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAAAATTC CCCTACTCGG AAGAATTGCA AACCGTCTCT
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2374; ORF 708.ng>:

```

g708.pep
1  MFFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSNPKNE LAWLVRAEIY QYLVNDRAQ ESFRQALSIK
101 PDSAEINNNY GWFLCGRILNR PAESMAYFDK ALADPTYPPT YIANLNKGIC
151 SAKQGQFGLA EAYLKRSLAA QPQFPAPFKE LARTEMLAGQ LGDADYFFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNVQAAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2375>:

```

m708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTCG TTCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCGA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCGACGGC AAGTATTGAA GACGCCCTGA AATCGGACCC
201 TAAAAACGAG CTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC GGTTGGTTCC TATGCGGCAG
351 GCTCAACCGC CTGCGGAAT CTATGGCATA TTTCGACAAA GCTCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAAAATTC CCCTACTCGG AAGAATTGCA AACCGTCTCT
751 ACCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2376; ORF 708>:

```

m708.pep

```



1141

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAQ ESFRQALSIK
101 PDSAEINNNY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSLLA QPQFPFAPKE LARTKMLAGQ LGDADYFFKK
201 YQSRVEVLQA DDLGLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

m708/g708 99.2% identity in 253 aa overlap

```

              10      20      30      40      50      60
m708.pep      MPFKPSKRISLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              |||||
g708           MPFKPSKRISLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              10      20      30      40      50      60

              70      80      90      100     110     120
m708.pep      DALKSDPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSEINNNYGWFLCGRLNR
              |||||
g708           DALKSNPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSEINNNYGWFLCGRLNR
              70      80      90      100     110     120

              130     140     150     160     170     180
m708.pep      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSLLAQPQFPFAPKE
              |||||
g708           PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSLLAQPQFPFAPKE
              130     140     150     160     170     180

              190     200     210     220     230     240
m708.pep      LARTKMLAGQLGDADYFFKKYQSRVEVLQADDLLGWKIAKALGNAQAAYEYEAQLQANF
              |||||
g708           LARTKMLAGQLGDADYFFKKYQSRVEVLQADDLLGWKIAKALGNVQAAYEYEAQLQANF
              190     200     210     220     230     240

              250
m708.pep      PYSEELQTVLTGQX
              |||||
g708           PYSEELQTVLTGQX
              250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

```

a708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGNGACGGC AAGTATTGAA GACGCCTTGA AATCAGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC NGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTGACAAA GCCCTGGCCG
401 ACCCCACNTA CCCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTGCT TGCTAGGCTG
651 GAAAAATGCC AAAGCCCTCG GCAACGCACA GCGGCATAC GAATATGAAG
701 CACAATTGCA GCGGAATTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2378; ORF 708.a>:

```

a708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQXTASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAQ ESFRQXLSIK
101 PDSAEINNNY XWFLCGRLNR PAESMAYFDK ALADPTYFPX YIANLNKGIC
151 SAKQGQFGLA EAYLKRSLLA QPQFPFAPKE LARTKMLAGQ LGDADYFFKK
201 YQSRVEVLQA DDLGLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 IGQ*

```

a708/m708 98.0% identity in 253 aa overlap

1142

	10	20	30	40	50	60
a708.pep	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQXTASIE					
m708	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a708.pep	DALKSDEPKNELAWLVRAEIQYLKVNDKAQESFRQXLSIKPDSAEINNXYWFLCGRLNR					
m708	DALKSDEPKNELAWLVRAEIQYLKVNDKAQESFRQALSIPDSAEINNXYWFLCGRLNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a708.pep	PAESMAYFDKALADPTYXPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
m708	PAESMAYFDKALADPTYTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a708.pep	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
m708	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
	190	200	210	220	230	240
	250					
a708.pep	PYSEELQTVLIGQX					
m708	PYSEELQTVLTGQX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2379>:

g709.seq

```

1  ATGTTTGCTT TCAAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
51  CGTCGTCGTC GCTCTGATTG CCGCAATGGG CTATACCATC ATTTCATTGG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGG CAGGGATGAT
201 AGGCGCGTTG AATCAGGGTA TGGCGCGCGT TTACCTGTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGGCTGAT TTCCCCGACT TATTTTATT TTTCGCGCTT
351 CGCGCTGTGT TCCGTCATCG GCGTGTCCAT CGGCAGCAGC CTGACCGCCT
401 GCGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC
451 GATATGGCGA TGACGgcggy cgcgattgTT tccggTGTGT TTTTCGCGCA
501 TAAATGTCC CCGCTTTCGG ACACCACGGG CATTTCGCGC TCCATCGTCG
551 GTATCGACCT GTTTGAACAC ATCAAAAACA TGATGTACAC CACCATCCCT
601 GCGTGGCTTA TCAGCGCGGC ACTGATGCTT TGGCTTCTTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACGGCTAT TCGCTGATTC CGTTTGCACT GTTGGTCGTT
751 TTGGCATTGA TCGCGCTCAA TGCCGTGGTC GCCATGCTCT TTACCGTCAT
801 TGCCGCGGTT GCCGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGCGCGGTG GTTTTATGGC GGTACAAAC TCGAAGGCGA AGCGTTTAAA
901 GCATTGCCA AACTGATTC GCGCGGCGGC TTGGAGAGTA TGTCTTTTAC
951 GCAGACCATC GTTATCCTCG GTATGAGTTT GGGCGGGCTG CTGTTTGCGC
1001 TCGGTGTGAT TCCTTCCTTG CTGGAGGCGG TCCGTACCTT CTTGACGAAT
1051 GCCGGACGCG CGACGTTTCA GCTTGCCATG ACTTCGGTCG GGGTCAATTT
1101 CCTGATTGGA GAGCAATATT TGAGCATCCT GCTTTCGGGA GAAACGTTCA
1151 AACCCGTTTA CGACAACTC GGCCTGCATT CGTGCAACCT GTCCGCGACT
1201 CTGGAAGATG CGGGGACGGT GATTAACCCG CTCGTGCCGT GGAGCGTGTG
1251 CCGCGTATTT ATCAGCCACG CCCTTGGCGT ACCCGTTTGG GAATATCTGC
1301 CTTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTAACCCT GTTATTCGGC
1351 TGGACGGGGC TGACTTTGAG CAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2380; ORF 709.ng>:

g709.pep

```

1  MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQAGMIGAL NQGMGAVYLF FFIGLMVSAL MNSGAIPTLM
101 YYGFGLISPT YFYFSAFALC SVIGVSISS LTACATVGVA FMGMAAFQA
151 DMAMTAGAIV SGVFFGDKMS PLSDTTGISA SIVGIDLFEL IKNNMYTTIP
201 AWLISAALML WLLPSVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVV
251 LALMRVNAV VAMLETVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
301 DIAKLISRG LLSMFFTQTI VILGMSLGL LFALGVIPSL LEAVRTFLTN

```

351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFFKPVYDKL GLHSCNLSRT  
401 LEDAGTVINP LVPWSVCGVF ISHALGVFVW EYLPYAFFCY LSLALTLLFG  
451 WTGLTLSKK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq  
1 ATGTTTCGCTT TCAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC  
51 CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTCATTGG  
101 AGTGGTTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG  
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT  
201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTGTTT TTCTTCATCG  
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG  
301 TATTACGGTT TCGGACTGAT TTCCCGGACT TATTTTATT TTCTCTCCTT  
351 CGCGCTGTGT TCCGTATCG CCGTGTCCAT CGGCAGCAGC CTGACCACCT  
401 GCGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGCGGCG GTTTCAGGCC  
451 GATATGGCGA TGACGGCGGG CGCGATTGTT TCGGGCGCAT TTTTGGCGA  
501 CAAAATGTCC CCGCTTTCGG ATACGACGGG TATTTCGCGC TCCATCGTCG  
551 GCATCGACTT GTTTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC  
601 GCGTGGCTCA TTAGTGCGGC ACTGATGCTT TGGCTTTTGC CGAATGTCCG  
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTGAAGCCA  
701 CGGGATTGGT GCACGGCTAT TCGCTGATTG CGTTTGCCTT GTTGGTCATT  
751 TTGGCATTGA TCGCATCAA CGCGCTCGTC GCCATGCTCT TTACCGTCAT  
801 GGTGCGCTT GCTGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC  
851 TCGGTGCGTG GTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTTTAA  
901 GATGTTGTCA AACTGATTTC GCGCGCGGCT TTGGAAGTA TGTTTTTCAC  
951 GCAAACCATC GTGATTCTCG GGATGAGTTT GGGCGGACTG TTGTTTGCCT  
1001 TCGGTGTGAT TCCTTCCTTG TTGGAGGCCA TCCGTACCTT CTGACGAAT  
1051 GCCGGACGCG CGACGTTTCC CGTTGCCATG ACTTCGCTCG GGGTTAATTT  
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTGCGGT GAAACGTTCA  
1151 AACCCTTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG  
1201 CTGGAAAGAT CCGGGACGGT GATTAACCCG CTCGTACCGT GGAGCGTATG  
1251 CCGCGTGTTC ATCAGCCACG CGCTGGCGCT GCCGGTTTGG GAATATCTGC  
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT  
1351 TGGACGGGGC TGACTTTGAG CAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep  
1 MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL  
51 YGLARGLKYN DMQQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM  
101 YYGFLISPT YFYFSSFALC SVIGVSIGSS LTTCATVGVA FMGMAAFQOA  
151 DMAMTAGAIV SGAFFGDKMS PLSDTTGISA SIVGIDLFEH IKNMYYTIP  
201 AWLISAALML WLLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI  
251 LALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK  
301 DVVKLISRG LLSMFFTQTI VILGMSLGL LFALGVIPSL LEAIRFTLN  
351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFFKPVYDKL GLHSCNLSRT  
401 LEDAGTVINP LVPWSVCGVF ISHALGVFVW EYLPYAFFCY LSLALTLLFG  
451 WTGLTLSKK\*

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAFKSLDDMPRGEALAVVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
g709	MFAFKSLDDMPRGEALAVVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
m709.pep	70	80	90	100	110	120
	DMQQGMIGALNQGMGAIYLF FFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSSFALC					
g709	DMQAGMIGALNQGMGAVYLF FFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSAFALC					
	70	80	90	100	110	120
m709.pep	130	140	150	160	170	180
	SVIGVSIGSSLTTCATVGVA FMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
g709	SVIGVSIGSSLTACATVGVA FMGMAAFQADMAMTAGAIVSGVFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
m709.pep	190	200	210	220	230	240
	SIVGIDLFEHIKNMYYTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFEHIKNMYYTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240

1144

	250	260	270	280	290	300
m709.pep	SLIPFALLVILALMRNAVAVAMLFTVMVAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK					
g709	SLIPFALLVILALMRNAVAVAMLFTVIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK					
	250	260	270	280	290	300
	310	320	330	340	350	360
m709.pep	DVVKLISRGGLESMTFTQIVILGMSLGGLLFALGVIPSLLEAIRTFLTNAGRATFSVAM					
g709	DIAKLISRGGLESMTFTQIVILGMSLGGLLFALGVIPSLLEAVRTFLTNAGRATFSVAM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m709.pep	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPWSVCGVF					
g709	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSCNLSTLEDAGTVINPLVPWSVCGVF					
	370	380	390	400	410	420
	430	440	450	460		
m709.pep	ISHALGVPVWEYLPYAFFCYLSLALTLFGWTGLTSLKXX					
g709	ISHALGVPVWEYLPYAFFCYLSLALTLFGWTGLTSLKXX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2383>:

```

a709.seq
1  ATGTTTCGCTT TCNAATCCTT ACTCGATATG CCGCGCGGTG AGGCNCTTGC
51  CGTCTGCTGC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTNNTTGG
101 AGTGGCTGCC GCATATGTCC ATTATGCGG CCATCGTNGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTNTTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCGACT TATTTTATT TTTCCGCCTT
351 CGCGCTGTGT TCCGTCATCG GCGTGTCAT CCGCAGCAGC CTGACCACCT
401 GCGCCACTGT CCGCGTTGCC TTNATGGGTA TNNNGNCGGC GTTTCNGGCC
451 NANATGGNGN NGNNGNNGN CNNGATTGTN NNGNCGCAT TNTTNGCGCN
501 CAAATGTGTC CCGCTTCCG ATACGNCGGG CATNTCCGCG TCCATTGTGC
551 GTATCGACCT GTTTGAACAC ATCAAAAATA TGATGTACAC NACCATTCCC
601 GCGTGGCTCA TCAGTGNNNC ACTGATGCTG TNGCTTCTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTGAAGCCA
701 CGGGATTGGT GCACTGCTAT TCGCTGATC CGTTTGCCT GTTGGTCGTT
751 TTGGCATTGA TCGCGCTCAA TGCCGTGGTC GCTATGCTCT TTACCGTCAT
801 TGCCGCCGTT GCCGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCCA AGCGTNTANA
901 GACATTGCCA AACTCATTTT TCGCGCGGTT TTGGAAAGTA TGTTTTTAC
951 GCAGACCATC GTGATTCCTT GGATGAGCCT TGGCGGGCTG CTGTTTGCAC
1001 TGGGCGCGAT TCCTTCCCTG CTGGATGCCG TCCGCAGCTT TTTGACGAAT
1051 GCCGGGCGTN CCACATTCAG CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTCNGGT GAAACGTTCA
1151 AACCTGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
1201 CTGGAAGATG CGGGGACGGT CATCAACCCG CTCGTACCGT GGAGCGTATG
1251 CGGCGTGTTT ATCANCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
1351 TGGACGGGGC TGACTTTGAG CAAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2384; ORF 709.a>:

```

a709.pep
1  MFAFXSLDDM PRGEALAVV ALIAAMGYTI IXLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFLISPT YFYFSAFALC SVIGVSISS LTTCATVGVA XMGXXXAFXA
151 XMXXXXXXIV XXAXXGXKMS PLSDTXGKSA SIVGIDLFH IKNNMYTTIP
201 AWLISXXLML XLLPSVAAQD LNSVESFRSQ LEATGLVHCY SLIPFALLV
251 LALMRVNAV AVAMLFTVIA AVTYLHSTPD LRQLGAWFYG GYKLEGEAXX
301 DIAKLISRGG LESMTFTQI VILGMSLGG LFLALGAIPSL LDAVRSFLT
351 AGRXTFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST

```

401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG  
451 WTGLTLSKK\*

a709/m709 91.1% identity in 459 aa overlap

a709.pep	10	20	30	40	50	60
	MFAFXSLDMPRGEALAVVVALIAAMGYTII	XLEWLP	PHMSII	AAIVVL	LILYGL	LARGLKYN
m709	10	20	30	40	50	60
	MFAFXSLDMPRGEALAVVVALIAAMGYTII	SLEWLP	PHMSII	AAIVVL	LILYGL	LARGLKYN
a709.pep	70	80	90	100	110	120
	DMQQGMIGALNQGMGAIY	FFFIGLMV	SALMM	SGAIP	TLMYYG	FGLISPTYFYFSAFALC
m709	70	80	90	100	110	120
	DMQQGMIGALNQGMGAIY	FFFIGLMV	SALMM	SGAIP	TLMYYG	FGLISPTYFYFSSFALC
a709.pep	130	140	150	160	170	180
	SVIGVSI	GSSLTTCATV	GVVAXMGXXXAF	XAMXXXXXIV	XXAXXG	KXKMSPLSDTXGXSA
m709	130	140	150	160	170	180
	SVIGVSI	GSSLTTCATV	GVVAFMGMAAFQ	ADMAMTAGAIV	SGAFFG	KXKMSPLSDTTGISA
a709.pep	190	200	210	220	230	240
	SIVGIDL	FEHIKNM	MYTTPAWL	ISXXLM	LXLLPS	VAAQDLNSVESFRS
m709	190	200	210	220	230	240
	SIVGIDL	FEHIKNM	MYTTPAWL	ISAALM	LWLLPN	VAAQDLNSVESFRS
a709.pep	250	260	270	280	290	300
	SLIPFALL	VVLALMR	NAVVM	LFTVIA	AAVAVTYL	LHSTPDLRQLGAWFYGGYKLEGEAXX
m709	250	260	270	280	290	300
	SLIPFALL	VILALMR	INAVVM	LFTVM	VAVAVTYL	LHSTPDLRQLGAWFYGGYKLEGEAFK
a709.pep	310	320	330	340	350	360
	DIAKLIS	RGGLES	MFFTQ	TIVIL	GMSL	GGLLFALGAI
m709	310	320	330	340	350	360
	DVVKLIS	RGGLES	MFFTQ	TIVIL	GMSL	GGLLFALGVI
a709.pep	370	380	390	400	410	420
	TSVGVN	FLIGE	QYLSIL	LSGET	FKPVY	DKLGLHSRNL
m709	370	380	390	400	410	420
	TSVGVN	FLIGE	QYLSIL	LSGET	FKPVY	DKLGLHSRNL
a709.pep	430	440	450	460		
	IXHALG	VPVWEY	LPYAFF	CYLSL	ALTLLF	GWGLTLSKKX
m709	430	440	450	460		
	ISHALG	VPVWEY	LPYAFF	CYLSL	ALTLLF	GWGLTLSKKX

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq

1	ATGGAAACCC	ACGAAAAAAT	CCGCCTGATG	CGCGAATTGA	ATAAATGGTC
51	CCAGGAGGAT	ATGGCGGAAA	AGCTGGCGAT	GTCGGCAGGC	GGGTATGCCA
101	AAATCGAACG	GGGCGAAACG	CAGTTAAATA	TCCCAGCTTT	GGAGCAGTTG
151	GCTCAGATT	TCAAAATCGA	TATGTGGGAC	TTGCTCAAA	CGGGCGGTGG
201	TGGGATGGTG	TTTCAGATTA	ATGAAGGTGA	TAGTGGTGCC	GATATTGCGT
251	TGTATGCGTC	GGGTGATGTT	TCGATGAAAA	TAGAATTTTT	AAAAATGGAG

m710.pep

1 METHEKIRLM RELNKSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL  
51 AQIFKIDMWD LLKSGGGGMV FQINEGDSGG DIALYASGDV SMKIEFLKME  
101 LKHCKEMLEQ KDKEIELLRK LTETV\*

a710.seq

```

1  ATGGAACCC  ACGAAAAAT  CCGCTGATG  CGCGAATGA  ATAAATGGTC
51  CCAGGAGGAT  AGTCGGGAAA  AGTGGCGAT  GTCGGCAGGC  GGGTATGCCA
101  AAATCGAAGC  AGGCGAAACG  CAGTTGAATA  TCCCGCGTTT  GGAGCAGTTG
151  GCGCAGATTT  TCAAAATTGA  TATGTGGGAC  TTGCTCAAT  CGGGCGCGGC
201  CGGGATGGTG  TTGCAGATTA  ACGATGTGGA  TACCAACAGC  GGGGAATTTG
251  CAATCTATAC  CGCTCAGGAT  GCATCNGTGA  AAGCTGGATT  TGTTAAATG
301  GAATTAAAC  ACTGTAAAGA  AATGTGGGAA  CACAAAGACA  AAGAAATCGA
351  GTGTGCTCCG  AAGCTGACCG  AACCCTTTTA  A

```

a710.pep

1 METHEKIRLM RELNKSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL  
51 AQIFKIDMWD LLKSGGGGMV LQINDVDTNS GEFAIYTAQD ASGKAGFVKM  
101 ELKHCKEMLE HKDKEIELLR KLTETV\*

	10	20	30	40	50	60
a710.pep	METHEKIRILMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLQLAQIFKIDMWD					
m710	METHEKIRILMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLQLAQIFKIDMWD					
	10	20	30	40	50	60
a710.pep	LLKSGGGGMVLQINDVDTSNGEFAIYTAQDASGKAGFVKMELKHCKEMLEHKDKIEILLR					
m710	LLKSGGGGMVFLQINEGDSG-GDIALYASGDVSMKIEFLKMKELKHCKEMLEQKDKIEILLR					
	70	80	90	100	110	120

```

a710.pep      KLTETVX
               |||||
m710          KLTETVX
               120

```

1147

g711.seq not found

g711.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

```
m711.seq
1  ATGCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACCTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTCCGCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAT ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAAATAT TGATGCACGA CCTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAAC TGCC
551 GCTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTTGGGC AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAAACTCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AGGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCCTATAAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:

```
m711.pep
1  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTASEIA KVYTIARMTD
51  LDMNDIKTS MVESAKSQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRRTPAHSAL DGLVYRYDDP FWATFYPPNG YNCRCVIAL SERDVERQQR
201 IVGQSTADNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFDDYNAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFSTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

```
a711.seq
1  ATGCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAAACCTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTTCCGCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAC ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAAATAT TGATGCACGA CCTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAAC TGCC
551 GTTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTCGGGC AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAAACTCTA
651 CAACAAAAAA GCGGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
```

1148

```

901 CCGGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AAGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2392; ORF 711.a>:

**a711.pep**

```

1 MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTAIEIA KVYTIARMTD
51 LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPASAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTSDNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFYDYNAGRM
251 NYRPDLKDYD RALAHQFAKA EMGGADFCTS FKQLEKEFYE VKQRDLIDGK
301 PDKEQIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

```

a711/m711 99.8% identity in 431 aa overlap

a711.pep	10	20	30	40	50	60
	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLDMLNDIKTS					
m711	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAIEIAKVYTIARMTDLDMLNDIKTS					
	10	20	30	40	50	60
a711.pep	70	80	90	100	110	120
	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
m711	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
	70	80	90	100	110	120
a711.pep	130	140	150	160	170	180
	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
m711	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
	130	140	150	160	170	180
a711.pep	190	200	210	220	230	240
	YNCRCSVIALSERDVERQGRIVGQSTSDNLVETHKIYNKKGDTYLTLAYKAPDGSLYTTD					
m711	YNCRCSVIALSERDVERQGRIVGQSTADNLVETHKIYNKKGDTYLTLAYKAPDGSLYTTD					
	190	200	210	220	230	240
a711.pep	250	260	270	280	290	300
	RGFDYNAGRMNYRPDLKDYDRALAHQFAKAEMGGADFCTSFKQLEKEFYEVKQRDLIDGK					
m711	RGFDYNAGRMNYRPDLKDYDRALAHQFAKAEMGGADFCTSFKQLEKEFYEVKQRDLIDGK					
	250	260	270	280	290	300
a711.pep	310	320	330	340	350	360
	PDKEQIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
m711	PDKEQIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
	310	320	330	340	350	360
a711.pep	370	380	390	400	410	420
	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
m711	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
	370	380	390	400	410	420

430



a711.pep	AKFMAKKKVLKX
m711	AKFMAKKKVLKX
	430

1150

g712.seq not found yet

g712.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2393>:

```
m712.seq
1  ATGATGCCCC ATATTGATTT TGACACGATT CCGGGCAGCA TCCGCGTGCC
51  CGGGCAGTAT ATTGAATTTA ACACCCGCAA TGCCGTACAA GGTTTGCCGC
101 AAAATCCGCA AAAGGTATTG ATGGTTGCAC CCATGCTGAC CGCGGGCATA
151 CAGCCCGCCT TAGAGCCGGT GCAACTATTT AGCGATGCCG AGGCGGCCGA
201 TTTGTTCCGA CAAGGCTCGC TGGCGCATTG GATGGTGCGC CAAGCATTTG
251 CCAACAACCC TTATTTGGAT TTGACCGTTA TCGGTATTGC CGACCACAGC
301 GCAGGCGTGC AGGCAACCGC AACCGTTACC CTTTCCGGCA CGGCCACCGC
351 GCCGGGCGTG GTGGAAATCA CGATTGGCGG CAAGCAGGTA AGCACGGCCG
401 TTAACACCGG CGAGACCGCC GCCACAGTGG CAGACCGTCT GAAAACCGCC
451 ATCACTGCCG CCGATGTAAC CGTTACCGCA TCCGGCAGCG GCGCAGCCGT
501 TACGCTGACG GCCAAACACA AAGGCGAGAT CGGCAACGAG AGCGGCTTAA
551 CCGTGAGCAC CGGCAATACC GGCCTAACTT ATCAAGCCAA TGCCTTTACC
601 GCGCGTGCCA AAATGCGGA CATTGCCACG GCCTTGTCCT AAGTGGCGGG
651 CAAGCATTAT CACATTATTT GCAGCCCGTT TAGCGATGAC GCCAACGCCA
701 AAGCCTTGAG CAACCATATT ACCAACGTAT CCAACGCCAT CGAGCAGCGC
751 GGCTGTATCG GCGTATTGGG TATGAGTGCG GCCTTGAGCA CGGCCACCAC
801 CGTACCGGCG GAAATCAACG ACGGCCGCGT GACCTGTGCT TGGTACAAAG
851 GTGCGGTAGA GCCAAACGCG ATCATCGCCG CAGGTTATGC GGCGGTGTTG
901 GCCTTTGAAG AAGACCCTGC CAAGCCGCTG AACACGCTGG AAATCAAAGG
951 GCTGGCCGTT ACACCTGATG CGCAATGGCC GCTGTTTGCA GAATGCAACA
1001 ATGCGCTGTA CAACGGCTTG ACCCGGCTCA CAGTGGTCAA CAACCGCGTG
1051 CAGATTATGC GTGCCGTATC CACCTATACC AAGTCGGCCA ACAACACCGA
1101 CGACCCGGCA CTACTCGACA TTACCACCAT CCGCACGCTG GATTATGTGC
1151 GCCGCAGCGT TAAAGAGCGC ATTGCCCTGC GTTTTCCGCG CGACAAATTG
1201 AGCGACCGCC TGCTGCCCAA GGTTAAGAGC GAGATTTTGG ACGTGTCTGAT
1251 TAAGCTCGAC CAAGCCGAAA TCATCGAAAA CGCCGAGGCC AACAAAGGCA
1301 AGCTGGTGGT GGCGCGTGCG CAAAACGACC CCAACCGTGT TAATGCCATT
1351 ATCCCGCGCG ATGTGGTCAA CGGCCGTGCAC GTCTTTGCCG GCGGCATTGA
1401 TTTGATTTTG TAA
```

This corresponds to the amino acid sequence <SEQ ID 2394; ORF 712>:

```
m712.pep
1  MMFHIDFTI PGSIRVPGQY IEFNTRNAVQ GLPQNPKVL MVAPMLTAGI
51  QPALEPVQLF SDAEAADLFG QGSLAHLNVR QAFANNPYLD LTVIGIADHS
101 AGVQATATVT LSGTATAPGV VEITIGGKQV STAVNTGETA ATVADRLKTA
151 ITAADVTVTA SGSGAAVTLT AKHKGEIGNE SGLTVSTGNT GLTYQANAFT
201 GGAKNADIAT ALSKVAGKHY HIICSPFSDD ANAKALSNHI TNVSNAIEQR
251 GCIGVLGMSA ALSTATTATG EINDGRMTCA WYKGAVEPNG IIAAGYAAVL
301 AFEEDPAKPL NTLKIKGLAV TPDAQWPLFA ECNNALYNGT TPLTVVNNRV
351 QIMRAVSTYT KSANNTDDPA LLDITTIRTL DYVRRSVKER IALRFPDRKL
401 SDRLLPKVKS EILDVLKLD QAEIENAEA NKGKLVVARA QNDPNRVNAI
451 IPADVNLGLH VFAGRIDLIL *
```

a712.seq not found yet

a712.pep not found yet

g713.seq not found yet

g713.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

m713.seq

```

1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGCGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCA
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 CCGAAAACAA CCCCGCTTTG GGCAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CCGAGGTTAC
651 TTTTGTGGCG CAATCGCACG GCCGCGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAACCCCGC GACGGCGTAT TGTGGCAACC TGGCCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CCCGATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCGC ACGCTTACCC CAAAAGGGC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
1101 CAAAAAGGC GGCAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2396; ORF 713>:

m713.pep

```

1  MQNNSYGYAV SVRVGKKEHR HWERYDIDS FLIPADSFDF VIGRLPEAA
51  IPDLSESCSE VVIDGQIVMT GIIGSQRHGK SKGSRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAKKL AAPWPQIKAV VLKAENNPAL GKIDIEPGET
151 VWQALHIAN SVGLHPWLEP DGTLVVGGAD YSSPPVATLC WSRTDSRCNI
201 ERMDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDLKWVYKD PTMTLHRPKT
251 VVVSADNLA ALQKQAKQL ADWRLEGFTL TITVGGHKTR DGVLWQPLR
301 VHVIDDEHGI DAVFFLMGRR FMSLRMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGRK KGVSHKGKKG GKKQAETAVF E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

a713.seq

```

1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGCGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCG
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 TCGAAAACAA CCCCGCTTTG GACAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGTGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CTGAGGTTAC
651 TTTTGTGGCG CAATCGCACG GCCGCGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAACCCCGC GACGGCGTAT TGTGGCAACC TGGCCGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CTCGATGGA TGGCAGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCGC ACGCTTACCC CAAAAGGGC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG

```

1101 CAAAAAAGGC GGCAAAAAC AAGCAGAAAC GCGGTGTTT GAATGA

This corresponds to the amino acid sequence <SEQ ID 2398; ORF 713.a>:

a713.pep

```
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLGSGESCE VVIDGQIVMT GIIGSQRHGK SKGGRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKVENNPAL DKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLVVGGVD YSSPPVATLC WSRTDSRRNI
201 ERMDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDWKVVKD PTMTLHRPKT
251 VVVSADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVWQPGQR
301 VHVIDDEHGI DAVFFLMGRR FLSRMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGR KGVSHKGGK GKKQAETAVF E*
```

a713/m713 98.4% identity in 381 aa overlap

a713.pep	10	20	30	40	50	60
	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDFVIGRLGPEAAIPDLGSGESCE					
m713	10	20	30	40	50	60
	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDFVIGRLGPEAAIPDLGSGESCE					
a713.pep	70	80	90	100	110	120
	VVIDGQIVMTGIIGSQRHGKSKGGRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAAKKL					
m713	70	80	90	100	110	120
	VVIDGQIVMTGIIGSQRHGKSKGSRRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAAKKL					
a713.pep	130	140	150	160	170	180
	AAPWPQIKAVVLKVENNPALDKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLVVGGVD					
m713	130	140	150	160	170	180
	AAPWPQIKAVVLKAENNPALGKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLVVGGAD					
a713.pep	190	200	210	220	230	240
	YSSPPVATLCWSRTDSRRNIERMDIEWDTDNRFSEVTFLAQSHGRSGDSAKHDLKVVYKD					
m713	190	200	210	220	230	240
	YSSPPVATLCWSRTDSRCNIERMDIEWDTDNRFSEVTFLAQSHGRSGDSAKHDLKVVYKD					
a713.pep	250	260	270	280	290	300
	PTMTLHRPKTVVVSADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGVWQPGQR					
m713	250	260	270	280	290	300
	PTMTLHRPKTVVVSADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGVWQPGLR					
a713.pep	310	320	330	340	350	360
	VHVIDDEHGI DAVFFLMGRRFMLS RMDGTQ TELRLKEDGI WTPDAYPKKAE AARKRKGR					
m713	310	320	330	340	350	360
	VHVIDDEHGI DAVFFLMGRRFMLS RMDGTQ TELRLKEDGI WTPDAYPKKAE AARKRKGR					
a713.pep	370	380				
	KGVS HKGKGGK KQAETAVFEX					
m713	370	380				
	KGVS HKGKGGK KQAETAVFEX					

1153

g714.seq not found yet

g714.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```
m714.seq
1  ATGAGCTATC AAGACATCTT GCGGGGCCTG TTGCCCCCGG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GCGGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
201 CGGTACGGGC AAAAACC GCCACCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAACCGC GCCGGCGACC GTCTTGC GCCAGGAAATC ATGTGGGTGT
401 GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGCTA A
```

This corresponds to the amino acid sequence <SEQ ID 2400; ORF 714>:

```
m714.pep
1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
51  RSAGQMLADW ERLVGLDGTG KNRQHRVLAV MAKLNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRERA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```
a714.seq
1  ATGAGCTATC AAGACATCTT GCGGGGTCTG TTGCCCCCGG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GCGGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
201 CGGTACGGGC AAAAACC GCCACCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAACCGC GCCGGCGACC GTCTTGC GCCAGGAAATC ATGTGGGTGT
401 GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGATA A
```

This corresponds to the amino acid sequence <SEQ ID 2402; ORF 714.a>:

```
a714.pep
1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
51  SSAGQMLADW ERLVGLDGTG KNRQRRVLAV MAKLNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRERA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

a714/m714 98.9% identity in 186 aa overlap

	10	20	30	40	50	60
a714.pep	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW					
m714	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPRSAGQMLADW					
	10	20	30	40	50	60
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPOPFRAGVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPOPFRAGVNR					
	70	80	90	100	110	120
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPOPFRAGVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDEPOPFRAGVNR					
	70	80	90	100	110	120
a714.pep	AGDRLAPQEIIMWVWHVNVRGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA					
m714	AGDRLAPQEIIMWVWHVNVRGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA					

1154

m714 AGDRLAPQEIMVWVHVNVVRGGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA  
 130 140 150 160 170 180

a714.pep IRFTYRX  
 |||||  
 m714 IRFTYRX

g715.seq not found yet

g715.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2403>:

m715.seq  
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA  
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT  
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT  
 151 CCGAAATGGG TTGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC  
 201 GGGTCGCTCG AAAGACAGTT TTCCACACT GTCAGACAAC GATACAGCCC  
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG  
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT  
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT  
 401 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2404; ORF 715>:

m715.pep  
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR  
 51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFEGGM  
 101 AGRNRKVRIP QREFLTLLDD DKQALMDDVQ DYFSGGLIP\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2405>:

a715.seq  
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA  
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT  
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT  
 151 CCGAAATGGT TGGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC  
 201 GGGTCGCTCG AAAGACAGTT TTCCACACT GTCAGACAAC GATACAGCCC  
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG  
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT  
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT  
 451 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2406; ORF 715.a>

a715.pep  
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR  
 51 PKWLGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFEGGM  
 101 AGRNRKVRIP QREFLTLLDD DKQALMDDVQ DYFSGGLIP\*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2407>:

g716.seq  
 1 ATGAACAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT  
 51 GGCCGCCGGC GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG  
 101 TTCAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT  
 151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC  
 201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA  
 251 AAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC  
 301 GAAGGCAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2408; ORF 716.ng>:

g716.pep  
 1 MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG  
 51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAKKHT KASKAKAKSA

1155

101 EGKCGEGKCG SK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2409>:

```
m716.seq
1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCGCGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA
```

-- This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:

```
m716.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*

m716/g716 86.6% identity in 112 aa overlap

      10      20      30      40      50
m716.pep MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----
      |||
g716      MNKNIAAALAGALSLSLAAGAAHKPASNATGVQKSAQGSAGSCGASKSAEGSCGASKSAEG
      10      20      30      40      50      60

      60      70      80      90      100
m716.pep ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
      |||
g716      SCGAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
      70      80      90      100      110
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2411>:

```
a716.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCGCGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2412.a>:

```
a716.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

a716/m716 100.0% identity in 102 aa overlap

```
      10      20      30      40      50      60
a716.pep MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
      |||
m716      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
      10      20      30      40      50      60

      70      80      90      100
a716.pep EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
      |||
m716      EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
      70      80      90      100
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2413>:

```
g717.seq
1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
```

```

51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCcccgCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  ACTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CGCCGCCGAC  AAAGACACTT  TGTCAAAC  CCTGTTCTTG  CCGCCGCTGC
251  TGTTTTCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCTGCGCG
301  TCTGAAATCC  TGTTTTCGCT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGTTTTCG
401  GTATGGAAGG  GCGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAA
451  CTCGCCATTC  TGCTGCTGTT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTC
501  GCGGAACACC  TCCGTCCTGA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGCTGAA  GGCCGTCGGG
601  CGCGCGCCGT  TTTGCCCGCG  CGTCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGCTCGCA  CTGAGCAGCC  TTGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTTCT  GAAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTTC
751  ATGGGTATTT  CGTTCGGCGG  GCGGGCATT  TTGCTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTCCGCTGC  AATCGAAGAA  AACGCCACGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAAATCC  CCGCCGCCCT  GCTTGCTTCC
901  GCCCTCTGCC  TGACCGGAAT  TTTCTCGCCC  CTCGCCCTCC  TCCTGCTGCC
951  GGAAGAACTAC  GCCGCCGTC  GGTTTACCGT  CGTATCGTGT  ATGCTGCCGC
1001  cgtGTTTATA  CACGCTGACC  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCCGATCGC  GCTTGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTACCGTC  CGCGGCGACG  CGCGGCGCGG
1151  CGGTTGCTTG  TGCCGCCTCA  TTCTGGTGT  TTTTGTGTTT  CAAGACAGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCGC  TTTATATGCA
1251  CACATTGTTT  TGCTTGGCCT  CCTCGCGGCG  CTACACCTGC  TTCGGCACAC
1301  CGGCAAACTA  CCCcctgttt  gccggcgtat  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AAATTTGCAC  AAATGTTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2414; ORF 717.ng>:

g717.pep

```

1  MDTKEILGYA  AGSIGSAVLA  VIILPLLSWY  FPADDIGRIV  LMQTAAGLTV
51  SVLCLGLDQA  YVREYAAAD  KDTLFKTLFL  PFLLFSAAlA  ALLLSRPSLP
101  SEILFSLDDA  AAGIGLVLE  LSFLPIRFL  LVLRMERAL  AFSSAQLVPK
151  LAIILLLPLT  VGLLHFPANT  SVLTAVYALA  NLAAAFLLF  QNRCRLKAVR
201  RAPFSPAVLH  RGLRYGIPLA  LSSLAYWGLA  SADRLFLKRY  AGLEQLGVYS
251  MGISFGGAAL  LLOSIFSTVW  TPYIFRAIEE  NATPARLSAT  AESAAALLAS
301  ALCLTGIFSP  LASLLLPENY  AAVRFTVVS  MLPPLFYTLT  EISGIGLNVV
351  RKTRPIALAT  LGALANLLL  LGLAVPSGGT  RGAAVACAAS  FWLFFVFKTE
401  SSCRLWQPLK  RPLMYHTLF  CLASSAAAYC  FGTANYPLF  AGVWAAYLAG
451  CILRHRKNLH  KLFHYLKKQG  FPL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2415>:

m717.seq

```

1  ATGGACACAA  AAGAAATCCT  CGGCTACGCG  GCAGGCTCGA  TCGGCAGCGC
51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCcccgCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  GCTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CACCGCCGAC  AAAGACACCT  TGTCAAAC  CCTGTTCTTG  CCGCCGCTGC
251  TGCTGCGCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCTGCGCG
301  TCTGAAATCC  TGTTTTCACT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGTTTTCG
401  GTATGGAAGG  ACGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAG
451  CTCGCCATTC  TGCTGCTGCT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTC
501  AGCGAACACC  GCCGTCCTGA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CCGCCGCCCT  TTTGCTGTTT  CAAAACCGAT  GCCGCTGAA  GGCCGTCGGG
601  CACGACCCGT  TTTGCCCGCG  CGTCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGATCGCA  CTGAGCAGCA  TCGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTTCT  GAAAAAATAT  GCCGGCCTGG  AACAGCTCGG  CGTTTATTTC
751  ATGGGTATTT  CGTTCGGCGG  GCGGGCATT  TTGTTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTCCGCGC  AATCGAAGAA  AACGCCCCGC
851  CCGCCCGCCT  CTCGGCAACG  GCAGAAATCC  CCGCCGCCCT  GCTTGCTTCC
901  GCCCTCTGCC  TGACCGGCAT  TTTCTCGCCC  CTTGCTCTCC  TCCTGCTGCC
951  GGAAGAACTAC  GCCGCCGTC  GGTTTATCGT  CGTATCGTGT  ATGCTGCCGC
1001  CGCTGTTTGA  CACGCTGGCG  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GCCGATCGC  GCTCGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTGCCTGC  CGGCGGCGCG  CGCGGCGCGG
1151  CGGTGCTGCT  TGCCGCCTCA  TTCTGGCTGT  TTTTGCCTT  CAAGACCGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCGC  TTTATCTGCA
1251  CACATTGTTT  TGCTGACCT  CCTCGGCGCG  CTACACCTGC  TTCGGCACGC
1301  CGGCAAACTA  TCCCCTGTTT  GCCCGCGTAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCATCCTGC  GCCACCGGAA  AGATTTGCAC  AAATGTTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```



This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

```
m717.pep
1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDQA YVREYYATAD KDTLFKTLFL PELLSSAAIA ALLLSRPSLP
101 SEILFSLDDA AAGIGLVLE LSFLPIRFL LVLMEGRAL AFSSAQLVVK
151 LAILLPLLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 HAPFSPAVLH RGLRYGIPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSFSTVW TPYIFRAIEE NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPPLFCTLA EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
401 SSCRLWQPLK RLPLYLHTLF CLTSSAAYTC FGTPANYPLF AGVWAAYLAG
451 CILRHRKDLH KLFHYLKKQG FPL*
```

m717/g717 96.4% identity in 473 aa overlap

m717.pep	10	20	30	40	50	60
	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
g717	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
m717.pep	70	80	90	100	110	120
	YVREYYATADKDTLFKTLFLPPLLSAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLE					
g717	YVREYYAARDKDTLFKTLFLPPLLSAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLE					
m717.pep	130	140	150	160	170	180
	LSFLPIRFLLLVLRMEGRALAFSSAQLVVKLAILLPLTVGLLHFPANTAVLTAVYALA					
g717	LSFLPIRFLLLVLRMEGRALAFSSAQLVVKLAILLPLTVGLLHFPANTSVLTAVYALA					
m717.pep	190	200	210	220	230	240
	NLAAAFLLFQNRCLKAVRHAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY					
g717	NLAAAFLLFQNRCLKAVRHAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY					
m717.pep	250	260	270	280	290	300
	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS					
g717	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENATPARLSATAESAAALLAS					
m717.pep	310	320	330	340	350	360
	ALCLTGIFSPASLLLPENYAAVRFIVVSCMLPPLFCTLAIEISGIGLNVVRKTRPIALAT					
g717	ALCLTGIFSPASLLLPENYAAVRFIVVSCMLPPLFCTLAIEISGIGLNVVRKTRPIALAT					
m717.pep	370	380	390	400	410	420
	LGALANLLLGLAVPSGGARGAACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF					
g717	LGALANLLLGLAVPSGGTRGAACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF					
m717.pep	430	440	450	460	470	
	CLTSSAAYTCFGTPANYPLFAGVWAAYLAGCILRHRKDLHKLHLYLKKQGFPLX					
g717	CLTSSAAYTCFGTPANYPLFAGVWAAYLAGCILRHRKDLHKLHLYLKKQGFPLX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

```
a717.seq
1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG
101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGGCGGCGGG GCTGACGGTG
151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
201 CGCCGCCGAC AAAGACACTT TGTTCAAAC CCTGTTCTG CCGCCGCTGC
```

1158

```

251 TGTCTGCCGC CGCGATAGCC GCCCTGCTGC TTTCCCGCCC ATCCCTGCCG
301 TCTGAAATCC TGTTTTTCGCT CGACGATGCC GCCGCCGGCA TCGGGCTGGT
351 GCTGTTTGAA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTCG
401 GTATGGAAGG ACGCGCCCTT GCCTTTTCGT CCGCGCAACT CGTGTCCAAG
451 CTCGCCATCC TGCTGCTGCT GCCGCTGACG GTCGGGCTGC TGCACCTTCC
501 GGCGAACACC GCCGTCCTGA CCGCCGTTA CCGGCTGGCA AACCTTGCCG
551 CCGCCGCCTT TTTGCTGTTT CAAAACCGAT GCCGTCTGAA GGCGTCCGG
601 CGCGCACCGT TTTTCATCCG CGTCCTGCAT CGCGGCCTGC GCTACGGCAT
651 ACCGATCGCA CTAAGCAGCA TCGCCTATTG GGGGTGCGCA TCCGCCGACC
701 GTTTGTCTCT GAAAAAATAT GCCGGCCTAG AACAGCTCGG CGTTTATTTCG
751 ATGGGTATTT CGTTCGGCGG AGCGGCATTA TTGTTCCAAA GCATCTTTTC
801 AACGGTCTGG ACACCGTATA TTTTCCGCGC AATCGAAGCA AACGCCCCGC
851 CCGCCCGCCT CTCGGCAACG GCAGAATCCG CCGCGCCCT GCTTGCCTCC
901 GCCCTCTGCC TGACCGGCAT TTTCTCGCCC CTCGCCTCCC TCCTGCTGCC
951 GGAAACTAC GCCGCGCTCC GGTTCATCGT CGTATCGTGT ATGCTGCCTC
1001 CGCTGTTTTG CACGCTGGTA GAAATCAGCG GCATCGGTTT GAACGTCGTC
1051 CGAAACACAC GCCCGATCGC GCTCGCCACC TTGGGCGCGC TGGCGGCAAA
1101 CCTGCTGCTG CTGGGGCTTG CCGTACCGTC CGCGGCGCGG CGCGGCGCGG
1151 CGGTTGCTCG TGCCGCTCA TTTTGGCTGT TTTTGTGTTT CAAGACCGAA
1201 AGCTCTGCC GCCTGTGGCA GCCGCTCAA CGCCTGCCG TTTATATGCA
1251 CACATGTGTC TGCTGGCCT CCTCGGCGGC CTACACCTGC TTCGGCACTC
1301 CGGCAAACTA CCCCTGTTT GCCGGCGTAT GGGCGGTATA TCTGGCAGGC
1351 TGCATCCTGC GCCACCGGAA AGATTGACAC AAATGTTTC ATTATTTGAA
1401 AAAACAAGGT TTCCATTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2418; ORF 717.a>:

```

a717.pep
1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDQA YVREYYAAAD KDTLEKTLFL PLLSAAAI AALLSRPSLP
101 SEILFSLDDA AAGIGLVLE LSELPPIRLL LVLMEGRAL AFSSAQLVSK
151 LAILLPLLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 RAPSSAVLH RGLRYGIPIA LSSIAYWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFSIFSTVW TPYIFRAIEA NAPPARLSAT AESAAALLS
301 ALCLTGIFSP LASLLPENY AAVRFIVVSC MLPPLEFCTLV EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFVEKTE
401 SSCRLWQPLK RFLYMHMTLF CLASSAAYTC FGTPANYPLF AGVWAVYLAG
451 CILRHRKDLH KLFHYLKKQG FPL*

```

a717/m717 97.9% identity in 473 aa overlap

	10	20	30	40	50	60
a717.pep	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
m717	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a717.pep	YVREYYAAADKDTLEKTLFLPPLLSAAAI AALLSRPSLPSEILFSLDDAAAGIGLVLE					
m717	YVREYYATADKDTLEKTLFLPPLLSAAAI AALLSRPSLPSEILFSLDDAAAGIGLVLE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a717.pep	LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA					
m717	LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA					
	130	140	150	160	170	180
	190	200	210	220	230	240
a717.pep	NLAAAFLLFQNRCLKAVRRAPSSAVLHRLRYGIPIALSSIAYWGLASADRLFLKKY					
m717	NLAAAFLLFQNRCLKAVRHAPSPAVLHRLRYGIPIALSSIAYWGLASADRLFLKKY					
	190	200	210	220	230	240
	250	260	270	280	290	300
a717.pep	AGLEQLGVYSMGISFGGAALLFSIFSTVWTPYIFRAIEANAPPARLSATAESAAALLS					

1159

```

|||||
m717      AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
           250      260      270      280      290      300

           310      320      330      340      350      360
a717.pep  ALCLTGIFSPLASLLLPENYA AVR FIVVSCMLPPLFCTLVEISGIGLVVRKTRPIALAT
|||||
m717      ALCLTGIFSPLASLLLPENYA AVR FIVVSCMLPPLFCTLAEISGIGLVVRKTRPIALAT
           310      320      330      340      350      360

           370      380      390      400      410      420
a717.pep  LGALAAANLLLLGLAVPSGGARGA AVACAASFWLFFVFKTESSCRLWQPLKRLPLYMHTLF
|||||
m717      LGALAAANLLLLGLAVPSGGARGA AVACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF
           370      380      390      400      410      420

           430      440      450      460      470
a717.pep  CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHKLFHYLKKQGFPLX
||:|||||
m717      CLTSSAAYTCFGTPANYPLFAGVWAAVYLAGCILRHRKDLHKLFHYLKKQGFPLX
           430      440      450      460      470

```

g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1   TCAGACGGCC TTTACGTACC CCGAACTTT ATCCACCGCC CGCAAAGCTG
51  GTTCAATGG  GACAAAGACA ACGGGCTGCT GCTGCGTACC CGCGAAAATC
101 CGGAAGGCGA AGCGTTGTGG CCGCTGGGCT GGGTCGTTCA TACCCAAAAA
151 TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTTCGCA  CGCTTTCCTG
201 GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTTGCC GAGTTTTTGG
251 AGCTGTACGG CATGCCCATC CGTATCGGCA AATACGGCGC GGGCGCAACC
301 AAAGAGGAAA AAAACACCCT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351 CGCGCCAGGC ATCATGCCAG AAGGTATGGA AATAGAGTC CACAACGCGG
401 CAAACGGTAC GACGGCAACC AGCAATCCGT TTTTGAGAT GGCCGACTGG
451 TCGCAAAAT  CGGCGGCGCG GCTGATTTG GGGCAAACGC TGACCAGCGG
501 TGCGGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551 TACGCCGCGA TTTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601 ACAAGCCAAA TCATCGGACC GTTCCTGCAA ATCAACTATC CCCATGCCGA
651 CCCAAACCGC GTGCCGAAAT TTGAATTGA CACGCGCGAG CCGAAGACA
701 TCGCGGTCTT TGCCGACGCT ATCCCAGAAC TGGTGGATGT CGGCGTACAA
751 ATCCCCGAAA GCTGGGTGCG CGACAACTG GTCATTCCAG ATGTGCAGGA
801 GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAAACAGAA
851 CTGCATTGGC GGCTTTATCC GCCCACACCG TACCATCTAA GGCTACGGGC
901 AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGGTTGAGCC
951 CGATTTCAAT TCTCAGCTCA ACCCGATGGT GCGTCAGGCG GTTGCCGCAC
1001 TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051 TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101 GTTTATCAGC GATATTTTGG GACAAGACCA TGCCCGCGCC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>:

```

m718.pep
1   SDGLYVRNF IHRPQSWFKW DKDNGLLRT RENPEGEALW PLGWVVHTQK
51  SRSVQQARNF LFRTLSWLYM FKHYAVHDFE EFLELYGMPI RIGKYGAGAT
101 KEEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTTAT SNPFLQMAW
151 CEKSAARLIL GOTLTSGADG KSSTNALGNI HNEVRDDLIV SDAKQVAQTI
201 TSQIIGPFLO INYPHADPNR VPKFEFDTRE PKDIAVFADA IPKLVGVQVQ
251 IPESWVRDKL VIPDVQEGEA VLVQRVPDNP VNRTALAALS AHTVPSKATG
301 RHQEILDGAL DDALVEPDFN SQLNPMVROA VAALNACNSY EEADAALNAL
351 YPNLDNAKLR TYMQQALFIS DILGQDHARA *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:

1160

## a718.seq

```
1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGGCTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCTGGC TGATATATGT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GGCGGAAATC GGTACAACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAT TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGGCG AAACCATCAC AAGCCAAATC
1051 ATCCGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A
```

This corresponds to the amino acid sequence <SEQ ID 2422; ORF 718.a>:

## a718.pep

```
1 MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51 LFEDAESGDI RAQHLEFADI EERDS DIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEEKLSQ QAYEMMDSLP TLEDLIMDLN DAVGHGFSAL EVEWVFSDDL
151 YLPNFIHRP QSWFKWDKDN GLLRLTREN EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRLAVAEI GHNAAGIMPE GMEIELHNA NGMTSAGNPF LQMAWCEKS
301 AARLILQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGFPLQINYP HADPNRPVKF EFDTRPKDI AVFADAI PKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNR ALAALSHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*
```

a718/m718 98.4% identity in 380 aa overlap

a718.pep	120	130	140	150	160	170
	DSLPTLEDLIMDLMDAVGHGFS	ALEVWVFS	SDGLYLPRNFIHRPQSWFKWDKDN	GLLLRT		
m718				SDGLYLPRNFIHRPQSWFKWDKDN	GLLLRT	
				10	20	30
a718.pep	180	190	200	210	220	230
	RENPEGEALWPLGWVVHTQKRSRV	QQARNGLFRTLSWLYMFKHYAVHDFAEFLE	LYGMPI			
m718						
	RENPEGEALWPLGWVVHTQKRSRV	QQARNGLFRTLSWLYMFKHYAVHDFAEFLE	LYGMPI			
	40	50	60	70	80	90
a718.pep	240	250	260	270	280	290
	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPF	LQMAW				
m718						
	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQMAW					

1161

	100	110	120	130	140	150
a718.pep	300	310	320	330	340	350
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGFFLQ					
m718	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGFFLQ					
	160	170	180	190	200	210
a718.pep	360	370	380	390	400	410
	INYPHADPNRPVKFEFDTREPKDIAVFADAIPKLVVDVGVQIPESWVRDKLVIPDVQEGEA					
m718	INYPHADPNRPVKFEFDTREPKDIAVFADAIPKLVVDVGVQIPESWVRDKLVIPDVQEGEA					
	220	230	240	250	260	270
a718.pep	420	430	440	450	460	470
	VLVRQVPDNFVNRTALAALSAHTVPKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
m718	VLVRQVPDNFVNRTALAALSAHTVPKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
	280	290	300	310	320	330
a718.pep	480	490	500	510	520	
	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	340	350	360	370	380	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

```

1  ATGGAGCCGA TAATGGCAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACGGCG ACCGGTCGGG
101 TTATCGCCGA GCATCCGTCC AATTTTATTA CGCCGCAAAA GATCGGGGCC
151 CTCTTCGAGG ACGCAGAAAG CGGCACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAT ATGGGGACGC
251 GCAACGCGCG GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCTTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCC CAAAGCTGGT TCAAATGGGA
501 CAAAGACACG GGGCTGCTGC TGGTACCCG CGAAATCCG GAAGCGGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAAATC GCGCAGCGTC
601 CAGCAGCGCG GCAACGGGCT TTTCCGACG CTTTCTTGGC TGATATGTT
651 CAAACACTAC GCGCTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCCTG TTCGAGCGGT GCGGGAATC GGTCAACAG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAG TAGAGCTCCA CAACGCGGCA AACGGTACGA
851 CGGCAACCAG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGCGCGCGG TGATTTTGGG GCAAACGCTG ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACG AACGCGCTGG GCAATATCCA CAACGAGGTA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCCG CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACCT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep.

```

1  MEPIMAKKN KTKIQPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFADI EERDS DIAAN MGRKRALLT LNRVAPPNN
101 ATPEEEEKLS QAYEMMSLPL TLEDLIMDL DAVGHGFSAL EVIEWFSDGL
151 YLPRNFIHRP QSWFKWDKDN GLLLRTRNP EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRICK YGAGATKEEK
251 NTLRLRAVAEI GHNAAGIMPE GMEIELHNA NGTTATSNPF LQMDWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEV RRDLLVSDAK QVAQTITSQI

```

351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES  
401 WVRDKLVI PD VQEGEAVLVR QVPDNPNVRT ALAALSHTV PSKATGRHQE  
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAAL NACNSYEEAD AALNALYPNL  
501 DNAKLRTYMQ QALFISDILG QDHARA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2425>:

a718.seq  
1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC  
51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG  
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC  
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT  
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC  
251 GCAACGCGCG GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCCGGAAAT  
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA  
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG  
401 GGCACGGATT TTCTGCGTTG GAGGTGAGT GGGTATTTTC AGACGCGCTT  
451 TACCTACCCC GAAACTTTAT CCACCGCCCC CAAAGCTGGT TCAATGGGGA  
501 CAAAGACAAC GGGCTGCTGC TGCCTACCCG CGAAATCCG GAAGGCGAAG  
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAATATC GCGCAGCGTC  
601 CAGCAGGCGC GCAACGGGCT TTTCGCGCAG CTTTCCTGGC TGTATATGTT  
651 CAAACACTAC GCCGTCCACG ATTTTGGCGA GTTTTGGAG CTGTACGGCA  
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA  
751 AACACCTGCT TTCGAGCGGT GCGGGAATC GGTCACAACG CGGCAGGCAT  
801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGCGATGA  
851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG  
901 GCGGCGCGCG TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA  
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT  
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC  
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT  
1101 CGCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG  
1151 CGGACGCTAT CCGGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC  
1201 TGGGTGCGCG ACAAACTGGT CATTCAGAT GTGCAGGAGG GTGAGGCTGT  
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG  
1301 CTTTATCCCG CCACACCGTA CCATCTAAGG CTACGGGCGA GCATCAGGAA  
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTAGGCCG ATTTCATTC  
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA  
1451 ACAGTACGGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTG  
1501 GACACGCGCA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA  
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

This corresponds to the amino acid sequence <SEQ ID 2426; ORF 718-1.a>:

a718.pep  
1 MEPIMAKKNN RTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA  
51 LFEDAESGDI RAQHELFADI EERDSIAAN MGRKRALLT LNWRVAPPRN  
101 ATPEEKLSLSD QAYEMMDSLP TLEDLIMDLN DAVGHGFSAL EWEVWFSDDL  
151 YLPRNFIHRP QSWFKWDKDN GLLLRTRNRP EGEALWPLGW VVHTQKRSRV  
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK  
251 NTLRLAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQMDWCEKS  
301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK OVAQTITSQI  
351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES  
401 WVRDKLVI PD VQEGEAVLVR QVPDNPNVRT ALAALSHTV PSKATGRHQE  
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAAL NACNSYEEAD AALNALYPNL  
501 DNAKLRTYMQ QALFISDILG QDHARA\*

a718/m718-1 99.0% identity in 526 aa overlap

a718.pep	10	20	30	40	50	60
m718-1	10	20	30	40	50	60
a718.pep	70	80	90	100	110	120
m718-1	70	80	90	100	110	120
a718.pep	130	140	150	160	170	180
m718-1	130	140	150	160	170	180

1163

	190	200	210	220	230	240
a718.pep	EGEALWPLGWVHTQKSRSVQQARNGLFRTLWLYMFKHYAVHDFAEFLELYGMPPIRIGK					
m718-1	EGEALWPLGWVHTQKSRSVQQARNGLFRTLWLYMFKHYAVHDFAEFLELYGMPPIRIGK					
	190	200	210	220	230	240
	250	260	270	280	290	300
a718.pep	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLQMDWCEKS					
m718-1	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTATSNPFLQMDWCEKS					
	250	260	270	280	290	300
	310	320	330	340	350	360
a718.pep	AARLILGQTLTSGADGKSSTNALGNIHNEIRDLLVSDAKQVAQTITSQIIGPFLQINYP					
m718-1	AARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGPFLQINYP					
	310	320	330	340	350	360
	370	380	390	400	410	420
a718.pep	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDPVGVQIPESWVRDKLVIPDVQEGEAVLVR					
m718-1	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDPVGVQIPESWVRDKLVIPDVQEGEAVLVR					
	370	380	390	400	410	420
	430	440	450	460	470	480
a718.pep	QVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAAAL					
m718-1	QVPDNPVNRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAAAL					
	430	440	450	460	470	480
	490	500	510	520		
a718.pep	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718-1	NACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	490	500	510	520		

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

1	ATGGCAAACG	GGAACATGAA	ACTGTCGTTG	GTGTTAACCG	CCCGAGATGA
51	CGGAGCGAGA	CGGCTACTGG	CTGATACTCA	ACGACAATTA	GATCGTACCG
101	CGAAATCGCG	GGCGCAACTT	GAACGGCAAA	GCCATACTTA	TGCGTTGACC
151	GGCATCCGCT	CAGAAAAACA	GATTCAACGC	GAAATCATGC	TGACACAGGC
201	TGCGTTTAAC	CGTTTGCGGC	GCAGCGGCAA	GGCATCACAA	AATGATTGG
251	CACGGGCGGC	GGTCGCTACG	CGTAACCGAA	TTCGCGAGCT	GAACGCGGAA
301	CTGAAACAGG	GCACGGGATT	TGCGGACAAG	ATGGGAAAAA	TCGGAAGATT
351	CGGTGCAGCT	GCGGTGGCTG	GTGGCGCGGC	AGCGTATACG	GTGCTTAAGC
401	CTGCTATGGA	CAACAGAAAG	CAGCTTGATG	AGAACATCAA	CCGCGTGTCC
451	AGACAGGCAT	TTATTGAGGA	TAACAGTAAA	TCGGCAGCGT	GGATTGCAAC
501	TGAAGGTGCG	CAACAGATCA	AGGATTGGC	ACTTGAACCT	GTCGAGAAAA
551	ATGGCGGGAC	CCACGATAAG	GCTTTGGATT	TAATCAGCGG	CATGATGACC
601	ACCGGTCTGA	ATTTTGCCCA	AACCAAGAAT	GAAGCGCAGG	CGGCATATGC
651	TTTGTCACTT	GCCTCAGAAG	GCAGTGGCGA	GGATACGGCA	AAACTGATTA
701	AAACCTGAA	AGATGGCGGC	ATGAGCGGTA	AAGACCTGCA	ACTCGGGCTT
751	GAGCACGTCT	TGCAATCGGG	TTTAGACGGC	ACTTTCGAGG	TGCGGGATAT
801	GGTTCGGGAG	CTGCCGAGCC	TGCTCTCTGC	CGCGCAACAG	GCAGGGATGA
851	ATGGTGTCTG	CGGTTTGGAC	TACCTGCTCT	CACTCTTACA	ATCTGCGGCG
901	AATAAATCGG	GCAGTCCTGC	CGAAGCGGCG	ACTAATGTGC	AAAATCTTTT
951	GAGTAAAACT	CTGTGCCTTG	ACACGATAGG	TCGTCTGAAG	AAGATGGCAA
1001	ATCCGAATGA	CCCGAAGAAA	GGTGTGCGATT	GGATAGGCTC	GGTTGTGCAA
1051	GGCAAGCAAA	ACGGCGAAAA	CGCAGTGCAG	GTGTTGTCCC	GTCTTGCCGA
1101	TGCCATGCTA	GTAAGGATA	AGCAATACCA	AGATTATAAG	AAACGCGCGG
1151	CTGCAGGCGA	TAAGACGGCG	GCGGAGCAGG	CAAAATATGCT	TAAGGGCGCG
1201	CTTTTGGCGC	AACTGCTGCC	TGATTTCAG	GCAAACAAG	GTTTGCTGGC
1251	TGCAACGGAT	ATGACGCAAA	TCCGTGAATA	TATGGCTTCG	TTGGCTGGCG

```

1301 TAACGTTGGA TAACGAAAA ATTGCTAAGA ACAACGAGGC GCGAATGTTG
1351 TCGGCAGCGG CGCAACAAGA GCAACAGGAA TCGCTGGCAA TGTTCGGGGA
1401 AAGTCTGACG GGAACATTGG TGGATATGGA AACCTCGTTT AAAAAGCTGG
1451 CAGCGGAATA CCCTAATGCC ACTCTAGCCC TGCAAGCATT GACGACGGCG
1501 GCAACAGCGG CGTCTGCCGC AATGTTATTA ACCGCCGGTG GCGGTAAAGG
1551 TGCAGGCTTT CTGAAAGATG TAGGTAGTAA AGCGTTGGGA TGGGGTAAGG
1601 CTTCCGCAGG CGGCGTGGCA GCAGGTGCCA CAGCGGCAGG CGGTAAGTTG
1651 CTGTCAATGG GAAATCTGC CGGTAGCGGG CTGATGAATA ATCCAGCGTT
1701 AGTTAAACGG GCGGGTTTGT TAGGTATGTT GCTGTATTCC GAGTCTTTGG
1751 GTGACGGCAC ATTGCCAAG GGTTCGCGT GTACCAAGAC AACTCCTGAA
1801 ATGATTAATC GTCTGAAAA CAACGGTATC CGATTGTAAC CTGCGCCGAA
1851 GCGGGAACAG GCGCGGGGTG GTGTCCCTCA GTATTTGGCT GCTCCGTCAG
1901 CGCAGCCTAC CGATAAGATG TTGTCTCCGT TGTTCCTAAC TCAGACGGCG
1951 GCGTATCAGG CAGCCATTCA GCAGCAGACG GCGCGGTATC AGGCAGCATT
2001 GCGCGAGGAT ACGGCTGCAG TTACAACAGG TTTGGCACAA GTGCAAAGTG
2051 CGATGGCGTC GGCAAGTCAG ACCATCAATA CCAATGTGAG CCTGAATATC
2101 GACGGACGTG TTATCGCGAA TGAGGTATCG CGGTATCAAG TGGCCATGTT
2151 CCGCGTGGGA GCGGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2428; ORF 719>:

```

m719.pep
1  MANGNMKLSL VLTARDDGAR RLLADTQRQL DRTAKSRAQL EROSHTYALT
51  GIRSEKQIQE EIMLTQAAFN RLARSGKASQ NDLARAAVAT RNRIRELNAE
101 LKQGTGFADK MGKIGRFGAA AVAGGAAAYT VLKPMADNRK QLDENINRVS
151 RQAFIEDNSK SAAWIATEGA QQIKDLALEL VEKNGGTHDK ALDLISGMMT
201 TGLNFAQTKN EAQAAAFAL ASEGSGEDTA KLIKTLKDGG MSGKDLQLGL
251 EHVLSGLDGL TFEVRDMVRE LPSLLSAAQO AGMNGVGGLD YLLSLLQSAA
301 NKSQSPAEAA TNVQNLLSKT LSPDTIGRLK KMANPNDPKK GVDWIGSVVQ
351 GKQNGENAVQ VLSRLADAML VKDKQYQDYK KRAAAGDKTA AEQANMLKGA
401 LLAQLLPDLQ AKQGLLAATD MTQIREYMAS LAGVTLNDGK IAKNNEARML
451 SAAQQEQEQE SLAMLRESLT GTLVDMETSF KKLAAEYPNA TLALQALTTA
501 ATAASAAMLL TAGGGKGAGF LKDVGSKALG WKGASAGGVA AGATAAGGKL
551 LSWGKSAGSG LMNPNALVKR AGLLGMLLYS ESLGDGTLPK GLRGTKTTPE
601 MINRLKNNGI RFEPAPKREQ ARGGVPOYLA APSAQPTDKM LSPLESTQTA
651 AYQAAIQQQT AAYQAALAQD TAAVTTGLAQ VQSAMASASQ TINTNVSLNI
701 DGRVIANEVS RYQVAMFGRG AGQ*

```

a719.seq not found yet

a719.pep not found yet

g720.seq not found yet

g720.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2429>:

```

m720.seq
1  ATGAGCGGAT GGCATACCTT ATTGCAGGAC GCATCTTACA AGGGCGTCCG
51  CTTTGATATT GAGGTGGTGG ACGAGAGCAA CGGCAAGGCA TTGGCCGAGC
101 ATGCGCGGCC GTTTGTGCAG GGTATCGACC TTGAAGACAT GGCATGACG
151 GGGCGGCAGG TGCAGATTAA TGCGGTGTTT TGGGGCAAGG GCTATGCAGG
201 CCGTCTGAAA AAGCTGCTGG ATGCGCTGGA GCAGCCGGGC GCGGCGTGC
251 TGGTGCACCC TGTTTGGGGG CGGATGCACA ACATGATTGC GGCATCATGG
301 AGTTACCGAC ATGAGGCCGA TTATGTGGAT TATGCGGGCA TCGATATTAC
351 TTTCCGCGAG GCGGCCGAAG CGCAGGAAAT CTTTGTTTT GAAAACGCCT
401 TTTTGGTCEA GCTTGAGGCG TTGATTGCTA ATATCGACAC CTACCGCGAG
451 GCGGCTATCG GCTTGTTGA TGCGGTGTTG GCGGTGGATG CCGGCGTATC
501 AGCTTTATGG GGCAGCGCGC TGGGCATTG GAGTGCAGCA TCGGGTACGT
551 TTGGCGCGGT GCGCGGTTT TTTGATTGGA ACAAATTGC CTTTCCCGAT
601 CCGGGCGGAT ACAGTGCAGC GCGGTTTAAA AACGGCTCGG CCAAGCTGTT
651 TGCGGATATA TCGGTCATGG TAGATACTGG CATACCGCGT GAGGCGGGTT
701 TGGCCGATAA TGCCATGCAC CATGCCGTT GGTCCGCGCG ACAGCGGTTT
751 GACGGGGCTG CGGCTGTTGC CGACCGCGCC GCCGCTATCC CTGATAATTT
801 GCTGACCGGC CGCTTTTCA GCGGCCTGCA AAACCGCCTG AACCGGTTAA

```



1165

```

851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CCGTGCGCCT GTTATCCACG
901 TCATCGCTGT TGTCGGTGGC AACGGCATTG ATCGAGGCGC ATGGCGAAGA
951 GATGACCGCG CCCGATTGTA TTGAGGTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TGCAGACGGC TGCTGCCGAG
1051 TCTGGTGGGC TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGCGGCGG CAGGCCGTCT GAATGCGTTG GTTGCGGCGG
1151 TCATCAACCA AAAGCCGCGG CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCA CGAGTTTAC GGCGATATAG CCCGCGCAGC
1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCGCGG TTTATCAAGC
1301 GCGGCACTTT GGTCAACAGC TATGCAAAAT AA

```

-- This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

```

m720.pep
1 MSGWHTLLQD ASYKGVGFDI EVVDESNGKA LAEHARPFVQ GIDLEDMGMT
51 GRQVQINAVF WGKGYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
101 SYRHEADYVD YAGIDITFRE AEAQEIVFV ENAFLEVELEA LIANIDTYRE
151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FDLDKIAFPD
201 RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPQRQF
251 DGAAAVADRA AAIPDNLLTG RFSDDLQNRL NRLTAKQVQF VAQAVRLLST
301 SLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAAAE
351 SGGLTANAVY TEAYQTAESL RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
401 TIHQIAHEFY GDIARAAELV RLNPHIHHPA FIKRGTLVNS YAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

```

a720.seq (partial)
1 GGCCTGCAAA ACCGCCTGAA CCGGTTAACC GCCAAACAGG TGACGCCGGT
51 AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
101 CGGCATTAAT CGAGGCGCAT GGCGAAGAGA TGACCGCGCC CGATTTGATT
151 GAGGTTAACC GCGCCATGCG CCGCCGTATG CAGGCCGAGA TTGCCGCCTT
201 ACGGGCGGTG CAGACGGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
251 CCGTGATATC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGGCGGCA
301 GGCCGTCTGA ATGCGTTGGT TGCGGCGGTC ATCAACCAAA AGCCGCCGCT
351 GATTGTGCGC CAAGCCCAA TCGACGGTAC GATACACCAA ATCGCCACG
401 AGTTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGGC GCTCAATCCC
451 CATATCCACC ACCCGCGGTT TATCAAGCGC GGCACCTTGG TCAACAGCTA
501 TGCAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

```

a720.pep (partial)
1 GLQNRLNRLT AKQVQFVAQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
51 EVNRRMRM QAEIAALRAV QTAASGGL TANAVYTEAY QTAESLRAAA
101 GRNLALVA V INQKPLIVR QAPIDGTI HQ IAHEFYGDIA RAAELVRLNP
151 HHHHPAFIKR GTLVNSYAK*

```

m720 / a720 100.0% identity in 169 aa overlap

```

          250      260      270      280      290      300
m720.pep  SPRQRFDGAAAVADRAAAIPDNLLTGRFSDGLQNRLNRLTAKQVQFVAQAVRLLSTSSLL
          |||||||||||||||||||||||||||||||||||||||
a720      GLQNRLNRLTAKQVQFVAQAVRLLSTSSLL
          10      20      30

          310      320      330      340      350      360
m720.pep  SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
          |||||||||||||||||||||||||||||||||||||||
a720      SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
          40      50      60      70      80      90

          370      380      390      400      410      420
m720.pep  QTAESLRAAAGRLNALVAAVINQKPLIVRQAPIDGTI HQIAHEFYGDIA RAAELVRLNP
          |||||||||||||||||||||||||||||||||||||||
a720      QTAESLRAAAGRLNALVAAVINQKPLIVRQAPIDGTI HQIAHEFYGDIA RAAELVRLNP
          100     110     120     130     140     150

          430      440
m720.pep  HHHHPAFIKRGTLVNSYAKX

```

1166

|||||  
a720      HIHHPAFIKRGTLVNSYAKX  
             160      170

g721.seq not found

g721.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2433>:

m721.seq  
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT...  
51 GCAGCCAAAA GACGGGCGAA TCCAACTGCT GCCATATGGC GAATTCGCG  
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA  
151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT  
201 TGTCGATTAT GAACACCAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG  
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG  
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA  
351 AGAGTATCGC TACATCTCTG CTGTGTTTC CTATGACACA AAGGGATATG  
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCGC GTTGGACGGT  
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC  
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GACCTGCCTG  
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGGAAAGCC  
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTGCGCG AGCTGGCGGA  
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT  
701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC  
751 GCCCGCGCTG CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC  
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAA  
851 AAGGCGTATT GAAACAGCCG GCGGCTTGG CATTTTTGAC CGGCTTTATT  
901 GAAACGCCCC AGCCGGTCCG TGCACCTGCA GGCTCGCAAA CGGGCGGCAA  
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TCGGGAAGAG GCAGCCGCAG  
1001 CAAAATGCT GGCATGTCC GCGAAGAAT TTGTAAAAAT CAAAGAAAGC  
1051 GAAGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2434; ORF 721>:

m721.pep  
1 MSKNAQKTL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAYWLTTEE  
51 NGHDVALLAN SSRNQLVVYD EHQTLYKEKN GQAPAPAGWM RWLEFTPKGM  
101 FAEVEWTDKA AAALAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG  
151 MDEVLAASA QILKPETEON PMKELLQOLF DLPDAGEEEL KAALSALVEA  
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTXYAPI SVVQELQSKV  
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAKGVLKQP GGLAFLTGFI  
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES  
351 EGK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2435>:

a721.seq  
1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT  
51 GCAGCCAAAA GACGGGCGAA TCCAACTGCT GCCATATGGC GAATTCGCG  
101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA  
151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT  
201 TGTCGATTAT GAACACTAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG  
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG  
301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA  
351 AGAGTATCGC TACATCTCTG CTGTGTTTC CTATGACACA AAGGGATATG  
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCGC GTTGGACGGT  
451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC  
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GGTCTGCCTG  
551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGGAAAGCC  
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTGCGCG AGCTGGCGGA  
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT  
701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC  
751 GCCCGCGCTG CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC  
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCA  
851 AAGGCGTATT GAAACAGCCG GCGGCTTGG CATTTTTGAC CGGCTTTATT  
901 GAAACGCCCC AGCCGGTCCG TGCACCTGCA GGCTCGCAAA CGGGCGGTAA  
951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TCGGGAAGAG GCAGCCGCAG  
1001 CAAAATGCT GGCATGTCC GCGAAGAAT TTGTAAAAAT CAAAGAAAGC

1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence &lt;SEQ ID 2436; ORF 721.a&gt;:

```

a721.pep
1  MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRVAVDGRPT DVPAYWLTEE
51  NGHDVALLAN SSRNQLVVDY EH*TLYKEKN GQPAPAAGWM RWLEFTPKGM
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON PMKELLQQLF GLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLT KYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

```

a721/m721 99.2% identity in 353 aa overlap

a721.pep	10	20	30	40	50	60
	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRVAVDGRPTDVPAYWLTEENGHDVALLAN					
m721	10	20	30	40	50	60
	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRVAVDGRPTDVPAYWLTEENGHDVALLAN					
a721.pep	70	80	90	100	110	120
	SSRNQLVVDYEHXTLYKEKNQPPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
m721	70	80	90	100	110	120
	SSRNQLVVDYEHQTLYKEKNQPPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
a721.pep	130	140	150	160	170	180
	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQQLF					
m721	130	140	150	160	170	180
	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQQLF					
a721.pep	190	200	210	220	230	240
	GLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
m721	190	200	210	220	230	240
	DLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
a721.pep	250	260	270	280	290	300
	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLVKQPGGLAFLTGFI					
m721	250	260	270	280	290	300
	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLVKQPGGLAFLTGFI					
a721.pep	310	320	330	340	350	
	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAKMLGMSGEEFVKIKESEGGKX					
m721	310	320	330	340	350	
	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAKMLGMSGEEFVKIKESEGGKX					

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

```

m722.seq
1  GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51  TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCTT GATACCGCGC ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGC GCGGCTT GAGCCGCCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTCA
301 GACGACCTGC AAGTGCCTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG

```

1168

```

401 AGCCGGGCGC GCGCGCCAAT GTGGGCGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCCGCCG GTGTGGCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCGGACCGCC CGCAGGCGGC AACCCTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGGTG TCGTCGGAAG
701 AAAGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GTATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTCGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCTGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCGCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2438; ORF 722>:

m722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLSRR NPPTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VGDGEAQLMA
151 APAGVATECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV SSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDRR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2439>:

a722.seq

```

1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCAT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGCGCGGCTT GCGCCGCCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGGCCTGC AAGTGCCTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG
401 AGCCGGGCGC GCGCGCCAAT GTGCGGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCGCGCG GTGTGTCCAC CGAATGCCGC CTTACCGTAC AAGCGCGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCGGACCGCC CGCAGGCGGC AACCCTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGGTG CCATCGGAAG
701 AAAGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GCATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTCGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GCGGGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCTCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2440; ORF 722.a>:

a722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLRRR NPPTASGTLT VSGIAQSMLS
101 DGLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VRDGEAQLMA
151 APAGVSTECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV PSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDLR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

g723.seq not found yet

g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

```
m723.seq
1  ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
51  AGTGATCACG CCGAACACCC TTATTTTAC  CGTTTACAAA CACAATACCG
101 TCTTCGCCCG CGGCCACTTC TTCGCCGCTA TCATCCACGC CCAGCTGCAC
151 TTCGCCTTGG GCCATAGCAC GCAGCAGGTC GAGCAGCTCG ATTTTGTAGC
201 GGTTCGGGAT TTCGTCGGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251 TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301 AAAAGGTCGT CTGAACCGCC CCAGATACGC GTCGATTTCG GCAGTGGCGT
351 CCACCAGCGC GGTTCGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
401 CCGTCGGTGA GCTGCAAGAC TTCCAGCTCA CCGAACGCGC CAACCATATC
451 CTCAACCGTC GCGTATGCCA TTAATCGACC GCCTTGCCTT GCAGCATAGG
501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551 CTTCGCGCCA GCCGCCGTCA AACAGCAGGC CGCCGCGCCA AAATTCTTTG
601 CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
651 GTCGGCGGCA CGTTGCGTAT GCTGCACTTT GAGTTCGGCA AGTTCGGCGG
701 ACAGTGCCTT TTTGTCGTCT TCGGCTTTT CCAAGGCTGT GGTTCAGCAT
751 TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
801 GGCTTTGATG TCTTCAAACG ACGGGCGGCG GGTTCGCGCG GTTTCTGGTT
851 TGTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901 CGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 2442; ORF 723>:

```
m723.pep
1  MRPKPRFRRS VIACISIVIT PEHLIFTVYK HNTVFARGHF FAAIHAQLH
51  FAFGHSTQOV EHVDFVAVAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFSGVHQH GLCDLAVNQP LVVAVGELQD FQLTETRNHI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARFTSRQPPS NSRPPRQNSL
201 PSAPVLTSIT SRLSAKASAA RVCCTLSSA SSADS AFLSS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGA AVSA VSGLLLVFAM MTPCFRRRI
301 RI*
```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pep not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

```
m724.map
ATGAGTTTGAGTAAATTGGCGAAAAAACGGCACAACTGCTAAAAATATCGGCGAAACC
1  -----+-----+-----+-----+-----+-----+-----+-----+ 60
a  TACTCAAACCTCATTTAACCGCTTTTGTGCGGTGTTGACGATTTTATAGCCGCTTTGG
   M S L S K L A K K T A Q T A K N I G E T -
CTGCGCGCGGCCTTTTCGGGAAAAATCACGCTGGTGGTGTCTCGGAGCCGATACAGCGC
61  -----+-----+-----+-----+-----+-----+-----+-----+ 120
a  GACGCGCGCCGGAAGCCCTTTTGTAGTGCAGCACACAGCAGGCTCGGCTATGTCGCG
   L R A A F R G K I T L V V S S E P I Q R -
GTGCAAGTTGAGCGGCTTGCGCGACGAAACCTGCAAGACCTGAACATTGTCAGGAATAC
121  -----+-----+-----+-----+-----+-----+-----+-----+ 180
a  CACGTCAACTCGCCGAACCGGCTGCTTTGGGACGTTCTGGAACCTGTAAACGTCCTTATG
   V Q L S G L A D E T L Q D L E H L Q E Y -
GGCTTTGCCAGCCATCCGCCGACGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
181  -----+-----+-----+-----+-----+-----+-----+-----+ 240
a  CCGAAACGGTCGGTAGGCGGGCTGCCGTCGCTTCGCCATCACTATGGCGACCCGCGTTA
   G F A S H P P D G S E A V V I P L G G N -
```

```

      ACTTCGCACGGTGTGATTGTGTGCAGCCAGCACGGCAGCTACCGCATCAAAAACCTTAAG
241  -----+-----+-----+-----+-----+ 300
      TGAAGCGTGCCACTAACACACGTCGGTCGTGCCGTCGATGGCGTAGTTTTGGGAATTC
a    T S H G V I V C S Q H G S Y R I K N L K -

      CCCGGCGAGACGGCGATTTTAAATCATGAGGGTGCAAAAATCGTGATTAAGCAAGGCAAA
301  -----+-----+-----+-----+-----+ 360
      GGGCCGCTCTGCCGCTAAAAATTAGTACTCCACGTTTTTAGCACTAATTCGTTCCGTTT
a    P G E T A I F N H E G A K I V I K Q G K -

      ATCATTGAGGCCGATTGCGACGTGTACCGGGTAACTGCAACAATACGAGGTTAATGCG
361  -----+-----+-----+-----+-----+ 420
      TAGTAACCTCCGGCTAACGCTGCACATGGCCCAATTGACGTTTGTATGCTCCAATTACGC
a    I I E A D C D V Y R V N C K Q Y E V N A -

      GCCACGGATGCCAAATTTAACGCTCCGTTGGTGGAGACCAGTGCAGTGTGACGGCGCAA
421  -----+-----+-----+-----+-----+ 480
      CGGTGCTACGTTTTAAATTGCGAGGCAACCACCTCTGGTCACGTCACAACGCGCGTT
a    A T D A K F N A P L V E T S A V L T A Q -

      GGCCAAATCAACGGCAACGGCGGCATGGCCGTCGAGGGCGGCGACGGAGCCACCTTTAGC
481  -----+-----+-----+-----+-----+ 540
      CCGGTTTAGTTGCCGTTGCCGCGGTACCGGCAGCTCCCGCGCTGCCCTCGGTGGAAATCG
a    G Q I N G N G G M A V E G G D G A T F S -

      GCGCATGTTAACCAACGGCGGCAGCTTTAACACCGACGGCGACGTTGGTGGCCGGCAAT
541  -----+-----+-----+-----+-----+ 600
      CCGCTACAATTGGTTTGGCCGCGTCGAAATTGTGGCTGCCGCTGCACCACGGCGCGTTA
a    G D V N Q T G G S F N T D G D V V A G N -

      ATATCGTTGCCAGCACCCGCATACCGACAGCATCGGCGGCAAAACCTTACCGGCGGAA
601  -----+-----+-----+-----+-----+ 660
      TATAGCAACGCGGTCGTGGGCGTATGGCTGTCTAGCCGCGTTTTGGAATGGCCGCGCTT
a    I S L R Q H P H T D S I G G K T L P A E -

      CCGGCATAG
661  ----- 669
      GGCCGTATC
a    P A * -

```

Enzymes that do cut: NONE

Enzymes that do not cut: BamHI BglII EcoRI HindIII KpnI NdeI NheI PstI SacI  
SalI SmaI SphI XbaI XhoI

This corresponds to the amino acid sequence <SEQ ID 2444; ORF 724>:

```

m724.pep
1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQKG IIEADCDVYR VNCKQYEVNA ATDAKENAPL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2445>:

```

a724.seq
1  ATGAGTTGA GTAAATTGGC GAAAAAACG GCACAAACTG CTAAAAATAT
51  CGGCGAAACC CTGCGCGCGG CCTTTCGGGG AAAAATCACG CTGGTGGTGT
101 CGTCCGAGCC GATACAGCGC GTGCAGTTGA GCGGCTTGGC CGACGAAACC
151 CTGCAAGACC TTGAACATTT GCAGGAATAC GGCTTTGCCA GCCATCCGCC
201 CGACGCGAGC GAAGCGGTAG TGATACCGCT GGGCGGCAAT ACTTCGCACG
251 GTGTGATTGT GTGCAGCCAG CACGGCAGCT ACCGCATCAA AAACCTTAAG
301 CCCGGCGAGA CGGCGATTTT TAATCATGAG GGTGCAAAA TCGTGATTAA
351 GCAAGGCAAA ATCATTGAGG CCGATTGCGA CGTGATCCGG GTTAACGTGA
401 AACAAATACG GGTAAATGCG GCCACGGATG CCAAATTTAA CGTCCCGTTG
451 GTGGAGACCA GTGCAGTGTT GACGGCGCAA GGCCAAATCA ACGGCAACGG

```

1171

501 CGGCATGGCC GTCGAGGGCG GCGACGGAGC CACCTTTAGC GGCGATGTTA  
 551 ACCAAACGGG CGGCAGCTTT AACACCGACG GCGACGTGGT GGCCGGCAAT  
 601 ATATCGTTGC GCCAGCACCC GCATACCGAC AGCATCGGCG GCAAACCTT  
 651 ACCGGCGGAA CCGGCATAG

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

a724.pep

1 MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET  
 51 LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKLNK  
 101 PGETAIFNHE GAKIVIKQGK IIEADCDVYR VNCKQYEVNA ATDAKFNAFL  
 151 VETSAVLTAQ GOINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN  
 201 ISLRQHPHTD SIGGKTLPAE PA\*

a724/m724 100.0% identity in 222 aa overlap

	10	20	30	40	50	60
a724.pep	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
m724	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a724.pep	GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKLNKPGETAIFNHEGAKIVIKQGK					
m724	GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKLNKPGETAIFNHEGAKIVIKQGK					
	70	80	90	100	110	120
	130	140	150	160	170	180
a724.pep	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGOINGNGGMAVEGGDGATFS					
m724	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGOINGNGGMAVEGGDGATFS					
	130	140	150	160	170	180
	190	200	210	220		
a724.pep	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
m724	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
	190	200	210	220		

g725.seq not found yet

g725.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

m725.seq

1 ATGGTGCGCA CGGTTAAAAG CTACAACGGC GAGGCCGACG ATTTGGCGGG  
 51 GCAAATCCAT ACGCTGCCTG CGGTTTGGGT AACGTATGGC GGCAGCAAAG  
 101 TTGAGCCTGC CAGCACCGGC GCGTATGCG GACGTTATCA GGATACCGCC  
 151 GAATTTGTGG TGATGGTGGC GCGCCGCAAT CTGCGCAACG AGCAGGCGCA  
 201 GCGGCAAGGC GGCATCGACA GCCGCGAAAT CGGCAGCAAC GATTTAATCC  
 251 GCGCTGTTGC CCGCCTGCTT GACGGCCAGC GGCTCGGTTT TGCCGATAGC  
 301 CGCGGCTTGG TGCCCAAAGC GGTGCGCGCG ATTGCCAATC ATGTGCTGGT  
 351 GCAAACGCGC GCAGTAAGCA TATATGCGGT TGAGTATGCC ATCCGCTTTA  
 401 ACACCTGCGG GTTGGAATAT GACCGCTACC CCGAACGCAC CGACAATCCC  
 451 GACGACCCCA ACCATATCTT TACCAAGTAT CAGGGTACAT TGAGCGAGCC  
 501 GTGGCCTGAT TTCGAGGGGT TGGACGGCAA AATTACGAC CCGCAATCCG  
 551 CCGATGAAAT ACCTGTAAAC CTAACCCTTA AGGATAAGCA ATGA

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

m725.pep

1 MVRTVKSNG EADDLAQIHL TPAVWVTYG GSKVEPASTG GVCGRYQDTA  
 51 EFVVMVAARN LRNEQAQRQG GIDSREIGSN DLIRAVRRLL DGQRLGFADS  
 101 RGLVPKAVRA IANHLVQNA AVSIYAVEYA IRENTCGLEN DRYPERTDNP  
 151 DDPNHIFTKY QGTLSEPPD FEGLDGKIYD PQSADEIPVN LTLKDKQ\*

a725.seq not found yet

a725.pep not found yet

g726.seq not found yet

g726.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2449>:

```
m726.seq
1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACAT TGGGCGGCAT
51  CCCCAGAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTAAACCC CGCCGCGCCC GTCCGATTAC CACGAATGGG ACGGCAAAAA
201 ATGGAAATC AGCAAAGCCG CGCCGCGCGC CCGTTTCGCC AAACAAAAAA
251 CCGCCTTGGC ATTCCGCCTC GCGGAAAAGG CGGACGAACT CAAAACAGC
301 CTCTTGGCGG GCTATCCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401 TGGCGCAAAT CGCCGCGCGC AGGGGCGTGG AATTGGACGT TTGATTGAA
451 AAAGTTATCG AAAAATCCGC CCGCCTGGCT GTTGCCGCGG GCGCGATTAT
501 CGGAAAGCGT CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551 CCGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAAATGGAC GCTAAACATC
601 GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2450; ORF 726>:

```
m726.pep
1  MTIYFKNGFY DDTLGGIPEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
51  VLTFFRPSPDY HEWDGKKWKI SKAAAAARFA KQKTALAFRL AEKADELKNS
101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDVLIE
151 KVIEKSARLA VAAGAIIGKR QLEDKLNTI ETAPGLDALE KEIEEWTLNI
201 G*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2451>:

```
a726.seq
1  ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACCT TGGGCGGCAT
51  CCCCAGAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTAAACCC CGCCGCGCCC GTCCGAATAC CACGAATGGG ACGGCAAGAA
201 ATGGGAAATC GGCGAAGCCG CTGCCGCGCG CCGTTTCGCC GAACAAAAAA
251 CCGCCACGGC ATTCCGCCTC GCGGCAAAGG CGGACGAACT CAAAACAGC
301 CTCTTGGCGG GCTATCCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401 TGGCGCAAAT CGCCGCGCGC AGGGGCGTGG AATTGGACGT TTGATTGAA
451 AAAGTTGTCG AAAAATCCGC CCGCCTGGCC GTTGCCGCGG GCGCGATTAT
501 CGGAAAGCGG CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551 CAGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAAATGGAC GCTAAACATC
601 GGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2452; ORF 726.a>:

```
a726.pep
1  MTIYFKNGFY DDTLGSIEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
51  VLTFFRPSEY HEWDGKKWEI GEAAAAARFA EQKTATAFRL AAKADELKNS
101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDVLIE
151 KVVEKSARLA VAAGAIIGKR QLEDKLNTI ETAPGLDALE KEIEEWTLNI
201 G*
```

a726/m726 95.5% identity in 201 aa overlap

```

          10      20      30      40      50      60
a726.pep  MTIYFKNGFYDDTLGSIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTTPRPSEY
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m726      MTIYFKNGFYDDTLGSIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTTPRPSEY
          10      20      30      40      50      60
```



1173

```

              70      80      90      100      110      120
a726.pep      HEWDGKKWEIGAAAAARFAEQKTATAFRLLAAKADELKNSLLAGYPQVEIDSFYRQEKEA
              |||||:::|||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          HEWDGKKWKISKAAAAARFAEQKTALAFRLAEKADELKNSLLAGYPQVEIDSFYRQEKEA
              70      80      90      100      110      120

              130      140      150      160      170      180
a726.pep      LARQADNNAPTPMLAQIAAARGVELDVLEIKVVEKSARLAVAAGAIIGKRQLEDKLNIT
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          LARQADNNAPTPMLAQIAAARGVELDVLEIKVIEKSARLAVAAGAIIGKRQLEDKLNIT
              130      140      150      160      170      180

              190      200
a726.pep      ETAPGLDALEKEIEEWTNIGX
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          ETAPGLDALEKEIEEWTNIGX
              190      200

```

g727.seq not found yet

g727.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2453>:

```

m727.seq
1  ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
51 CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTTGC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAAGT
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
251 TGGCTTTGGC GAAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAGA
301 GACCTTTGCA AAATTCCTTT CCTCCCGAC AGCCGAAACC CAAACACAGG
351 TTTTCGGCTG TTTTCGCCCC AAATACCGCC TAATTTTACC CAAATACCCC
401 CTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2454; ORF 727>:

```

m727.pep
1  MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTER
101 DLCKIPFPFD SRNPNTGFRL FSPQIPPNET QIPP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2455>:

```

a727.seq
1  ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GGCAGCTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA
251 TGGCTTTGGC GAAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
301 AAAAAGGAAA TCGAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2456; ORF 727.a>:

```

a727.pep
1  MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DFGHGLQL YKRALGYGN*

```

a727/m727 83.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
a727.pep      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

g728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCCTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCTGTGT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGTATC CCGGCTCAGT
301 CGTTTGAAGG AAAAGGCGAA ATGCTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTCGGG
401 TTTCCCTTTC GCACGCTCGC CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGCTCCGT TTTCTGAAAT GTGTACGGCG TGACCGGCTCA
501 CGGGGAAAAA TATGAAACGA CAGGGAATA TCGGGTTGTT GGACACCCGG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAAATCCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTTATCAGATG GCCCAGGATT ATTTGGCGAA
651 ATACCCGGAT STCCGCAATG ACGAGCAGAA GGTTTGGGAC TTCCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTTATCAGAT
751 ATGCGGGAAT TGATGCCCCG GGGGATGAAG GCGAACAGTC TTGTGTCGG
801 CTATGATGCG GACGGTCTCG CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAAACG CACGAGTTTC GAATATTATT TGAAAAACCG AAATCTTTTT
901 ATTGCACAAT CTTTCGACGT AGCATTGAAA GCGGATGGCG TAACCGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTTGGAT GGCGGGCGGAG
1001 TTATCCGCGA AGAGAAACAG GGAGACAGAC TGCTGATTT TCCTTTGAAC
1051 TTGGAAGATT TGAAAAAAGA GGTGAGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCGGGCGCG GCCTTCTCA CTGA

```

```

g728.pep
1  MFKKKFKPVLL  SFFALVFAFW  LGTGIAYEIN  PRWFLSDTAT  EVPENPNFAV
51  AKLARLFRNA  DRAVVIVKES  MRTEESLAGA  VDPGPLESEK  DYALALAIRLS
101  RLKEKAKWFH  VTEQHEGEEV  WLDYIYIGEGG  LVAVSLSQRS  PEAFVNAEYL
151  YRNDRPFSVN  VYGGTAHGEN  YETTGYRRV  WQPDGSLQRA  AGRGKAGEDV
201  YEHCLGCYQM  AQVYLAKYRD  VANDEQKVWD  FREESNRIAS  DSRDYVFYQN
251  MRELMPRGMK  ANSLVVGYDA  DGLPQKVYVS  FDNGKKRQSF  EYYLKNGNLF
301  IQSSTVALK  ADGVTADMQT  YHAQQTWYLD  GGRIIREEKQ  GDRLPDPFLN
351  LEDLEKEVSR  YAEAAARRSG  GRRGLSH*

```

```
m728.seq
1 ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51 TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAAT CCGCGTTGGT
101 TTTTGAAGCGA TACGGCAACT CAGGTACCTA AAAATCCGAA TGCTTTTGTG
151 CGGAAACTGT CCGCGCTGTT CGAAGATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAAATCT TGCCGGAAT TGCGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGTTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTGCTTTTC GCACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAT GTGTACGGCG GAACGGTTCA
```

1175

```

501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCAG
551 ACGGTTTCGGT ATTTGATGCG GCGGGGCGCG GGAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAA
751 ATGCGGGAAT TGATGCCCGG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCACAAT CTTTCGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATT TCCTTTGAAC
1051 TTGGAATAAT TGAAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2460; ORF 728>:

m728.pep

```

1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVKPNPNAFV
51 AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGVSFDA AGRGKIGEDV
201 YEHLGCGYQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVIFYQN
251 MRELMPRGMK ANSLVVGIDA DGLPQKVYWS FDNGKKRQSF EYLLKNGNLF
301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
351 LENLEKEVRR YAEAAARRSG GRRDLSH*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

m728 / g728

m728.pep	10	20	30	40	50	60
	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKPNPNAFVAKLARLFRNA					
g728	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNAFVAKLARLFRNA					
	10	20	30	40	50	60
m728.pep	70	80	90	100	110	120
	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
g728	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
	70	80	90	100	110	120
m728.pep	130	140	150	160	170	180
	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSNVYGGTVHGENYETTGEYRVV					
g728	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSNVYGGTAHGENYETTGEYRVV					
	130	140	150	160	170	180
m728.pep	190	200	210	220	230	240
	WQPDGVSFDAAGRGKIGEDVYEHCLGCGYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
g728	WQPDGVSFDAAGRGKIGEDVYEHCLGCGYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
	190	200	210	220	230	240
m728.pep	250	260	270	280	290	300
	DSRNSVIFYQNMRELMPRGMKANSLVVGIDADGLPQKVYWSFDNGKKRQSF EYLLKNGNLF					
g728	DSRDYVIFYQNMRELMPRGMKANSLVVGIDADGLPQKVYWSFDNGKKRQSF EYLLKNGNLF					
	250	260	270	280	290	300
m728.pep	310	320	330	340	350	360
	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					

1176

```

g728      IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIIREEKQGDRLPDFPLNLEDLEKEVSR
           310      320      330      340      350      360
           370
m728.pep  YAEAAARRSGGRRDLSHX
           |||||
g728      YAEAAARRSGGRRGLSHX
           370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2461>:

```

a728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAAATCCGA ATGCTTTTGT GGCAGAACTT
151 GCCCGCCTGT TCCGAAATGC CGACAGGGCG GTTGTCATCG TGAAGGAATC
201 GATGAGGACG GAGGAAAGTC TTGCCGGAGC TGTGGATGAC GGTCCGTTGC
251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCGTTGAAA
301 GAAAAGGCGA AATGGTTTCA CGTAACGGAG CAGGAACATG GGAAGAGGT
351 TTGGCTGGAT TACTATATCG GCGAGGGCGG TTTGGTTGCG GTTTCGCTT
401 CGCAACGCTC GCCGGAAGCG TTTGTAAATG CCGAATATCT GTATCGGAAC
451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
501 TTATGAAACG ACAGGAGAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
551 TATTTGATGC GTCGGGGCGC GGGAAAATCG GGAAGATGT TTATGAGCAT
601 TGCCTCGGGT GTTATCAGAT GGCCAGGTA TATTTGGCGA AATATCGGGA
651 TGTCGCGAAT GATGAGCAGA AGGTTTGGGA CTTCCGCGAA GAGAGTAACC
701 GGATTGCGTC GGAATGCGC GATTCTGTGT TTTATCAGAA TATGCGGGAA
751 TTGATGCCCC GAGGGATGAA GGCAACAGT CTTGTGGTCG GCTATGATGC
801 GGACGGTCTG CCGCAGAAAG TCTATTGGAG TTTGACAAAT GGGAAAAAAC
851 GCCAGAGTTT CGAATATTAT TTGAAAAACG GAAATCTTTT TATTGCACAA
901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC
951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTTGAA CTGGAAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGGCAGGCGC GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2462; ORF 728.a>:

```

a728.pep
1  MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYI ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGQYMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKQRQSFYFY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

a728 / m728 96.3% identity in 377 aa overlap

```

a728.pep      10      20      30      40      50
               MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATE---NPNAFVAKLARLFNA
               |||||
m728           MFKKFKPVLLSFFALVFVFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFNA
               10      20      30      40      50      60

a728.pep      60      70      80      90      100     110
               DRAVVIVKESMRTESLAGAVDDGPLQSEKDYIALAVRLSRLKEKAKWFHVTEQEHGEEV
               |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
m728           DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYIALAIRLSRLKEKAKWFHVTEQEHGKEV
               70      80      90      100     110     120

a728.pep      120     130     140     150     160     170
               WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
               ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
m728           WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
               130     140     150     160     170     180

```

1177

	180	190	200	210	220	230
a728.pep	WQPDGSVFDASGRKIGEDVYEHCLGQYMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m728	WQPDGSVFDAAAGRKIGEDVYEHCLGQYMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
	240	250	260	270	280	290
a728.pep	DSRDSVFYQNMRELMPRGMKANSILVVGYDADGLPQKVYWSFDNGKKRQSF EYYLKNGNLF					
m728	DSRNSVFYQNMRELMPRGMKANSILVVGYDADGLPQKVYWSFDNGKKRQSF EYYLKNGNLF					
	250	260	270	280	290	300
	300	310	320	330	340	350
a728.pep	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGIRIVREEKQGDRLPDFPLNLEDEKEVSR					
m728	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGIRIVREEKQGDRLPDFPLNLEKEVRR					
	310	320	330	340	350	360
	360	370				
a728.pep	YAEAAAARRSGRRDL SHX					
m728	YAEAAAARRSGRRDL SHX					
		370				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2463>:

g729.seq

```

1  ATGAATACTA  CATTGAAAAC  TACCTTGACC  TCTGTTGCAG  CAGCCTTTGC
51  ATTGTCTGCC  TGCACCATGA  TTCCTCAATA  CGAGCAGCCC  AAAGTCGAAG
101  TTGCGGAAAC  CTTCCAAAAC  GACACATCGG  TTTCTTCCAT  CCGCGCGGTT
151  GATTTGGGTT  GGCATGACTA  TTTTGCCGAC  CCGCGCCTGC  AAAAGCTGAT
201  CGACATCGCA  CTCGAGCGCA  ATACCAGTTT  GCGTACAGCC  GTATTGAACA
251  GCGAAATCTA  CCGCAAAACA  TACATGATCG  AGCGCAACAA  CCTCTGCCCC
301  ACGCTTGCCG  CCAATGCGAA  CGGCTCGCGC  CAAGGCAGCT  TGAGCGGCgg
351  caaTGTCAGC  AGCAGCTACA  ATGTCGGAAT  GGGTGcGGca  tCTTACGAAC
401  TCGATCTGTT  CgGGCGCGTG  CGCagcaaca  GcgaagcAGC  ACTGcaggGC
451  tATTTTGCCA  GCGTTGCCAA  CcgCGATGCG  GCACATTTGa  ttCtGATTGC
501  CACCGTTGCC  AAAGCCTATT  TCAAcgaGcG  TTATGCCGAA  AAAGcgatgT
551  CTTTGGCGCA  gcGTGTCTTG  AAAACGCGCG  AGGAAACCTA  CAAGTGTGCC
601  GAATTGCGGT  ACAAGGCAGG  CGTGATTTCG  GCCGTCGCCC  TGCGCCAGCA
651  GAAAGCCTTG  ATTGAATCTG  CCAAAGCCGA  TTATGCCCAT  GCCGCGCGCa
701  gcCGGCAACA  GGCGCGCAAT  GCCTTGCGAA  CCTTGATTAA  ccGTCCGATA
751  CCCGAaGaCC  TGCCCGCCCG  TTTGCCGTTG  GACAagcAGT  TTTTGTGTA
801  AAAATGCCT  GCCGGTTTGA  GTTCCGAAGT  ATTGCTCGAC  CGTCCCGACA
851  TCCGCGCGCG  CGAACACGCG  CTCAAACAGG  CAAACGCCAA  TATCGGTGCG
901  gcgCGCGCCg  ccTTTTTCCC  GTCCATCCGC  CTGACCGGAA  GCGTCGGTAC
951  GGGTTCTGTC  GAATTGGGCG  GGCTGTTCAA  AAGCGGCACG  GCGGTTTGGG
1001  CGTTCGCTCC  GTCTATTACC  CTGCCGATTT  TTAATTGGGG  AACGAACAAG
1051  GCGAACCTTG  ATGTGGCAAA  ACTGCGCCAA  CAGGCACAAA  TTGTTGCCTA
1101  TGAATCCGCC  GTCCAATCCG  CCTTTCAAGA  CGTGGCAAA  GCATTGGCGG
1151  CGCGCGAGCA  GCTGGATAAA  GCCTATGACG  CTTTAAGCAA  ACAAGCCGC
1201  GCCTCTAAAG  AAGCGTTGCG  CTTGGTCGGA  CTGCGTTACA  AACACGGCGT
1251  ATCCGGCGCG  CTCGATTGTC  TCGATGCGGA  ACGCATCAGC  TATTCGGCGG
1301  AAGGTGCGGC  TTTGTGCGCA  CAACTGACCC  GCGCCGAAAA  CCTTCCGAT
1351  TTGTACAAGG  CGCTCgacGG  CGGATTGAAA  CGGGATACCC  AAACCGGCAA
1401  ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

g729.pep

```

1  MNTTLKTTLT  SVAAAFALSA  CTMIPQYEQP  KVEVAETFQN  DTSVSSIRAV
51  DLGWHDFYAD  PRLOKLIDIA  LERNLSLRTA  VLNSEIYRKQ  YMIERNLLP
101  TLAANANGSR  QGSLSGGNVS  SSYNVGLGAA  SYELDLFGRV  RSNSEALQG
151  YFASVANRDA  AHLILIATVA  KAYFNERYAE  KAMSLAQRLV  KTREETYKLS

```

m729.seq

1	ATGGATACTA	CATTGAAAAC	CACCTTGACT	TCTGTTGCAG	CAGCCTTTGC
51	ATTGTCGTCC	TGCACCATGA	TTCCCCAATA	CGAGCAGCCC	AAAGTCGAAG
101	TTGCCGAAAC	GTTCAAAAAC	GATACGCCCG	ACAGCGGCAT	CCGCGCCGTC
151	GATTTAGGTT	GGTCAGACTA	TTTTGCCGAC	CCCGCGCTGC	AAAGCTGAT
201	CGACATCGCA	CTCGAGCGCA	ATACCAGTTT	CGGTACCGCC	GTATTGAACA
251	GCGAAATCTA	CCGCAAAACAA	TACATGATTG	AGCGCAACAA	CCTCCTGCCC
301	ACGCTTGCCG	CCAATGCGAA	CGACTCGCGC	CAAGGCAGCT	TGAGCGGCGG
351	CAATGTAAAG	AGCAGTCTCA	AGAGTCGGAT	GGGTGCGGCA	CTCTACGAAC
401	TCGATCTGTT	CGGGCGTGTA	CGCAGCAGCA	GCGAGGCGGC	ACTCGAAGGC
451	TATTTCGCGA	GCACCGCCAA	CGCGATATGC	GCACATTGTA	GCCTGATTGC
501	CACCGTTGCC	AAAGCGCTATT	TCAACGAAAG	TTACGCCGAA	GAAGCGATGT
551	CTTTGGCGCA	ACGTGTTTTG	AAAACGCGCG	AGGAAAACCTA	CAAGCTGTCC
601	GAATTACGTT	ACAAGGCAGG	CGTGATTTC	CCCGTCGCCC	TACGTACAGA
651	GGAAGCCCTG	ATCGAATCTG	CCAAAGCCGA	TTATGCCCAT	GCCGCGCGCA
701	GCCGCGCAAC	GGCGCGCAAT	GCCTTTGGCA	CCTTGATTAA	CCAACCGATA
751	CCCGAAGACC	TGCTGCGCGG	TTGCCCGCTG	GACAAGCAGT	TTTTTGTGTA
801	AAAACCTGCC	GCCGGTTTGA	GTTCCGAAGT	ATTGCTCGAC	CGTCCCGATA
851	TCCGTGCTGC	CGAACACGCG	CTCAAACAGG	CAAACGCCAA	TATCGGTGCG
901	GCAAGCGCGC	CCTTTTTTCC	ATCCATTCCG	CTAGCCGGAA	CGGTGCGTAC
951	GGTTCCTGCC	GAATTGGGTG	GGTTGTTCAA	AAGCGGCACG	GGCGTTTGGT
1001	CGTTTCGCGC	GTCATTATAC	CTGCCGATTT	TTACCTGGGG	TACGAACAAG
1051	GCGAACCCTG	ATGTAGCCAA	GCTGCGCCAA	CAGGTACAAA	TCGTTGCCTA
1101	TGAATCCGCG	GTCCTAATCC	CATTTCAAAG	CGTGGCAAAC	GCATTGGCGG
1151	CGCGCGAGCA	GCTGGATAAA	GCCTATGACG	CTTTAAGCAA	ACAAAGCCCG
1201	GCCTCTAAAG	AAGCGTTGCG	CTTGTCGCG	CTGCGTTACA	AGCAGCGGCT
1251	ATCCGGCGCG	CTCGACTTGC	TCGATGCGGA	ACGCAGCAGT	TATGCGGCGG
1301	AGGTTGCGGC	TTGTGCGGCA	CAACTGACCC	GCGCCGAAAA	CCTTGCCGAT
1351	TTGTACAAGG	ACTCGGGCGG	CGGATTGAAA	CGGGATACCC	AAACCGACAA
1401	ATAA				

m729.pgp

1	MDTTLKTLTI	SVAAAFALSA	CTMIPQYEQP	KVEVAETFKN	DTADSGIRAV
51	DLGWHDYFAD	PRLQKLIDIA	LERNTSLRTA	VLNSEIYRKQ	YMIERNLLLP
101	TLAANANDSR	QGSLSGNGVS	SSYKVG LGAA	SYELDLFGRV	RSSEEAALQG
151	YFSTANNDRA	AHLSLIATVA	KAYFNERYAE	EAMSLAQ RVL	KTREETYKLS
201	ELRYKAGVIS	AVALRQOEAL	IESKADYAH	AARSREQARN	ALATLINQPI
251	PEDLPAGLPL	DKOFFVEKLP	AGLSSEVLLD	RPDIRAEHA	LKQANANIGA
301	ARAAFFPSIR	LTGTGTG TGA	ELGGLFKSGT	GVWSFAPSIT	LPIFTWGTNK
351	ANLDVAKLRQ	QVQIVAYESA	VQSAFQDVAN	ALAAREQLDK	AYDALSKQSR
401	ASKEALRLVC	LYRKHGVSGA	LDLLDAERSS	YAAEGAALSA	QLTRAENLAD
451	LYKALGGGLK	RDTOTDK*			

ORF 729 shows 95.7% identity over a 467 aa overlap with a predicted ORF (ORF729.a) from *N. gonorrhoeae*:

m729 / g729 95.7% identity in 467 aa overlap

```
m729.pep      10          20          30          40          50          60
               MDTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFKNDTADSGIRAVDLGWHDYFAD
               |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g729           MNTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFQNDTSVSSIRAVDLGWHDYFAD
               10          20          30          40          50          60
```

1179

m729.pep	70	80	90	100	110	120
	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNNLLPTLAANANDSRQGSLSGGNV					
g729	70	80	90	100	110	120
	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNNLLPTLAANANGSRQGSLSGGNV					
m729.pep	130	140	150	160	170	180
	SSYKVGGLGAASYELDLFGRVRSSEALQGYFASTANRDAHLSLIATVAKAYFNERYAE					
g729	130	140	150	160	170	180
	SSYNVGLGAASYELDLFGRVRSNSEALQGYFASVANRDAHLILIATVAKAYFNERYAE					
m729.pep	190	200	210	220	230	240
	EAMSLAQRLVLTREETYKLSELRYKAGVISAVLRQOEALIESAKADYAHARSREQARN					
g729	190	200	210	220	230	240
	KAMSLAQRLVLTREETYKLSELRYKAGVISAVLRQOEALIESAKADYAHARSREQARN					
m729.pep	250	260	270	280	290	300
	ALATLINQPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
g729	250	260	270	280	290	300
	ALATLINQPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
m729.pep	310	320	330	340	350	360
	ARAAFFPSIRLTGTGTGSAELGGLFKSGTGVSFAPSITLPIFTWGTNKANLDVAKLRQ					
g729	310	320	330	340	350	360
	ARAAFFPSIRLTGSGTGSVELGGLFKSGTGWAFAPSITLPIFTWGTNKANLDVAKLRQ					
m729.pep	370	380	390	400	410	420
	QVQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVS					
g729	370	380	390	400	410	420
	QAQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVS					
m729.pep	430	440	450	460		
	LDLLDAERSSYAAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX					
g729	430	440	450	460		
	LDLLDAERISYSAEGAALSAQLTRAENLADLYKALDGGGLKRDQTQDKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

1	ATG	GATACTA	CATTG	AAAC	CACCTT	GACT	TCTGT	TGCAG	CAGCCT	TCCG
51	ATT	TATCC	GCC	TGCAC	CATGA	TTCCCA	AATA	CGAGC	AGCCC	AAAGT
101	TTG	CCGAA	C	GTTCA	AAAC	GATACC	GCCG	ACAGC	GGCAT	CCGTG
151	GATT	TGGGT	GGCAT	GACTA	TTTG	CCCGAC	CCGCG	CCTGC	AAAAG	CTGAT
201	CGAC	ATCGCA	CTCGA	GCGCA	ATACC	AGTTT	GCGT	ACCGC	GTATT	GAACA
251	GCGAA	ATCTA	CCGCA	ACAA	TACAT	GATTG	AGCGC	AACA	CCTCT	GCCC
301	ACGCT	TGCCG	CCAAT	GCGAA	CGACT	CGCGC	CAAGG	CAGCT	TGAGC	GGCGG
351	CAATG	TAAGC	AGCAG	CTACA	AAGTC	GGAAT	GGGT	GCGGA	TCTTA	CGAAC
401	TCGAT	CTGTT	CGGGC	GTGA	CGCAG	CAGCA	GCGAG	GCGGC	ACTGC	AAGGC
451	TATTT	CGCCA	GCACC	GCCAA	CCGCG	ATGCG	GCACA	TTTGA	GCCTG	ATTGC
501	CACCG	TGCC	AAAGC	CTATT	TCAAC	GAAAC	TTATG	CCGAA	GAAGC	GATGT
551	CTTTG	GCGCA	ACGTG	TTTG	AAAAC	GCGCG	AGGAA	ACCTA	CAAGC	TGTCC
601	GAATT	ACGTT	ACAAG	GCAAG	CGTGA	TTTCC	GCCGT	CGCCC	TACGT	CAGCA
651	GGAAG	CCCTA	ATCGA	ATCTG	CCAAG	CCCA	TTATG	CCCAT	GCCGC	GCGCA
701	GCCGC	GCAACA	GGCGC	GCAAT	GCCTT	GGCAA	CCCTG	ATTAA	CCAAC	CAGTA
751	CCCGA	CAGAC	TGCCG	CCCGG	TTGCC	GTTG	GACA	AAGCA	TTTTT	GTTGA
801	GAAGC	TGCCG	GCGGT	TTGA	GTTCC	GAAAG	ATTGC	TCGAC	CGTCC	CGATA
851	TCCGT	GCTGC	CGAAC	ACGCG	CTCAA	ACAGG	CAAAC	CGCAA	TATCG	GTCGG
901	GCACG	CGCGG	CCTTT	TCCC	ATCCAT	CCCG	CTGAC	CGGAA	GCGTC	GATAC
951	GCATT	CTGCC	GAATT	GGGCG	GGCTG	TTCAA	AAGCG	GCAAC	GGCGT	TTGGT
1001	TGTT	CGCAC	TTCCAT	TACC	CTGCC	GATTT	TTACT	TGGGG	TACGA	ACAAG

1180

1051 GCGAACCTCG ATGTAGCCAA GCTGCGCCAA CAGGCACAAA TCGTTGCCTA  
1101 TGAAGCCGCC GTCCAATCCG CATTTCAGA CGTGGCAAAC GCATTGACCG  
1151 CGCGCGAGCA GTTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC  
1201 GCCTCTAAG AAGCGTTGCG TTTGGTCGGT CTGCGTTACA AACACGGCGT  
1251 ATCCGGCGCG CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATTGCGCGG  
1301 AAGGTGCGGC TTTGTCGGCA CAACTGACCC GCGCCGAAA CTTGCCGAT  
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA  
1401 ATAA

This corresponds to the amino acid sequence <SEQ ID 2468; ORF 729.a>:

a729.pep

1 MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV  
51 DLGWHDFAD PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNLLP  
101 TLAANANDSR QGSLSGGNVS SSKVGLGAA SYELDLFGRV RSSSEALQG  
151 YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRLV KTREETYKLS  
201 ELRYKAGVIS AVALRQREAL IESAKADYAH AARSREQARN ALATLINQPI  
251 PDDLPAFLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA  
301 ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK  
351 ANLDVAKLRQ QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR  
401 ASKEALRLVG LRYKHGVSQA LDLLDAERSS YSAEGAALSA QLTRAENLAD  
451 LYKALGGGLK RDTQTDK\*

a729 / m729 98.1% identity in 467 aa overlap

a729.pep	10	20	30	40	50	60
	MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDFAD					
m729	MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDFAD					
a729.pep	70	80	90	100	110	120
	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNVS					
m729	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNVS					
a729.pep	130	140	150	160	170	180
	SSKVGLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVAKAYFNERYAE					
m729	SSKVGLGAASYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVAKAYFNERYAE					
a729.pep	190	200	210	220	230	240
	EAMSLAQRLVKTREETYKLS ELRYKAGVIS AVALRQREAL IESAKADYAH AARSREQARN					
m729	EAMSLAQRLVKTREETYKLS ELRYKAGVIS AVALRQREAL IESAKADYAH AARSREQARN					
a729.pep	250	260	270	280	290	300
	ALATLINQPI PDDLPAFLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
m729	ALATLINQPI PDDLPAFLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
a729.pep	310	320	330	340	350	360
	ARAAFFPSIR LTGSVDTHSA ELGGLFKSGTGVWLFAPSITLPIFTWGTNKANLDVAKLRQ					
m729	ARAAFFPSIR LTGSVDTHSA ELGGLFKSGTGVWLFAPSITLPIFTWGTNKANLDVAKLRQ					
a729.pep	370	380	390	400	410	420
	QAQIVAYEAA VQSAFQDVANALTAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
m729	QAQIVAYEAA VQSAFQDVANALTAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					



1181

```

          430      440      450      460
a729.pep  LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m729      LDLLDAERSSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX
          430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2469>:

```

g730.seq
1  GTGAAACCGC  TGC GCAGACT  GACAAACCTC  CTTGCCGCCT  GCGCCGTAGC
51  GCGGGTCGCA  CTCATACAGC  CCGCCCTCGC  GCGGGACTTG  GCGCAAGACC
101 CGTTCATTAC  CGATAACACC  CAACGGCAGC  ACTACGAACC  CGGCGGCAAA
151 TACCACCTCT  TCGGcgaCCC  GCGCGGCAGC  GTTTCGACCC  GCACCGGCAA
201 AATCAACGTC  ATCCAAGACT  ATACCCACCA  GATGGGCAAC  CTGCTCATCC
251 AACAGGCGGC  AATCCAAGGC  AATCTTGTT  ACACCGTCCG  CTTTTCGGA
301 CACGGACACG  AAGAACACGC  CCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 AAGCGAAGAA  AAAGGCAACG  TTGACGACGG  CTTTACCGTG  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCGCGCG  ATGCCTACGA  CGGCCCGAAG
451 GCGGGCAATT  ACCCCAAACC  TACGGGCGCA  CGAGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCCCGCA  GTATCAAAC  CAATCCGACC  GACACCCGCA
551 GCATCCGGCA  ACGCATATTC  GACAACATA  ACAACCTCGG  CAGCAATTTT
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TGTCACGGC  GTCGCGCGCG
701 GCGCGCTCAA  CCCCTTTATC  AGCGCGGCG  AAGCCTTGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCGA  TGCGCAACAT
801 CGCCCCCTTA  CCCGCCGAGG  GCAAATTCG  CGCCATCGGC  GGCTTGGGCA
851 GCGCGGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTGTA  CCGGTGGATA
901 CAGGAAACCC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCCT
951 GCCGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GCGCGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  TGGGGATTTT  TCTAAATCCT  ACACCTGCTC  CTTCCACGGC
1051 AGCACCTTGG  TCAAAACGGC  AGACGGCTAC  AAAGCCATTG  CCCATATTCA
1101 AGCCGGAGAC  CGCGTCCTTT  CCAAGGACGA  GGCAAGCGGA  GAAACGGGAT
1151 ACAAAACCGT  TACCGCCCGA  TACGGCAATC  CGTATCAAGA  AACCCTTTAC
1201 ATTGAAGTTT  CAGACGGCAT  CGGCAACAGC  CAAACCTGTA  TTTCCAACCG
1251 CATCCACCGG  TTTTATTCGG  ACGGCAATG  GATTAAGGCG  GAAGATTTAA
1301 AAGCGGGAAG  CCGGTGTGTA  TCCGAAAGCG  GCAAAACCCA  AACCCTCCGC
1351 AACATCGTTG  TCAAACCAAA  ACCGCTCAA  GCCTACAATC  TGACCGTTGC
1401 CGATTGGCAT  ACCTACTTCG  TCAAGGGTAA  TCAGGCGGAA  ACGGAAGGGG
1451 TTTGGGTTCA  TAATGATTGT  CCGCCTAAAC  CAAAACCAAC  CAATCATGCC
1501 CAACAAAGAA  AAGAAGAAGC  TAAAAACGAT  TCTCATCGAA  GTGTGGGAGA
1551 TTCCAATCGT  GTCGTTCGCG  AAGGAAAGCA  ATATTTAGAT  TCCGACACAG
1601 GAAACCATGT  TTATGTAAAA  GGAGATAAAG  TGGTTATTCT  AACTCCTGAT
1651 GGAAGACAGG  TAACTCAATT  TAAGAACTCG  AAAGCCAATA  CGTCAAAAAG
1701 GGTAAAAAAT  GGAATATGGA  CACCAAAATA  A

```

This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

```

g730.pep
1  VKPLRLRLTNL  LAACAVAAVA  LIQPALAADL  AQDPFITDNT  QRQHYEPGGK
51  YHLFGDPRGS  VSDRTGKINV  IQDYTHQMG  LLIQAAAIQ  NLGYTVRFSG
101 HGHEEHAPFD  NHAADSASEE  KGNVDDGFTV  YRLNWEGHEH  HPADAYDGPK
151 GGNYPKPTGA  RDEYTYHNG  TARSIKLNPT  DTRSIRQRIF  DNYNNLGSNF
201 SDRADENR  MFEHNAKLDR  WGNMSEFVNG  VAAGALNPFI  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPI  PAEGKFAAIG  GLGSAAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVKNLTKAAK  PGKAAVSGDF  SKSYTCSFHG
351 STLVKTAGDY  KAIAHIQAGD  RVLKDEASG  ETGYKPV TAR  YGNPYQETVY
401 IEVSDGIGNS  QTLISNRIHP  FYSDGKWIKA  EDLKAGSRL  SESGKTQTVR
451 NIVVKPKPLK  AYNLTVADWH  TYFVKGNQAE  TEGVWVHND  PPKPKPTNHA
501 QORKEEAKND  SHRSVGDSNR  VVREGKQYLD  SDTGNHVYVK  GDKVVILTPD
551 GRQVTQFKNS  KANTSKRVKN  GKWTFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2471>:

```

m730.seq
1  GTGAAACCGC  TGC GCAGACT  GACAAACCTC  CTTGCCGCCT  GCGCCGTAGC
51  GCGGGCCGCA  CTCATACAGC  CCGCCCTCGC  GCGGGACTTG  GCGCAAGACC

```

1182

```

101 CGTTCATTAC CGATAACGCC CAACGGCAGC ACTACGAACC CGCGGGCAAA
151 TACCACCTCT TCGGCGACCC GCGCGGCAGC GTTTCGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
251 AACAGGCAAA CATCAACGGC ACAATCGGCT ACCACACCCG CTTTTCCGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 GAGCGAAGAA AAAGGCAACG TTGACGAAGG CTTTACCGTA TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCCGCCG ATGCCTACGA CGGCCGGAAG
451 GCGGGCAATT ACCCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAAC CAATCCGACC GACACCGCA
551 GCATCCGCA ACGCATATCC GACAATTACA GCAACCTCGG CAGCAATTTT
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTTCGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TATCAACGGC GTCGCGCCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGCGGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCAA TGCGCAACAT
801 CGCCCCCTTG CCGCGCGAGG GCAAATTCGC CGTCATCGGC GGCTTGGGCA
851 GCGTGGCGGG CTTTGAAAAG AATACGCGCG AAGCCGTTGA CCGGTGGATA
901 CAGGAAAATC CCAATGCGCG CGAAACCGTC GAAGCCGTCT TCAACGTTGC
951 CGCAGCAGCC AAAGTCGCGA AGTTGGCAAA GGCGGCAAAA CCAGGGAAGG
1001 CTGCGGTTAG CGGGGATTTT GCTGATTCTT ATAAAAAGAA ATTGGCTTTG
1051 TCTGATAGTG CGAGACAGTT ATATCAAAAT GCAAAGTATA GAGAAGCTCT
1101 AGATATACAT TATGAAGATT TAATTAGAAG AAAAAGTAT GGTTCATCAA
1151 AATTTATTAA CGGCAGAGAA ATTGACGCTG TTACGAATGA TGCTTTAATA
1201 CAAGCCAAA GAACAATTTT AGCAATAGAT AAACCTAAAA ATTTCTTAAA
1251 TCAAAAAAAT AGAAAGCAAA TTAAAGCAAC CATCGAAGCA GCAAACCAAC
1301 AGGGAAAACG TGCAGAATTT TGGTTTAAAT ACGGTGTTCA TTCACAAGTT
1351 AAGTCATATA TTGAATCAAA AGGCGGCATT GTTAAACAG GTTTAGGAGA
1401 TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2472; ORF 730>:

```

m730.pep
1  VKPLRRRLTNL LAACAVAAAA LIQPALAADL AQDPFITDNA QRQHYEPGGK
51  YHLFGDPRGS VSDRTGKINV IQDYTHQMG NLLIQQANING TIGYHTRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDEGFTV YRLNWEGHEH HPADAYDGPK
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIS DNYSNLGSNF
201 SDRADANRK MFEHNAKLDR WGNSEFING VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAVIG GLGSVAGFEK NTREAVDRWI
301 QENPNAAETV EAVFNVAAAA KVAKLAKAAK PGKAAVSGDF ADSYKKKLAL
351 SDSARQLYQN AKYREALDIH YEDLIRKTD GSSKFINGRE IDAVTNDALI
401 QAKRTISAID KPNFLNQKN RKQIKATIEA ANQQGKRAEF WFKYGVHSQV
451 KSYIESKGGI VKTGLGD*

```

g730 / m730 93.0% identity in 344 aa overlap

```

          10      20      30      40      50      60
g730.pep  VKPLRRRLTNLLAACAVAAVALIQPALAADLAQDPFITDNTQRQHYEPGGKYHLFGDPRGS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      VKPLRRRLTNLLAACAVAAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS
          10      20      30      40      50      60

          70      80      90      100     110     120
g730.pep  VSDRTGKINVIQDYTHQMG NLLIQQAIIQGNLGYTVRFSGHGHEEHAPFDNHAADSASEE
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      VSDRTGKINVIQDYTHQMG NLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE
          70      80      90      100     110     120

          130     140     150     160     170     180
g730.pep  KGNVDDGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT
          130     140     150     160     170     180

          190     200     210     220     230     240
g730.pep  DTRSIRQRIFDNYNNLGSNFSRDEANRKMFEHNAKLDRWGNSEFVNGVAAGALNPFI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      DTRSIRQRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGNSEFINGVAAGALNPFI
          190     200     210     220     230     240

```

1183

	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
m730						
	250	260	270	280	290	300
	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSAAGFEKNTREAVDRWI					
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNVLPFAKVNLTAAKPGKAAVSGDFSYSYTCSPHGSTLVKTADGY					
m730						
	310	320	330	340	350	360
	QENPNAAETVEAVFNVAATAAKVAKLAKAAGKPGKAAVSGDFADSYKKKLALSDSARQLYQN					
	370	380	390	400	410	420
g730.pep	KAIAHIQAGDRVLSKDEASGETGYKPVYTARYGNPYQETVYIEVSDGIGNSQTLISNRIHP					
m730	AKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIKPKNLFNLQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

```

a730.seq
1  GTGAAACCGC  TGCGAAGACT  CATCAAGCTC  CTTGCCGCCT  GTGCCGTAGC
51  GCGGCGCCGC  CTCATACAGC  CCGCCCTCGC  GCGCGACTTG  GCACAAGACC
101 CGTTCATTAC  CGATAACGCC  CAACGGCAGC  ACTACGAACC  CGGAGGCAAA
151 TACCACCTCT  TCGGCGACCC  GCGCGGCAGC  GTCTCCGACC  GCACCGGTCA
201 AATCAACGTC  ATCCAAGACT  ATACCCACCG  GATGGGCAAC  CTGCTCATCC
251 AGCAGGCAAA  CATCAACGGC  ACAATCGGCT  ACCACACCCG  CTTTCCGGA
301 CACGGATACG  AAGAACACGC  CCCCTTCGAC  AACCACGCCG  CCGACAGCGC
351 GAGCGAAGAA  AAAGGCAACG  TTGACGAAGG  CTTTACCGTA  TACCGGCTCA
401 ACTGGGAAGG  ACACGAACAT  CATCCCGCCG  ATGCCTACGA  CGGCCCGAAG
451 GCGGCAATT  ACCCAAACC  TACGGGTGCA  CGCGACGAAT  ACACCTATCA
501 CGTCAACGGC  ACAGCACGCA  GCATCAACT  CAATCCGACC  GACACCCGCA
551 GCATCCGGCA  ACGCATATCC  GACAATTACA  GCAACCTCGG  CAGCAATTTC
601 TCCGACCGCG  CCGATGAAGC  CAACAGAAAA  ATGTTTCGAGC  ACAATGCCAA
651 GCTCGACCGC  TGGGGCAACA  GCATGGAGTT  TATCAACGGC  GTCGCGCCCG
701 GCGCGCTCAA  CCCCTTTATC  AGCGCGGGCG  AAGCCTTGGG  CATAGGCGAC
751 ATACTGTACG  GAACGCGCTA  TGCCATAGAC  AAAGCCGCAA  TGCACAACAT
801 CGCCCCCTTG  CCCGCCGAGG  GCAAATTCGC  CGTCATCGGC  GGCTTGGGCA
851 GCGTGGCGGG  CTTTGAAAAA  AATACGCGCG  AAGCCGTGTA  CCGGTGGATA
901 CAGGAAAACC  CCAATGCCGC  CGAAACCGTC  GAAGCCCTGG  TCAACGTCTT
951 GCGGTTTGCC  AAAGTCAAAA  ACCTGACAAA  GGCGGCAAAA  CCGGGGAAGG
1001 CTGCGGTTAG  CGGGGATTTT  TCTGCTGCAT  ACAATACAAG  AACAACCTAG
1051 AAAGTTACTA  CAGAAACAGA  GGGGTTAAT  AGAATCAGAC  AGAACCAGAA
1101 AAATAGTAAT  ATACATGAGA  AAAATTATGG  AAGAGATAAT  CCTAATCATA
1151 TTAATGTTTT  ATCTGGAAT  TCTATACAAC  ATATACTGTA  TGGAGATGAA
1201 GCAGGAGGTG  GGCATCTTTT  TCCTGGCAAA  CCTGGTAAGA  CAACATTCCC
1251 CCAACATTGG  TCAGCCAGTA  AAATAACTCA  TGAAATTAGT  GATATCGTTA
1301 CATCCCCAAA  AACGCAATGG  TATGCACAGA  CTGGAACAGG  CGGCAATAT
1351 ATTGCTAAAG  GAAGACCAGC  TAGGTGGGTA  TCATATGAAA  CGAGAGATGG
1401 AATTCGTATC  AGAACAGTTT  ATGAACCTGC  AACAGGAAAA  GTGGTAACGT
1451 CATTCCCCGA  TAGAACCTCT  AATCCCAAAT  ATAACCCTGT  AAAATAAA

```

This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

```

a730.pep
1  VKPLRRLIK  LAACAVAAAA  LIQPALAADL  AQDPFITDNA  QRQHYEPGGK
51  YHLFGDPRG  VSDRTGQINV  IQDYTHRMGN  LLIQQANING  TIGYHTRFSG
101 HGYEEHAFD  NHAADSASEE  KGNVDEGFTV  YRLNWEGHEH  HPADAYDGPK
151 GGNYPKPTGA  RDEYTYHVNG  TARSIKLNPT  DTRSIRQRIS  DNYSNLGSNF
201 SDRADEANRK  MFEHNAKLDR  WGNMSEFING  VAAGALNPFI  SAGEALGIGD
251 ILYGTRYAID  KAAMRNIAPL  PAEGKFAVIG  GLGSVAGFEK  NTREAVDRWI
301 QENPNAAETV  EALVNVLPFA  KVNLTAAK  PGKAAVSGDF  SAAYNTRTTR
351 KVTTETEGLN  RIRQONQNSN  IHEKNYGRDN  PNHINVLSGN  SIQHILYGDE
401 AGGGHLFPK  PGKTTFPQHW  SASKITHEIS  DIVTSPKTQW  YAQTGTGGKY
451 IAKGRPARWV  SYETRDGIRI  RTVYEPATGK  VVTAFDPRTS  NPKYNPVK*

```

a730 / m730 88.6% identity in 376 aa overlap

	10	20	30	40	50	60
a730.pep	VKPLRLRIKLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
m730	VKPLRLRLTNLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
a730.pep	VSDRTGQINVIQDYTHRMGNLLIQQANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
m730	VSDRTGKINVIQDYTHQMGNLLIQQANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
a730.pep	KGNVDEGFTVYRLNWEGHEHHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
a730.pep	DTRSIRQIRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGSMEFINGVAAGALNPFI					
m730	DTRSIRQIRISDNYSNLGSNFSRDEANRKMFEHNAKLDRWGSMEFINGVAAGALNPFI					
	190	200	210	220	230	240
a730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSGVAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSGVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
a730.pep	QENPNAAETVEALVNVLPFAKVKNLTAAKPGKAAVSGDFSAAYNTRTRTKVTETEGLN					
m730	QENPNAAETVEAVFNVAATAKVAKLAKAAGKPGKAAVSGDFADSY-----KKKLALSDSAR					
	310	320	330	340	350	360
a730.pep	RIRQNQKNSNIHEKNYGRDNPNIHINVLSGNSIQHILYGDEAGGHLFPKGPKGKTTFFQHW					
m730	QLYQNAKYREALDIHYEDLIRKTDGSSKFINGREIDAVTNDALIQAKRTISAIDKPKNF					
	370	380	390	400	410	420
a730.pep	RIRQNQKNSNIHEKNYGRDNPNIHINVLSGNSIQHILYGDEAGGHLFPKGPKGKTTFFQHW					
m730	QLYQNAKYREALDIHYEDLIRKTDGSSKFINGREIDAVTNDALIQAKRTISAIDKPKNF					
	360	370	380	390	400	410

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2475>:

g731.seq  
 1 gattttcag cgttttcatg CGAGAACGGT TTGTCTGTGC GCGTCCGCAA  
 51 TTTGGACGGC GGCAAATCG CGTTGCGGCT GGACGGCAGG CGTGCCGTCC  
 101 TCTCTCCGA CGTTGCCGCA TCCGGCGAAC GCTATACCGC CGAACACGGT  
 151 TTGTTCCGAA ACGGAACCGA GTGGCACCAG AAAGGCGGCG AAGCCTTTT  
 201 CGGCTTTACC GATGCCTACG GCAATTCGGT CGAACTTCC TGCCGCGCCC  
 251 GTTAA

This corresponds to the amino acid sequence &lt;SEQ ID 2476; ORF 731.ng&gt;:

g731.pep  
 1 DFRAFSCENG LSVVRNLDG GKIALRLDGR RAVLSSDVAA SGERYTAEHG  
 51 LFGNGTEWHQ KGGEAFFGFT DAYGNSVETS CRAR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2477>:

m731.seq  
 1 ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTTGT CTTTGGCGGC  
 51 CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGCGGG CATATGCCGC  
 101 CCGTTCAAAA CCAAGCCGGC ACGGACGATT TTCGGGCGTT TTCTGCGAG  
 151 AACGGTTTGT CTGTGCGCGT CCGCCATTG GACAGCGGCA AAGTCGCGTT  
 201 GCGGCTGGAC GGCAGGCGTG CCGTCTCTC TTCCGACGTT GCCGCATCCG

1185

251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG  
 301 CACCAGAAAG GCGGCGAAGC CTTTTCGGC TTTACCGATG CCTACGGCAA  
 351 TTCGGTCGAA ACTTCCTGCC GCGCCCGTTA A

This corresponds to the amino acid sequence <SEQ ID 2478; ORF 731>:

m731.pep  
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TDDFRAFSCE  
 51 NGLSVRVRHL DSGKVALRLD GRRAVLSSDV AASGERYTAE HGLFGNATEW  
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR\*

g731/m731 95.2% identity in 84 aa overlap

g731.pep					10	20	30
					DFRAFSCE	GLSVRVRNLDGGKIALRLDGR	
m731	LSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCE	GLSVRVRHLD	DSGKVALRLDGR				
	20	30	40	50	60	70	
g731.pep		40	50	60	70	80	
		RAVLSSDV	AASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVETSCRARX				
m731		RAVLSSDV	AASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVETSCRARX				
		80	90	100	110	120	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2479>:

a731.seq  
 1 ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTGT CTTTGGCGGC  
 51 CTGTGCCGTG CCGGAGGCGT ATGATGACGG CCGACGAGGG CATATGCCGC  
 101 CCGTTCAAAA CCAAGCCGGC ACGGCAGATT TTCGGGCATT TTCCTGCGAG  
 151 AACGGTTTGT CTGTGCACGT CCGCCGTTTG GACGGCGGCA GAATCGCGTT  
 201 GCGGTTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG  
 251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG  
 301 CATCAGAAAG GCGGCGAAGC CTTTTCGGC TTTACCGATG CCTACGGCAA  
 351 TTCGGTCGAA ACCTCCTGCC GCGCCCGCTA A

This corresponds to the amino acid sequence <SEQ ID 2480; ORF 731.a>:

a731.pep  
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TADFRAFSCE  
 51 NGLSVHVRRL DGGRIALRLD GRRAVLSSDV AASGERYTAE HGLFGNGTEW  
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR\*

a731/m731 94.4% identity in 126 aa overlap

a731.pep		10	20	30	40	50	60
		MNIRFFALTV	PVLSLAACAV	PEAYDDGGRGHMPPVQNQAGTADFRAFSCE	GLSVHVRRL		
m731		MNIRFFALTV	PVLSLAACAV	PEAYDDGGRGHMPPVQNQAGTDDFRAFSCE	GLSVRVRHL		
		10	20	30	40	50	60
a731.pep		70	80	90	100	110	120
		DGGRIALRLD	GRRAVLSSDV	AASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVE			
m731		DSGKVALRLD	GRRAVLSSDV	AASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVE			
		70	80	90	100	110	120

a731.pep TSCRARX  
 |||||  
 m731 TSCRARX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2481>:

g732.seq  
 1 ATGTCGAAAC CTGTTTTTAA GAAATCGCA CTTTATACTT TGGGTGCAAT  
 51 CAGCGGCGTG GCCGTAAGTC TGGCGGTGCA GGGTTTGGC GCCGagaagg  
 101 ACGGgcgGGA TAACGAagtc CTGCCGTGTC AATCCATCCG TACGATGGCG

```

151 GAGGTTTACG GTCAGATTAA GGCAAACTAC TATCATGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCGGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGTTT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGCGCGAGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACGCGCGGT
451 ATGACGGTCA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGTTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTGC CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACCGGCG CGGTCGGCGT GTCGGCGGCG TTTCTGCCGT CTGAAGCGGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GTACTGAAAG
851 CCGTCCCGA GGATTATGTG TACGGTATGG GCGGCGACCC TTTGGCGGGT
901 ATTCTGCGG AGTTGAAAAC GATTCGGATG ACGgtatTTGG TcaaTTCCGG
951 TTCggcttCC CGGTCGGAGA TTGtcgCCGG CGCATTGCAG GACCACAAAC
1001 GCGCGGTCA TCGCGGTACG CAGAGCTTCG GTAAAGGTTT GGTTCAGACT
1051 TTGATTCCCT TGTCCAACGG CAGCGCGGTC AAGTTGACGA CCGCCCTGTA
1101 TTACACGCGG AACGACCGTT CCATTCAGGC ACAGGGGATT GTTCCCGATG
1151 TCgaaGTAAA AGATAAGGAA CGTACTTTTG AAAGCCGCGA GCGGACCTG
1201 LTGCGACACA TCGGCAATCC CTTgggcGGC GAGGATGTGA ACAGTGAAAC
1251 CCTtgccGTA CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GCAAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGTG CTTCAAGGCG GATTCCGAAC
1351 CCTGCGAAAG ACGATCAGTT GCGTAAGGCT TTGGATTGTTG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GGCGAAAAAA CCGGTTTCAA
1451 ATAAAGATAA AAAAGATAAG AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2482; ORF 732>:

```

g732.pep
1 MSKPVFKKIA LYTLGAISGV AVSLAVQGF A EKDGRDNEV LPVQSIRTMA
51 EVYGOIKANY YHDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAEVKSDFI VKIDNVSTRG
151 MTVSEAVKMK RGKPGTKITL TSLRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGYIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGDGDM VLKAVPEDYV YMGGDPLAG
301 IPAELEKTI PMTVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFKGKSVQT
351 LIPLSNGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RTFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA AKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKDK K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2483>:

```

m732.seq
1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51 CAGCGGCGTG GCCGTAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAATCAA GGCAAACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCGGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGCGGGGGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTGC CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GTACTGAAAG
851 CCATTCCTGA AGATTATGTG TACGGGATGG GCGGCGATTC GTTGGCGGGC
901 ATTCTGCGG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC CGGTCGGAGA TTGTGCGAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCA TCGCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCCT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA

```

1187

```

1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GGCGGATTTG
1201 GTCGGACACA TCGGCAATCC CTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCCGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGT CTTCAAGGCG GATTCCCAAC
1351 CTGCCCAAAG ACGACCACTT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGCTT TGGGGCTGGC GGCGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

```

m732.pep
1 MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51 EVYGOIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGFEFGLGME IGQEDGFVKV VSPIEDTPAE RAGVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAIPEDYV YGMGGDSLAG
301 IPAEKLTIPM TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSGKGSVQT
351 LIPLSNGSAV KLTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKADKPA VKEGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAK PVSNDKKDK KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

m732/g732 98.2% identity in 491 aa overlap

m732.pep	10	20	30	40	50	60
	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY					
g732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY					
	10	20	30	40	50	60
m732.pep	70	80	90	100	110	120
	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGFEFGLGMEIGQEDGFVKV					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGFEFGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
m732.pep	130	140	150	160	170	180
	VSPIEDTPAERAGVKSDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
g732	VSPIEDTPAERAEVKSDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
m732.pep	190	200	210	220	230	240
	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGPLKGLV					
g732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGPLKGLV					
	190	200	210	220	230	240
m732.pep	250	260	270	280	290	300
	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAIPEDYVYGMGGDSLAG					
g732	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKGMVLKAVPEDYVYGMGGDPLAG					
	250	260	270	280	290	300
m732.pep	310	320	330	340	350	360
	IPAEKLTIPMTVLVNNGSASASEIVAGALQDHKRAVIVGTQSGKGSVQTLIPLSNGSAV					
g732	IPAEKLTIPMTVLVNNGSASASEIVAGALQDHKRAVIVGTQSGKGSVQTLIPLSNGSAV					
	310	320	330	340	350	360

1188

	370	380	390	400	410	420
m732.pep	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV					
g732	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERTFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
g732	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	430	440	450	460	470	480
	490					
m732.pep	PVSNDKKDKKKX					
g732	PVSNDKKDKKKX					
	490					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2485>:

a732.seq

1	ATGTCGAAAC	CTGTTTTTAA	GAAAATCGCA	CTTTATACTT	TGGGTGCAAT
51	CAGCGGCGTG	GCCGTCAGTC	TGGCGGTGCA	GGGTTTTGCC	GCCGAGAAGG
101	ACAGGCGGGA	TAACGAAGTC	CTGCCGGTGC	AATCCATCCG	CACAATGGCG
151	GAGGTTTACG	GTCAAATCAA	GGCAAACCTAC	TATCAGGACA	AACCCGATGC
201	CGATTTGTTT	GAAGGTGCGA	TGAAGGGTAT	GGTGGCCGGT	TTGGATCCGC
251	ATTCGGAATA	TATGGATAAA	AAAGGTTATG	CCGAGATAAA	GGAGTCCACC
301	AGCGGCGAAT	TTGGCGGCTT	GGGGATGGAA	ATCGGGCAGG	AAGACGGATT
351	TGTCAAAGTG	GTTTCGCCGA	TTGAGGACAC	GCCTGCGGAA	CGGGCGGGGG
401	TGAAAAGCGG	CGATTTCATT	GTGAAAATCG	ATAATGTTTC	GACACGCGGC
451	ATGACGGTCA	GCGAAGCGGT	GAAGAAAATG	CGGGGCAAGC	CGGGTACGAA
501	GATTACTTTG	ACGCTGTTCG	GCAAAAATGC	CGACAAGCCG	ATAGTCGTCA
551	ACCTGACCCG	TGCCATTATT	AAAGTGAAAA	GCGTCCGCCA	TCACCTGATC
601	GAACCCGATT	ACGCTATAT	CCGCTGTGTC	CAGTTCCAAG	AGCGGACGGT
651	CGAAAGCGTC	AATACCGCCG	CAAAAGAGCT	GGTAAAGGAA	AATAAAGGAA
701	AACCGCTCAA	GGGCTGGTG	TTGGATTGTC	GCGACGACCC	CGGCGGGCTT
751	TTGACTGGCG	CGGTCGGCGT	GTCGGCGGCA	TTTCTGCCGT	CTGAAGCAGT
801	CTCGTCAAG	ACCAAGGGAC	GCGACGGCAA	AGACCGCATG	GTAAGGAAAG
851	CCGTTCTGA	AGATTATGTG	TACGGGATGG	GCGGCGATTC	GTGGCGGGC
901	ATTCTGCGG	AGTTGAAAC	CATACCGATG	ACGGTATTGG	TCAATTCCGG
951	TTGCGCTTCC	GCGTCGGAGA	TTGTCGCAGG	TGCATTGCAG	GATCATAAAC
1001	GCGGGGTCA	CGTCGGTACG	CAGAGCTTCG	GCAAAGGTTT	GGTTCAGACT
1051	TTGATTCCCT	TGTCCAACGG	CAGCGCGGTC	AAGCTGACAA	CGGCACTGTA
1101	TTATACGCCG	AACGACCGTT	CTATTCAGGC	GCAGGGGATT	GTTCCCGATG
1151	TCGAAGTAAA	AGATAAGGAA	CGCATTTTGT	AAAGCCGCGA	GGCGGATTGT
1201	GTCGGACACA	TCGGCAATCC	TTTGGGCGGC	GAGGATGTGA	ACAGTGAAAC
1251	CCTTGCCGTG	CCGCTTGAAA	AAGATGCGGA	TAAGCCCGCT	GTAAGAGAAA
1301	AAGGTAAAAA	GAAAAAGGAC	GAGGATTGT	CTTCAAGGCG	GATTCCCAAC
1351	CCTGCCAAAG	ACGACCAAGT	GCGGAAAGCT	TTGGATTAG	TCAAGTCGCC
1401	CGAGCAGTGG	CAGAAGTCTT	TGGGGCTGGC	GGCGAAAAAG	CCGGTTTCAA
1451	ATAAAGATAA	GAAAGATAAA	AAAGATAAGA	AGTAG	

This corresponds to the amino acid sequence <SEQ ID 2486; ORF 732.a>:

a732.pep

1	MSKPVFFKIA	LYTLGAISGV	AVSLAVQGFA	AEKDRRDNEV	LPVQSIRTMA
51	EVYGIKANY	YQDKPDADLF	EGAMKGMVAG	LDPHSEYMDK	KGYAEIKEST
101	SGEFGGLGME	IGQEDGFVKV	VSPIEDTPAE	RAGVKSGDFI	VKIDNVSTRG
151	MTVSEAVKKM	RGKPGTKITL	TLSRKNADKP	IVVNLTRAI	KVKSVRHHLI
201	EPDYGIVRS	QFQERTVESV	NTAAKELVKE	NKGKPLKGLV	LDLRDDPGGL
251	LTGAVGVSA	FLPSEAVVVS	TKGRDGDKDM	VLKAVPEDYV	YGMGGDSLAG
301	IPAEKLTIPM	TVLVNNGSAS	ASEIVAGALQ	DHKRAVIVGT	QSFKGVSQVT
351	LIPLNSGSAV	KLTTALYYTP	NDRSIQAQGI	VPDVEVKDKE	RIFESREADL
401	VGHIGNPLGG	EDVNSETLAV	PLEKDADKPA	VKEKGKKKKD	EDLSSRRIPN
451	PAKDDQLRKA	LDLVKSPEQW	QKSLGLAAKK	PVSNDKKDKD	KDKK*



a732/m732 99.6% identity in 494 aa overlap

a732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVL	10	20	30	40	50	60
m732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVL	10	20	30	40	50	60
a732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV	70	80	90	100	110	120
m732	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV	70	80	90	100	110	120
a732.pep	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTL	130	140	150	160	170	180
m732	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTL	130	140	150	160	170	180
a732.pep	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV	190	200	210	220	230	240
m732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV	190	200	210	220	230	240
a732.pep	LDLRDDPGGLLTGAVGVSAFLPSEAVVVSTKGRDGGKDRMVLKAVPEDYVYGMGGDSL	250	260	270	280	290	300
m732	LDLRDDPGGLLTGAVGVSAFLPSEAVVVSTKGRDGGKDRMVLKAVPEDYVYGMGGDSL	250	260	270	280	290	300
a732.pep	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKGSVQTLIPLSNGSAV	310	320	330	340	350	360
m732	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKGSVQTLIPLSNGSAV	310	320	330	340	350	360
a732.pep	KLTTALYYTPNDRSIQAQGI	370	380	390	400	410	420
m732	KLTTALYYTPNDRSIQAQGI	370	380	390	400	410	420
a732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK	430	440	450	460	470	480
m732	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK	430	440	450	460	470	480
a732.pep	PVSNKDKKDKKDKKX	490					
m732	PVSNKDKKDKKDKKX	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq

```

1  ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51 GGCTCTGACC GCCTGCGCCG GCGGCGGGCA TAAAAACCTG TATTATTACG
101 GCGGTATACC CGATACCGTC TATGAAGGTT TGAAAAACGg cgACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGCGG AAGCCGCCAA
201 CAAAAAATG AATGCCGCCG CGGGTGCGCA CGCCATTG GGA CTGCTGC

```

1190

251 TTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAATT TGAAGAAGAG  
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC  
 351 CGGtaaAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2488; ORF 733>:

**g733.pep**

1 MNPKTLGRL SLCAAVLALT ACAGGGHKNL YYYGGYPDTV YEGLKNDDTS  
 51 LGKQTEKMEK YFAEAANKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE  
 101 KRLFPESGVF MDFLMKTGKG GKR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2489>:

**m733.seq**

1 ATGATGAATC CGAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT  
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG  
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG  
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA  
 201 CAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCCATCTG GGAAGTCTGC  
 251 TTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG  
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC  
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2490; ORF 733>:

**m733.pep**

1 MNPKTLSRL SLCAAVLALT ACGNGQKSL YYYGGYPDTV YEGLKNDDTS  
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE  
 101 KRLFPESGVF MDFLMKTGKG GKR\*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 733 shows 94.3% identity over a 123 aa overlap with a predicted ORF (ORF733.a) from *N. gonorrhoeae*:

**m733/g733**

m733.pep	10	20	30	40	50	60
	MNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
g733	:     :     :     :     :     :     :     :     :     :     :					
	10	20	30	40	50	60
m733.pep	70	80	90	100	110	120
	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEERLFPESGVFMDFLMKTGKG					
g733	:     :     :     :     :     :     :     :     :     :					
	70	80	90	100	110	120
m733.pep	GKRX					
g733	GKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2491>:

**a733.seq**

1 ATGATGAATC CGAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT  
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG  
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG  
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA  
 201 CAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCCATCTG GGAAGTCTGC  
 251 TTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG  
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC  
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2492; ORF 733.a>:

**a733.pep**

1191

1 MNPKTSLRSL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGKNDTDS  
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEE  
 101 KRLFPESGVF MDFLMKTGKG GKR\*

a733/m733 100.0% identity in 123 aa overlap

	10	20	30	40	50	60
a733.pep	MNPKTSLRSLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGKNDTSLGKQTEKMEK					
m733	MNPKTSLRSLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGKNDTSLGKQTEKMEK					
	10	20	30	40	50	60
a733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG					
m733	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG					
	70	80	90	100	110	120
a733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG					
m733	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEKRLFPESGVFMDFLMKTGKG					
	70	80	90	100	110	120
a733.pep	GKRX					
m733	GKRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

g734.seq

1	ATGATGAAAA	AGATACTGGC	AGTATCGGCA	CTATGCCTGA	TGACTGCGGC
51	GGCACAGGCT	GCCGATACTT	ACGGCTATCT	CGCCGTTTGG	CAGAATCCGC
101	AGGATGCAAA	CGATGTTTTG	CAGGTTAAAA	CCACAAAAGA	AGATTGCGCG
151	AAAAGCGAAG	CGTTTGCCGA	GTTGGAAGCC	TTTTGCAAAG	GTCAGGACAC
201	GCTTGCGGGC	ATTGCCGAAG	ACGAGCCGAC	CGGATGCCCG	TCGGTCGTGT
251	CGCTGAACAA	TACCTGTGTC	TCGCTGGCAT	ACCCGAAAGC	CTTGGGCGCG
301	ATGCGCGTTG	AAAACGCCGT	CGTGATTACT	TCTCCGCGTT	TTACGAGCGT
351	TCATCAGGTC	GCACTCAACC	AGTGCATAAA	AAAATACGGC	GCACAGGGAC
401	AATGCGGCTT	GGAAACAGTG	TATTGCACGT	CATCTTCTTA	TTACGGCGGG
451	GCTGTTGCT	CCTTAATCCA	ACACCTGAAA	TAA	

This corresponds to the amino acid sequence <SEQ ID 2494; ORF 734.ng>:

g734.pep

1	MMKKILAVSA	LCLMTAAAQA	ADTYGYLAVW	QNPQDANDVL	QVKTTKEDSA
51	KSEAFAELEA	FCKGQDTLAG	IAEDEPTGCR	SVVSLNNTCV	SLAYPKALGA
101	MRVENAVVIT	SPRFTSVHQV	ALNQCIKKYG	AQGQCGLTV	YCTSSSYGG
151	AVRSLIHLK	*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

m734.seq (partial)

1	TCGGGCATTG	CTGAAGACGA	GCCGACCGGA	TGCCGGTCGG	TCGTGTCGCT
51	GAACAATACC	TGTGTGCGCG	TGGCATAACC	GAAAGCCTTG	GGCGCGCTGC
101	GTGTCGACAA	CGCCGTCGTG	ATTACTTCTC	CGCGTTTTAC	GAGCGTTCAT
151	CAGGTCGCAC	TCAACCAGTG	CATCAAAAAA	TACGGCGTAC	AGGGACAATG
201	CGGCTTGGAA	ACAGTGTATT	GCACATCTTC	TTCTTATTAC	GGCGGAACTG
251	TGCGCTCTTT	GATTCAAAAT	CTCAAATAA		

This corresponds to the amino acid sequence <SEQ ID 2496; ORF 734>:

m734.pep (partial)

1	SGIAEDEPTG	CRSVVSLNNT	CVALAYPKAL	GALRVDNAVV	ITSRFTSVH
51	QVALNQCIKK	YGVQGQGLE	TVYCTSSSY	GGTVRSLIQN	LK*

m734/g734 92.4% identity in 92 aa overlap

	10	20	30
m734.pep	SGIAEDEPTGCRSVVSLNNTCVALAYPKAL		
g734	VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKAL		

1192

	40	50	60	70	80	90
m734.pep	GALRVDNAVVITSPRFTSVHQVALNQCIKKYGVQGCGLQETVYCTSSSYGGTVRSLIQN					
g734	GAMRVENAVVITSPRFTSVHQVALNQCIKKYGAQGCGLQETVYCTSSSYGGAVRSLIQH					
	100	110	120	130	140	150

m734.pep	LKX
g734	LKX
	160

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2497>:

```
a734.seq
1  ATGATGAAAA AGATACTGGC CGTATCGGCA CTATGCCTGA TGAATGCGGC
51  GGCACGGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGAATGCAAA CGATGTTTGG CAGGTTAAAA CCACAAAAGA AGATTCGACG
151 AAAAGCGAAG CGTTTGCCGA GTTGAAGCT TTCTGCAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC GCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT TGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TTATCAGGTC GCACTCAACC AGTGCATCAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAAACAGTG TATGCACGT CTTCTTCTTA TTACGGGGGA
451 ACTGTGCGCT CTTTGATTCA AAATCTCAA TAA
```

This corresponds to the amino acid sequence <SEQ ID 2498; ORF 734.a>:

```
a734.pep
1  MMKKILAVSA LCLMTAAARA ADTYGYLAVW QNPQNANDVL QVKTTKEDST
51  KSEAFAELEA FCKGQDTLAG IEDEPTGCR SVVSLNNTCV ALAYPKALGA
101 MRVENAVVIT SPRFTSVYQV ALNQCIKKYG AQGCGLQETV YCTSSSYGG
151 TVRSLIQNLK *
```

a734/g734 95.6% identity in 160 aa overlap

	10	20	30	40	50	60
a734.pep	MMKKILAVSALCLMTAAARAADTYGYLAVWQNPQNANDVLQVKTTKEDSTKSEAFAELEA					
g734	MMKKILAVSALCLMTAAQAADTYGYLAVWQNPQDANDVLQVKTTKEDSAKSEAFAELEA					
	10	20	30	40	50	60
a734.pep	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVYQV					
g734	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVHQV					
	70	80	90	100	110	120
a734.pep	ALNQCIKKYGAQGCGLQETVYCTSSSYGGTVRSLIQNLKX					
g734	ALNQCIKKYGAQGCGLQETVYCTSSSYGGAVRSLIQHLKX					
	130	140	150	160		

g735.seq not found yet  
g735.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2499>:

```
m735.seq
1  ATGAATCTCG TGAAGCTGCT GCGCAATAAC TGGCAACCGA TTGCCATTAT
51  CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTGTC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAAGT
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
301 AAAAAGGAAA TCGAAATGT CCTTACTCAA GACCGTAAAA ATGCAAGCGG
```

1193

351 CGGTTGCATT GACGGCTTTG GCTCTCACGG CCTGCAGCTC TACAACCGCG  
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>:

m735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK  
51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN  
101 KKEIENVLTQ DRKNASGGCI DGFGSHGLQL YNRALGYGN\*

-- The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2501>:

a735.seq

1 ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT  
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT  
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG  
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA  
201 GCGCGGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA  
251 TGGCTTTGTC GAAAAACAG GCGGAAGTCA GCCGTCGTAA AACGGAAAAAT  
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG  
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG  
401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK  
51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN  
101 KKEIENVLTQ DRKNAGGGCI DGFGHHGLQL YKRALGYGN\*

a735/m735 95.7% identity in 139 aa overlap

	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN					
m735	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a735.pep	YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARA EAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
	130	140				
a735.pep	DGFGHHGLQLYKRALGYGNX					
m735	DGFGSHGLQLYNRALGYGNX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2503>:

g736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC  
51 CTTCGGCAGT ATCACGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA  
101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGCG  
151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTG TCGGTATGGT  
201 TTTGGGTTTG CAGGCTATA CGCAGTTGTC GAAATTCAA TCCGCCGATA  
251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGGCGAACT GGGTCCCGTG  
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTGCGA TGACCAGCGA  
351 AATCGGTTTG ATGAAAACGA CCGACAGCT CGAAGCGATG AACGTGATGG  
401 CGGTCAACCC CGTCGCCCGC GTGGTTGCC CCGGTTTTG GCGGGCGGTG  
451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCG GCATTTTCGG  
501 CGCGTATTTG GTCGCGGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT  
551 GGCCGCGAGT GCAGAACAA ATTACGATAC ATTACGATGT AATCAACGGT

601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA  
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA  
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA  
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2504; ORF 736>:

**g736.pep**

1 MNFIRSVGAK TLGLIQSFGS ITLFLNLA KSGTAFARPR LSVRQVYFAG  
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV  
 101 LAAILFASSA GGAMTSEIGL MKTTQOLEAM NVMAVNPVAR VVAPRFWAGV  
 151 FSMPLLASIF NVAGIFGAYL VGVSWLGLDS GIFWPQMNN ITIHYDVING  
 201 LIKSAAFGVA VTLIAVHQGF HCIPTSEGIL RASTRTVVSS ALTILAVDFI  
 251 LTAWMFTD\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2505>:

**m736.seq**

1 ATGAATTTTA TCCGTTCCGT CGGGCGGAAA ACCCTCGGCC TTATTCAATC  
 51 CTTCGGCAGT ATCAGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA  
 101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGGCGGC  
 151 GTGCTGTCGG TGCTGATTGT TGCGTTTCG GGGCTGTTCG TCGGTATGGT  
 201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA  
 251 TTTGGGCTA TATGGTCGCG GCTTCTCTGT TCGCGAACT GGGTCCCGTG  
 301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GGCGGTGCGA TGACCAGCGA  
 351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG  
 401 CGGTCAACCC CGTCGCCCGC GTGGTTGCC CGCGTTTTCG GCGGGCGGTG  
 451 TTTTCTATGC CGCTTTTGGC TTCGATTTC AACGTCGCG GCATTTTCGG  
 501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT  
 551 GGCCGCAGAT GCAGAACAAC ATTACGATAC ATTACGATGT AATCAACGGT  
 601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA  
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA  
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA  
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2506; ORF 736>:

**m736.pep**

1 MNFIRSVGAK TLGLIQSLGS ITLFLNLA KSGTAFVRPR LSVRQVYFAG  
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV  
 101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMAVNPVAR VVAPRFWAGV  
 151 FSMPLLASIF NVAGIFGAYL VGVTWLGLDS GIFWSQMNN ITIHYDVING  
 201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI  
 251 LTAWMFTD\*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 736 shows 97.7% identity over a 258 aa overlap with a predicted ORF (ORF736.ng) from *N. gonorrhoeae*:

**m736/g736**

	10	20	30	40	50	60
m736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNLA KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
g736	MNFIRSVGAKTLGLIQSFGSITLFLNLA KSGTAFARPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
m736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
g736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
m736.pep	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLGLDS					
g736	MKTGQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					
	130	140	150	160	170	180

1195

	130	140	150	160	170	180
	190	200	210	220	230	240
m736.pep	GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					
g736	GIFWPQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					
	190	200	210	220	230	240
	250	259				
m736.pep	ALTILAVDFILTAWMFTDX					
g736	ALTILAVDFILTAWMFTDX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2507>:

```

a736.seq
1  ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51  TCTCGGCAGT ATCACGCTGT TTCTGCTGAA TATTCTGGCG AAATCCGGTA
101 CGGCTTTCGT CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCGG TGTGATTGT TGCCGTTTCA GGGCTGTTG TCGGCATGGT
201 CTTGGGTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCGCTGT TCGCGAACT GGGTCCGGTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GGCGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGAACAGCT CGAAGCGATG AACGTGATGG
401 CGGTAAACCC CGTCGCCCGA GTGGTTGCGC CGCGCTTTTG GCGGGGCGTG
451 TTTTCCATGC CGCTTTTGGC TTCGATTTC AACGTGGCGG GTATTTTCGG
501 CGCGTATTTG GTCGGTGTA CCTGGCTGGG CTGGACAGC GGTATTTCT
551 GGTGCGAAAT GCAGAACAAC ATCACGATAC ATTACGATGT AATCAACGGT
601 CTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGGCTC CACTGCGTCC CGACCTCGGA AGGCATTTTG CGCGCCAGCA
701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2508; ORF 736.a>:

```

a736.pep
1  MNFIRSVGAK TLGLIQSLGS ITLFLNILA KSGTAFVRPR LSVRQVYFAG
51  VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMVNPVAR VVAPRFWAGV
151 FSPMLLASIF NVAGIFGAYL VGVTLWLGLDS GIFWSQMNN ITIHYDVING
201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
251 LTAWMFTD*
  
```

a736/m736 100.0% identity in 258 aa overlap

	10	20	30	40	50	60
a736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
m736	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
m736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a736.pep	MKTTEQLEAMNVMVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLWLGLDS					
m736	MKTTEQLEAMNVMVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVTLWLGLDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a736.pep	GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS					

1196

```

m736      GIFWSQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRVTVSS
           190      200      210      220      230      240
           250      259
a736.pep  ALTILAVDFILTAWMFTDX
           |||||
m736      ALTILAVDFILTAWMFTDX
           250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2509>:

```

g737.seq
1  atgaACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51  CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2510; ORF 737>:

```

g737.pep
1  MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2511>:

```

m737.seq..
1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2512; ORF 737>:

```

m737.pep
1  MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 737 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF737.a) from *N. gonorrhoeae*:

m737/g737

```

m737.pep      10      20      30      40      50      60
               MNIKHLLLTSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRQAQEAALAR
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g737           MNIKHLLLTAAATALLGISAPALAHHDGHGDDDHGHAHQHGKQDKIISRQAQEAALAR
               10      20      30      40      50      60

m737.pep      70      80      90      100     109
               VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
               |||||:|||||:|||||:|||||:|||||:|||||:|||||
g737           VGGKITDIDLEHDDGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
               70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2513>:



## a737.seq

```

1 ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51 CATTTCGGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

## a737.pep

```

1 MNFKRLLLLTA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLLTA	AATALMGISA	PALAHHDGHG	DDDHGHAHQ	HSKQDKIISR	AQAEKAALAR
m737	MNIKHL	LLTSAAT	ALLSIS	APALAH	HDGHG	DDDHGHAHQ
	10	20	30	40	50	60

	70	80	90	100	109
a737.pep	VGGKITDIDL	EHDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX
m737	VGGKITDIDL	EHDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX
	70	80	90	100	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

## g738.seq

```

1 ATGTCGCGTG AACGACCGT ATCCGGCGCG CGCCCCGCGG CCAAACCTGCC
51 GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT
101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCGCGC
151 GCGGCGCGCC TGATTGTCTT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCCCGCCA TCAGCTTCCT CCTGTTTGCA ATGGCGGCAT
251 TTTGGTGGCT TCAGGCACGC CTGATGAACC TGATTATCC CGGAATGAAC
301 GACATCGCCT CTTGGGTTTT CATCTTGCTC GCCGTCAGCG CGTGGGCGCTG
351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCAtcgt ACCCTGTTTG
401 CCTGGTCCGT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC
451 CAGTTTGCCG GCTGGGAAAA CACCCCTCGT CTTCAAACA TCATCGTTCA
501 CAGAGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCTCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCCG CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAATTTCG GCACCATCTT GACCTACATA GCGGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGACGG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC GCCATTCTGG AAACCTTTAC AGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GCGGGTTTCA CAGACTTGCC GCGCCAAAGC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA
951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTGATCAAT GCCGAACAGC
1001 ACACCATACA CGACAACCTC CTCAGCACCT TGTTACCCCA TTCCCACAAC
1051 ATCATCCTCC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCTCCCTGA
1151 CCCCCGCATC ACTTTTCTCG CTGTGCGCGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCTTCCG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCGC CATATTCGCA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC
1401 CCCC GCCGCT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAAC
1451 TGCGCTATAT TTCCGC AAAC AGCCCGATGC TGTCTTTT TA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAG CACTAAATA CCGCCCTAC TCCGCCACCT

```

1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA  
 1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA  
 1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTGCCCGAAC  
 1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAAACA  
 1801 AAACCCTGCA AATGA

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>:

g738.pep

1 MSAETTVSGA RPAAKLPIYI LPCFLWIGII PFTFALRLKP SPDFYHDA  
 51 AAGLIVLLFL TAGKKLFDVK IPAISFLFA MAAFWWLOAR LMNLIYPGMN  
 101 DIASWVFILL AVSAWACKSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI  
 151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR  
 201 KIPALGAIC LIMQTAVLGL VNSRTILTYI AATIALILPFW YFRSDKSNRR  
 251 TMLGIAAAVF LTALFQFSMN AILETFTGIR YETAVERVAN GGFTDLPRQS  
 301 EWNKALAAFQ SAPIFGHWGN SFAQQTFLIN AEQHTIHDNF LSTLFTSHSN  
 351 IILQLLAEMG ISGTLVLAAT LLTGIAGLLK RSLTPASLFL LCAVAVSMCH  
 401 SMLEYPLWYV YFLIPFGLML FLSPAESDGL IAFKKAANLG ILTASAIIFA  
 451 GLLHLDWYTY RLVSFSPAA DDSAKTLNRK INELRYISAN SPMLSFYADF  
 501 SLVNFALPEY PETQTWAEA TLKALKYRKY SATYRIALYL MRQGVKVAEK  
 551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPET  
 601 KPCK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2517>:

m738.seq

1 ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACCTGCC  
 51 GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTACCT  
 101 TCGCGCTCAA ACTGAAACCG TCGCCGACT TTTACCACGA TGCCGCGGCC  
 151 GCAGCCGGCC TGATTGTCTT GTTGTCTCTC ACGGCAGGAA AAAAAGTGT  
 201 TGATGTCAA ATCCCGCCA TCAGCTTCTT TCTGTTGCA ATGGCGCGCT  
 251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTACCC CGGTATGAAC  
 301 GACATCGTCT CTGGATTTT CATCTTGCTC GCCGTCAGCG CGTGGCCCTG  
 351 CCGGAGCTTG GTCGCACACT TCGGACAAGA ACGCATCGTG ACCCTGTTTG  
 401 CCTGGTCTGT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC  
 451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAACA TCATCGTTTA  
 501 CAGCGGGCAA GCGCTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC  
 551 ACTACCTCAT GTGGGGCATA CTCGCCGCCG CCTACCTCAA CGGACAACGA  
 601 AAAATCCCCG CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCCGT  
 651 TTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG  
 701 CCCTCATCTT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG  
 751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCGAATT  
 801 TTCCATGAAC ACCATCTCTG AAACCTTTAC TGGCATCCGC TACGAAACTG  
 851 CCGTCGAACG CGTCGCAAC GCGGTTTCA CAGACTTGCC GCGCCAAATC  
 901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGCA TATTGGGGCA  
 951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC  
 1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTTCAACCA TTCCACAAC  
 1051 ATCGTCTCTC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT  
 1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA  
 1151 CCCCCGCATC GCTTTTCTTA ATCTGCACGC TTGCCGTCAG TATGTGCCAC  
 1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCTTTCGG  
 1251 ACTGATGCTC TTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA  
 1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTGCA  
 1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACGCCTTTTC  
 1401 CCCCGCCACT GACGACAGTG CCAAACCTT CAACCGGAAA ATCAACGAGT  
 1451 TGGCTATAT TTCCGCAAAC AGTCCGATGC TGTCCTTTTA TGCCGACTTC  
 1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCGGAAACCC AGACTTGGGC  
 1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT  
 1601 ACCGCATCGC CCTTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA  
 1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA  
 1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCCGCTG CTACCCGAAC  
 1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA  
 1801 AAACCCTGCA AATGA

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>:

m738.pep

1 MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALKLKP SPDFYHDA

```

51  AAGLIVLLFL TAGKKLFDVK IPAISFLFA MAAFYLOAR LMNLIYPMN
101 DIVSWIFILL AVSAWACRSL VAHFGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWEDTFL FQNIIVYSGQ GVIGHIGORN NLGHYLMWGI LAAAYLNGQR
201 KIPAAALGVIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN TLETFGTGIR YETAVERVAN GGFTDLPRQI
301 EWNKALAAFO SAPIFGHGWN SFAQQTFLIN AEQHNIYDNL LSNLFTHSHN
351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAESDGS IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTF RLVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFAPEY PETQTWAEAE TLKSLKYRPH SATYRIALYL MRQGVAEAK
551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
601 KPCK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 738 shows 95.0% identity over a 604 aa overlap with a predicted ORF (ORF738.a) from *N. gonorrhoeae*:

m738/g738

	10	20	30	40	50	60
m738.pep	MPAETTVSGAHPAAKLPIIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
g738	MSAETTVSGARPAAKLPIIYILPCFLWIGIIPFTFALRLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
m738.pep	TAGKKLFDVKIPAISFLLFAMAAFWYLOARLMNLIYPMNDIVSWIFILLAVSAWACRSL					
g738	TAGKKLFDVKIPAISFLLFAMAAFWLQARLMNLIYPMNDIASWVFILLAVSAWACKSL					
	70	80	90	100	110	120
m738.pep	TAGKKLFDVKIPAISFLLFAMAAFWYLOARLMNLIYPMNDIVSWIFILLAVSAWACRSL					
g738	TAGKKLFDVKIPAISFLLFAMAAFWLQARLMNLIYPMNDIASWVFILLAVSAWACKSL					
	70	80	90	100	110	120
m738.pep	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTFLFQNIIVYSGQGVIGHIGORN					
g738	VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWENTPLLQNIIVHRGQGVIGHIGORN					
	130	140	150	160	170	180
m738.pep	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTFLFQNIIVYSGQGVIGHIGORN					
g738	VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWENTPLLQNIIVHRGQGVIGHIGORN					
	130	140	150	160	170	180
m738.pep	NLGHYLMWGI LAAAYLNGQRKIPAAALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
g738	NLGHYLMWGI LAAAYLNGQRKIPAAALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
m738.pep	NLGHYLMWGI LAAAYLNGQRKIPAAALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
g738	NLGHYLMWGI LAAAYLNGQRKIPAAALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
m738.pep	YFRSDKSNRR TMLGIAAAVFLTALFQFSMN TLETFGTGIR YETAVERVANGGFTDLPRQI					
g738	YFRSDKSNRR TMLGIAAAVFLTALFQFSMN AILETFGTGIR YETAVERVANGGFTDLPRQS					
	250	260	270	280	290	300
m738.pep	YFRSDKSNRR TMLGIAAAVFLTALFQFSMN TLETFGTGIR YETAVERVANGGFTDLPRQI					
g738	YFRSDKSNRR TMLGIAAAVFLTALFQFSMN AILETFGTGIR YETAVERVANGGFTDLPRQS					
	250	260	270	280	290	300
m738.pep	EWNKALAAFO SAPIFGHGWN SFAQQTFLINAEQHNIYDNL LSNLFTHSHN IVLQLLAEMG					
g738	EWNKALAAFO SAPIFGHGWN SFAQQTFLINAEQHTIHDN FLSTLFTHSHN IILQLLAEMG					
	310	320	330	340	350	360
m738.pep	EWNKALAAFO SAPIFGHGWN SFAQQTFLINAEQHNIYDNL LSNLFTHSHN IVLQLLAEMG					
g738	EWNKALAAFO SAPIFGHGWN SFAQQTFLINAEQHTIHDN FLSTLFTHSHN IILQLLAEMG					
	310	320	330	340	350	360
m738.pep	ISGTLLVAAT LLTGIAGLLKRPLTPASLFLICTLAVSMCH SMLEYPLWYVYFLIPFGLML					
g738	ISGTLLVAAT LLTGIAGLLKRSLTPASLFLCALAVSMCH SMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
m738.pep	ISGTLLVAAT LLTGIAGLLKRPLTPASLFLICTLAVSMCH SMLEYPLWYVYFLIPFGLML					
g738	ISGTLLVAAT LLTGIAGLLKRSLTPASLFLCALAVSMCH SMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
m738.pep	FLSPAESDGI AFKKAANLG ILTASAAIFAGLLHLDWYTYRLVNAFSPAT DDSAKTLNRK					
g738	FLSPAESDGI AFKKAANLG ILTASAAIFAGLLHLDWYTYRLVNSFSPAADDSAKTLNRK					
	430	440	450	460	470	480
m738.pep	FLSPAESDGI AFKKAANLG ILTASAAIFAGLLHLDWYTYRLVNAFSPAT DDSAKTLNRK					
g738	FLSPAESDGI AFKKAANLG ILTASAAIFAGLLHLDWYTYRLVNSFSPAADDSAKTLNRK					
	430	440	450	460	470	480

1200

	430	440	450	460	470	480
	490	500	510	520	530	540
m738.pep	INELRYISANSEPLSFYADFSLVNFALPEYPETQTWAEELTKSLKYPHRSATYRIALYL					
g738	INELRYISANSEPLSFYADFSLVNFALPEYPETQTWAEELTKALKYRPYSATYRIALYL					
	490	500	510	520	530	540
	550	560	570	580	590	600
m738.pep	MRQGVKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
g738	MRQGVKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEP					
	550	560	570	580	590	600
m738.pep	KPCKX					
g738	KPCKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2519>:

a738.seq

```

1  ATGCCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACCTGCC
51  GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TTGCGCTCAG GCTGCAACCG TCGCCCGACT TTACCACGA TGCCGCGCGC
151 GCAGCCGGCC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCACCTA TCAGCTTCCT TCTGTTTGA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTACTC GCCGTCAGCG CGTGGGCGCTG
351 CCGGAGCTTG GTCGCACACT ACGGACAAGA ACGCATCGTT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAACA TCATTGTTTA
501 CAGCGGGCAA GCGTAATCG GACACATCGG ACAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGCGATA CTCGCCCGCG CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CCGCCTTGGG TGCAATCTGC CTGATTATGC AGACCGCGGT
651 TTTAGGTTTG GTCAATTGCG GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGATACTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC CGGCATCCGC TACGAAACCG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACCTGCC GCGCCAAATC
901 GAATGGCGCA AAGCCCTCGC CGCCTTCCAG TCCGCCCGGA TATTCGGGCA
951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATACA CGACAACCTC CTCAGCAACT TGTTCACCCA TTCCACAAC
1051 ATCGTTCTCC AACTCCTTGC AGAGATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGTGAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCTGT ATCTGCACAC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCTTCTCG
1251 ACTGATGCTC TTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTAACCG CCTCCGCCG CATATTCGCA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGATGGTTA ACGCCTTTTC
1401 CCCC GCCACT GACGACAGTG CCAAACCCCT CAACCGGAAA ATCAACGAGT
1451 TCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAACT TGCCCGTATG GCGCGCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCGG CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2520; ORF 738.a>:

a738.pep

```

1  MPAETTVSGA HPAAKLPYI LPCFLWIGIV PFTFALRLQP SPDFYHDAAD
51  AAGLIVLLFL TAGKKLFDVK IPPISFLLFA MAAFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHYGQERIV TLFWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR

```

1201

201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR  
 251 TILGIAAAVF LTALFQFSMN TILEFTTGIR YETAVERVAN GGFTDLPRQI  
 301 EWRKALAAFO SAPIFGHGWN SFAQQTFLIN AEQHNHNDNL LSNLFTHSHN  
 351 IVLQLLAEMG ISGTLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH  
 401 SMLEYPLWYV YFLIPFGLML FLSPAASDG IAFKKAANLG ILTASAAIFA  
 451 GLLHLDWYTT RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMSFYADF  
 501 SLVNFALEPY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQKVAEAK  
 551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA  
 601 KPCK\*

a738/m738 98.3% identity in 604 aa overlap

a738.pep	10	20	30	40	50	60
	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALRLQPSPDFYHDAAGLIVLLFL					
m738	10	20	30	40	50	60
	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
a738.pep	70	80	90	100	110	120
	TAGKKLFDVKIPPIISFLLFAMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
m738	70	80	90	100	110	120
	TAGKKLFDVKIPAIISFLLFAMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
a738.pep	130	140	150	160	170	180
	VAHYGQERIVTLFAWSLLIGSLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
m738	130	140	150	160	170	180
	VAHFGQERIVTLFAWSLLIGSLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
a738.pep	190	200	210	220	230	240
	NLGHYLMWGILAAAYLNGQRKIPPALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
m738	190	200	210	220	230	240
	NLGHYLMWGILAAAYLNGQRKIPALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
a738.pep	250	260	270	280	290	300
	YFRSDKSNRRRTILGIAAAVF LTALFQFSMNTILEFTTGIRYETAVERVANGGFTDLPRQI					
m738	250	260	270	280	290	300
	YFRSDKSNRRRTMLGIAAAVF LTALFQFSMNTILEFTTGIRYETAVERVANGGFTDLPRQI					
a738.pep	310	320	330	340	350	360
	EWRKALAAFO SAPIFGHGWN SFAQQTFLINAEQHNHNDNL LSNLFTHSHNIVLQLLAEMG					
m738	310	320	330	340	350	360
	EWNKALAAFO SAPIFGHGWN SFAQQTFLINAEQHNHNDNL LSNLFTHSHNIVLQLLAEMG					
a738.pep	370	380	390	400	410	420
	ISGTLVAATLLTGIAGLLKRLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
m738	370	380	390	400	410	420
	ISGTLVAATLLTGIAGLLKRLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
a738.pep	430	440	450	460	470	480
	FLSPAASDGIAFKKAANLGILTASAAIFAGLLHLDWYTRMVNAFSPATDDSAKTLNRK					
m738	430	440	450	460	470	480
	FLSPAASDGIAFKKAANLGILTASAAIFAGLLHLDWYTRLVNAFSPATDDSAKTLNRK					
a738.pep	490	500	510	520	530	540
	INELRYISANSPMSFYADFSLVNFALEPYPETQTWAEATLKSLKYRPHSATYRIALYL					
m738	490	500	510	520	530	540
	INELRYISANSPMSFYADFSLVNFALEPYPETQTWAEATLKSLKYRPHSATYRIALYL					

1202

	550	560	570	580	590	600
a738.pep	MRQ GKVAEAKQWMRATQSYYPYLM	PRYADEIRKLPVWAPLLPELLK	DCKAF	AAAPGH	PEA	
m738	MRQ GKVAEAKQWMRATQSYYPYLM	PRYADEIRKLPVWAPLLPELLK	DCKAF	AAAPGH	PEA	
	550	560	570	580	590	600

a738.pep	KPCKX
m738	KPCKX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2521>:

g739.seq

```

1   ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGGCGCGTA TTGCTCATCT GTATCACC GC CATCGGCGCA TTGGCAGTAG
101 GCATCGTCAG CACATTC AAC CCGAACGGCG ACAAACCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGCCGTCGGA CAAGATGCCG CCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGAAG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCAAGAA AAACCGGGTc AAACCGCGCC CTTCGGATGC
351 GGCCCGGGCA GCGGATTCGT TAACCGGCAC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGCCCCCA TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACAA ACCGGACACC CCGAAAAACA
551 CGCCGGCCAA ACCCCATAAA GAGATTCTCG ACAACCTCTT TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2522; ORF 739>:

g739.pep

```

1   MAKKENKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTE
51  PQHTDSPRET EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSGLP
101 SPAAPKKNRVKPRPSDAARAADSLTGTGTQAENTLKETPVLPNTNAPHPEP
151 RKETPEKQAQPKETPKEKETPKENHTKPDTPKNTPAKPHKEILDNLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2523>:

m739.seq

```

1   ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGGCGCGTA TTGCTCATCT GTATCACC GC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTC AAC CCGAACGGCG ACAAACCCT TCAAGCCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CGCCCAAGA
501 AAACCATACC AAACCGGACA CCGCAAAA CACGCCGCC AAACCCATA
551 AAGAAATTCT CGACAACTC TTC

```

This corresponds to the amino acid sequence <SEQ ID 2524; ORF 739>:

m739.pep

```

1   MAKKENKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAE
51  PQHTDSPRET EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDES GSGLP
101 SPAAPKKNRVKQFADTAQTDROPDDAGTQAENTLKETPVLPNTNVPREPEP
151 RKETPEKQAQPKETPKENHTKPDTPKNTPPKPHKEILDKL F

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 739 shows 86.3% identity over a 197 aa overlap with a predicted ORF (ORF739.a) from *N. gonorrhoeae*:

m739/g739

1203

```

      10      20      30      40      50      60
m739.pep  MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAE PQHTDSPRET
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g739      MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTE PQHTDSPRET
          10      20      30      40      50      60

      70      80      90      100     110     120
m739.pep  EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g739      EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSLPSPAAPKKNRVKPRPSDAARA
          70      80      90      100     110     120

      130     140     150     160     170
m739.pep  DRQPDAGTQAENTLKETPVLPNTVPRPEPRKETPEKQAQPKETPK-----NHTKPD
          :  : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g739      ADSLTGTGTAENTLKETPVLPNTNAPHPEPRKETPEKQAQPKETPKETPKENHTKPD
          130     140     150     160     170     180

      180     190
m739.pep  PKNTPPKPHKEILDKLF
          ||||| |||||:|||||
g739      PKNTPAKPHKEILDNLF
          190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

```

a739.seq
1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCTCCTCAT
251 CCGCACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACAA GCTGAAAACA
401 CACTCAAAGA AACCCTCGTA CTGCCACAA ACGTCCCCCG TCCCGAACC
451 CGAAAAGAAA CACCCGAAA ACAGGCACAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAACA
551 CGCCGCCTAA ACCCATATAA GAAATTCTCG ACAACCTCTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

```

a739.pep
1  MAKKPNKPFRLTPKLLIRAV LLICITAIGA LAIGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH ASSSAPAQPD GTDESGSLP
101 SPAAPKKNRV KPQADTAQT DRQPDAGAQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAQ PKETPKEKET PKENHTKPD PKNTPPKPHK EILDNLF*

```

a739/m739 93.9% identity in 197 aa overlap

```

      10      20      30      40      50      60
a739.pep  MAKKPNKPFRLTPKLLIRAVLLICITAIGALAIGIVSTFNPNGDKTLQTE PQHTDSPRET
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m739      MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAE PQHTDSPRET
          10      20      30      40      50      60

      70      80      90      100     110     120
a739.pep  EFWLPNGVVGQDAAQPEHHHASSSAPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m739      EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT
          70      80      90      100     110     120

      130     140     150     160     170     180
a739.pep  DRQPDAGAQ AENTLKETPVLPNTVPRPEPRKETPEKQAQPKETPKETPKENHTKPD
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m739      DRQPDAGTQAENTLKETPVLPNTVPRPEPRKETPEKQAQPKETPK-----ENHTKPD
          130     140     150     160     170

```

1204

```

              190
a739.pep      PKNTPPKPKHKEILDNLFx
              |||||
m739          PKNTPPKPKHKEILDKLF
              180      190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2527>:

```

g740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTC GCCGTCTGCC TCATCCCCTT
51 GgcgACGCTT GCCGTTTTCG CCGCCAATcc gcCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTAAa
151 ttcgtgctCT TTGAAACCAT CAAGCATCAT CTTAaacaag gGTTTGATT
201 GAAACgtcaa ACCATGTTTC TGTTATTCC GATTGTTTG CTGGTTGTGT
251 ATTTGTTCCA CTATTTCCGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2528; ORF 740.ng>:

```

g740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQGFDLKRQ TMLFIFIPLV LVVYLPHYFG AF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2529>:

```

m740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GCCGTCTGCC TCATCCCCTT
51 GCGGACGCTT GCCGTTTTCG CCGCCAATCC GCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTAAa
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTTATTCC GATTATTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2530; ORF 740>:

```

m740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQGFDLKRQ TMLFIFIPLV LVVYLPHYFG AF*

```

m740/g740 93.5% identity in 92 aa overlap

```

              10      20      30      40      50      60
m740.pep      MSRNLLVRWLA VCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK FVLFDTIKHH
              |||||
g740          MSRNLLVRWLA VCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK FVLFDTIKHH
              10      20      30      40      50      60

              70      80      90
m740.pep      LKQGFDLKRQ TMLFIFIPLV LVVYLPHYFG AFX
              |||
g740          LKQGFDLKRQ TMLFIFIPLV LVVYLPHYFG AFX
              70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2531>:

```

a740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GTCGTCTGCC TGATACCCTT
51 GCGGACGCTT GCCGTTTTCG CCGCCAATCC GCCGAAGAC AAACCCAGC
101 ATCTGATTAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTCAAA
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTTATTCC GATTATTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2532; ORF 740.a>:

```

a740.pep
1  MSRNLLVRWL VVCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQGFDLKRQ TMLFIFIPLV LVVYLPHYFG AF*

```

a740/m740 97.8% identity in 92 aa overlap

```

              10      20      30      40      50      60

```



1205

```

a740.pep  MSRNLLVRWLVVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFDTIKHH
m740      MSRNLLVRWLVVCLIPLATLAVFAANPPEDKLOHLINGIILACEATFLFKFVLFDTIKHH
           10      20      30      40      50      60

           70      80      90
a740.pep  LKQEFDLKRQTMLLFPIILLIVYLFHYFGAFX
m740      LKQEFDLKRQTMLLFPIILLIVYLFHYFGAFX
           70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1   GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCCG GCCCTGATTG
51  TGACCGCCTG CAGCAGCGGA GGGGCGGAGG CGGTGGTGTC GCCGCCGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAACCG CGCCGCTCGA CCATAAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCGCC AAAACGGAAAC
201 ACTGACCCCTG TCGGCACAAG GTGCGGAAAA AACTTTCAAA GCCGCGCGCA
251 AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TGCAAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAAAATAT ACAAACAGGA TCACTCCGcc gtcgtTgcCC
401 TacgGATTGA AAAAATCAAC AACCCCGACA AAATCGACAG CCTGATAAAC
451 CAACGCTCCT TCCTTGTCAG CGATTTGGGC GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGGCAAAG CCGAGTATCA CGGCAAAGCA TTCAGCTCCG
551 ACGATGCCGA CGGAAACTG ACCTATACCA TAGATTTCGC CGCCAACAG
601 GGACACGGCA AAATCGAACA CCTGAAACA CCGAGCAGA ATGTTGAGCT
651 TGCCTCCGCC GAACTCAAAG CAGATGAAAA ATCACACGCC GTCATTTGG
701 GCGACACGCG CTACGGCGGC GAAGAGAAAG GCACTTACCG CCTCGCCCTT
751 TTCGGCGACC GCGCCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
801 GAAAAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1   VNRTTFCCLS LTAGPDSDDL QRRGGGGGV AADIGTGLAD ALTAPLDHKD
51  KGLKSLTLEA SIPQNGTLTL SAQGAETFK AGGKDNSLNT GKLNKDKISR
101 FDFVQKIEVD GQTITLASGE FQIYKQDHS VVALRIEKN NPDKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAKQ
201 GHGKIEHLKT PEQNVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGKEV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1   GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCCGAC ATCGGTGCGG
101 GGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAAGA CAAAGGTTTG
151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
201 GCGGCACAA GGTGCGGAAA AACTTATGG AACCGGTGAC AGCCTCAATA
251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGCGAGCT CATTACCTTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CCTTAACCGC CTTTCAGACC GAGCAAATAC
401 AAGATTCGGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GCGGACATAG CGGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGCGGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGCGCGAA
551 AACTGACCTA CACCATAGAT TTCGCGCGCA AGCAGGAAA CGGCAAAATC
601 GAACATTTGA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
651 CAAGCCGGAT GGAAGGAGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
751 CAGGAAGTTG CCGGCGAGCG GGAAGTGAAA ACCGTAAACG GCATACGCCA
801 TATCGGCCTT GCCGCCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1   VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT APLDHDKDKL
51  QSLTLDQSVR KNEKLKLAAQ GAEKTYGNGD SLNTGKLKND KVSRLFDFIRQ
101 IEVDGQLITL ESGEFQVYKQ SHSALTAFQT EQIQDSEHSG KMLVAKRQFRI

```

1206

151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLTYTID FAAKQGNNGKI  
 201 EHLKSPELNV DLAAADIKPD GKRHAVISGS VLYNQAEKGS YSLGIFGGKA  
 251 QEVAGSAEVK TVNGIRHIGL AAKQ\*

m741/g741 61.4% identity in 280 aa overlap

	10	20	30	40	50
m741.pep	VNRTAFCCLSLTT---ALILTACSSGGGGVAAADIGAGLADALTAPLDHKDKGLQSLTLDQ				
g741	VNRTTFCCLSLTTAGPDSRLQQRGGGGVAAADIGTGLADALTAPLDHKDKGLKSLTLEA				
	10	20	30	40	50
	60	70	80	90	100
m741.pep	SVRNEKELKLAQAQAEKTY---GNGDSLNTGKLNKDKVSRFDFIRQIEVDGQLITLESGE				
g741	SIPQNGTTLTSAQGAEKTFKAGGKDNSLNTGKLNKDKISRFDVQKIEVDGQTITLASGE				
	70	80	90	100	110
	120	130	140	150	160
m741.pep	FQVYKQSHSALTAFQTEQIQDSEHSGKMKVAKRQFRIGDIAGEHTSFDKLPEGGRATYRG				
g741	FQIYKQDHSASVALRIEKNPNPKIDSLINQSRFLVSDLGGEHTAFNQLPDG-KAEYHGK				
	130	140	150	160	170
	180	190	200	210	220
m741.pep	AFGSDDAGGKLTYTIDFAAQQNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYN				
g741	AFSSDDADGKLTYTIDFAAQQGHGKIEHLKTPEQNVELASAEKKADEKSHAVILGDTRYG				
	180	190	200	210	220
	240	250	260	270	
m741.pep	QAEKGSYSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAQKQX				
g741	GEEKGTYRLALFGDRAQEIAGSATVKIGEKVHEIGIADKQX				
	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2537>:

a741.seq

1	GTGAACCGAA	CTGCCTTCTG	CTGCCTTTCT	TTGACCGCCG	CCCTGATTCT
51	GACCGCCTGC	AGCAGCGGAG	GCGGCGGTGT	CGCCGCCGAC	ATCGGCGCGG
101	TGCTTGCCGA	TGCACTAACC	GCACCGCTCG	ACCATAAAGA	CAAAAGTTTG
151	CAGTCTTTGA	CGCTGGATCA	GTCCGTCAGG	AAAAACGAGA	AACTGAAGCT
201	GGCGGCACAA	GGTGGGAAA	AAACTTATGG	AAACGGCGAC	AGCCTCAATA
251	CGGGCAAATT	GAAGAACGAC	AAGGTCAGCC	GCTTCGACTT	TATCCGTCAA
301	ATCGAAGTGG	ACGGGCAGCT	CATTACCTTG	GAGAGCGGAG	AGTCCAAGT
351	GTACAAACAA	AGCCATTCCG	CCTTAACCGC	CCTTCAGACC	GAGCAAGTAC
401	AAGATTCCGA	GCATTTCAGG	AAGATGGTTG	CGAAACGCCA	GTCAGAATC
451	GGCGATATAG	CGGGTGAACA	TACATCTTTT	GACAAGCTTC	CCGAAGGCGG
501	CAGGGCGACA	TATCGCGGGA	CGGCATTCGG	TTGAGACGAT	GCCAGTGGAA
551	AACTGACCTA	CACCATAGAT	TTGCGCGCCA	AGCAGGGACA	CGGCAAAATC
601	GAACATTTGA	AATCGCCAGA	ACTCAATGTT	GACCTGGCCG	CCTCCGATAT
651	CAAGCCGGAT	AAAAAACGCC	ATGCCGTCAT	CAGCGGTTCC	GTCCCTTTACA
701	ACCAAGCCGA	GAAAGGCAGT	TACTCTCTAG	GCATCTTTGG	CGGGCAAGCC
751	CAGGAAGTTG	CCGGCAGCGC	AGAAGTGGAA	ACCGCAAACG	GCATACGCCA
801	TATCGGTCTT	GCCGCCAAGC	AGTAA		

This corresponds to the amino acid sequence &lt;SEQ ID 2538; ORF 741.a&gt;:

a741.pep

1	VNRTAFCCLS	LTAALILTAC	SSGGGGVAAAD	IGAVLADALT	APLDHKDKSL
51	QSLTLDQSVR	KNEKLKLAQ	GAEKTYGNGD	SLNTGKLNK	KVSRFDFIRQ
101	IEVDGQLITL	ESGEFQVYKQ	SHSALTALQT	EQVDSEHSG	KMVAKRQFRI
151	GDIAGEHTSF	DKLPEGGRAT	YRGTAFGSDD	ASGKLTYTID	FAAKQGHGKI
201	EHLKSPELNV	DLAASDIKPD	KKRHAVISGS	VLYNQAEKGS	YSLGIFGGQA
251	QEVAGSAEVE	TANGIRHIGL	AAKQ*		

a741/m741 95.6% identity in 274 aa overlap

1207

	10	20	30	40	50	60
a741.pep	VNRTAFCCLSLTAALILTACSSGGGGVAADIGAVLADALTAPLDHKDKSLQSLTLDQSVR					
m741	VNRTAFCCLSLTTALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a741.pep	KNEKLKLAQAQAEKTYGNGDSLNTGKLNKDKVSRFDIFIRQIEVDGQLITLESGEFQVYKQ					
m741	KNEKLKLAQAQAEKTYGNGDSLNTGKLNKDKVSRFDIFIRQIEVDGQLITLESGEFQVYKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
a741.pep	SHSALTALQTEQVQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLEGGGRATYRGTAFGSDD					
m741	SHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLEGGGRATYRGTAFGSDD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a741.pep	ASGKLTYYTIDFAAQQGHGKIEHLKSPELNVDLAASDIKPKRRAVIGSVLYNQAEKGS					
m741	AGGKLTYYTIDFAAQQNGKIEHLKSPELNVDLAAADIKPDGKRRAVIGSVLYNQAEKGS					
	190	200	210	220	230	240
	250	260	270			
a741.pep	YSLGIFGGQAQEVAGSAEVETANGIRHIGLAQKX					
m741	YSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAQKX					
	250	260	270			

g742.seq not found yet

g742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

m742.seq

1	ATGTTTACG	GCATTGCCGA	AGCCGATGCG	GGCGACAGCA	GTGTGCTTAC
51	TTTGGGCGGC	ATGTATCAGA	AGAGTAGGGA	GGTTCCTGAT	TTTTCGGGCA
101	TTATTTTGCC	CTGTGAAAT	CAGAAACTG	CCCCGTTTCA	TTCAACGCCT
151	GCCTGCAACC	GGCCTTTGCA	ACTGCCGCGC	AACACTTATT	TGGGGGAGGA
201	TTGGTCGCGG	TAAAGTGCCG	ACAAATACAA	CCTTTTCTCA	GGATTCAAAC
251	ATGTGTTTGA	CAACGGTTGG	CAGCTCAATG	CCGAAGTGTC	TTATACCAAG
301	AATGAATCCG	ATGCCAAGGT	GGGGCAGTTT	TTTCTGAAAA	ACGAATATGC
351	GGCGGGTTTG	TCGGGTGAGG	ATGCCGTAGG	CTTTTGACT	GAAAAAACG
401	AAGTCATCCC	GTTGAGCCG	AAAGATAAGG	CATTGGAGAA	ACTGAAAGCA
451	TATCGTGATG	AAACCGCCAA	GGAATACCGG	GAGCGCAAAG	ACGATTTTGT
501	TAAAAACCGT	TTCGATAATA	CTGCTTTCGA	ACAGTATCGC	AGCCGCCGTG
551	CCGCAGAACG	CAAAGCCGGT	TTTGACAAGT	GTATGAGTGA	CCCTTTCGCG
601	CTGGACTTTA	TCTGTCAAGG	TTCTTGGGGG	GATCCGGGCG	TTGATGCCGA
651	CAAGGCGGAA	TTTGTGATA	AAGCCCTTGC	GAAGGAGGGC	ATCTTTAATA
701	ATGCCGCACA	ACGTTTTCCT	AACAGCCTGT	ATGACTCTTC	CTTTAATCGG
751	AAGGCTACCG	CCAACCGACG	ATACAGTTAT	ATGCCGTTGC	GGCATACCAA
801	AGACGACCGC	CAATGGGGAA	TTAAACTTGA	CCTGACCGGC	ACATATGGGC
851	TGTTTCGGCG	GGAGCATGAT	TTCTTTGTCG	GCTATGCCTA	CGGTGATGAA
901	AAGATACGTT	CGGAATATCT	AGAAATCTAC	GAACGCCGCT	ACAGAGTACG
951	TCCGAATACG	GGGGCAACGC	ACGGCGTGTA	TGCGGGAAGT	TGTCAGGAGG
1001	AGCCGGACCG	CGATTTGTCG	TCTCCTTTGG	TCAGGGGGCA	TAAAGAACCC
1051	GATTGGCAGG	CGTACGATGA	AAAAGGCAAC	CGTACCGTTT	ATGCCGAAGA
1101	ATGCAGGAAC	GCCAAGAAAA	TAAAAACCGA	GCCCAAGCTC	GATGCCGAAG
1151	GCAAGCAGGT	GTATTACTAT	GACGAATACA	GCGGCAGCCG	GACACCGGTA
1201	TATGTCGATG	TATATGAGCT	GGACGAAAAA	GGCAACAAGA	TTCAGGAGAG
1251	CAATCCCGAC	GGCACGCCTG	CCTTTACCGG	TTTTTCCGGT	ACGGTGCCCG
1301	TTTGGAAAAC	CGTCAAAGTG	GCAGACGACC	ATGTTCTTGC	GCTGTATAAC
1351	TACGCCAAAT	ACCTCAACAC	CAACAAAACC	CATTGCGTGA	CTGCCAGCAC
1401	GCGTTTCAAC	GTAACCGGCC	GACTGCACCT	TTTGGGCGGG	CTGCACTACA

```

1451 CGCGCTATGA GACTTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAGGGCGG ATCAGGACCA
1551 TTACACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGACTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCGGC ACAAACATATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTC GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTCCGGTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTCGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAAGT CTTTGGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTTGCC AAAAATTTCA GTGCAGACCC GTACAACTTC AGCAATTTCA
2051 CACCGGTGCA CATATTCGGT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCC AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAACAA
2301 CTTCTACGGA GAGCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2540; ORF 742>:

```

m742.pep
1  MVGIGAEADA GDSSVLTGG MYQKSREVPD FSGIILPCEN QKTAPFSSTP
51  ACNRPLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFDNGW QLNAEVSYTK
101 NESDAKVGQF FLKNEYAAGL SGEDAVGFLT EKNEVIPFEP KDKALEKLKA
151 YRDETAKEYR ERKDDFVKNR FDNATAFEQYR SRRAAERKAG FDKCMSDPFA
201 LDFICQGSWG DPGVDADKAE FVDKALAKEG IFNNAAQRFN NSLYDSSFNH
251 KATANRRYSY MPLRHTKDDR QWGIKLDLTG TYGLFGREHD FVGYAYGDE
301 KIRSEYLEIY ERRYRVRPNT GATHGVYAGS CQEEPdGDLs SPLVRGHKEP
351 DWQAYDEKGN RTVYAEECRN AKKIKTEPKL DAEGKQVYYY DEYSGSRTPV
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKTVMV ADDHVPALYN
451 YAKYLNTNKT HSLTASTRFN VTGRLHLLGG LHYTRYETSQ TKDMPVRYGQ
501 PASDFQTASS IRADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551 FKQDQNDVDS AKTVLPPLVG TNYEVGWKGA FLQGRNLASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGVVVS RGAEFELSGE LNEWDKVFAG
651 YTYNKSRYKN AAEVNAERLA KNSSADPYNF SNFTPVHIFR FGTSFHIPNT
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRTYFENNYN RTRGANNFYG EPRTVSMKLD WQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2541>:

```

a742.seq
1  ATGGTTTACG GCATTGCCGA AGCCGATGCG GCGCACAGCA GTGTGCTTAC
51  TTTGGGCGGC ATGTATCAGA AGAGTAGGGA GGTTCCTGAT TTTTCGGGCA
101 TTATTTTGTG CTGTGAAAAT CAGAAACTG CCCCCTTCAG TTCAACGCCT
151 GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCGCGG TTGAGTGCTG ACAAATACAA CCTTTTCTCA GGTTCAAAC
251 ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGGCAGTTT TTTCTGAAAA ACGAACATGC
351 GCGGGGTTTG TCAGATGAGG ATGCGGTAGG CTTTTTGACC GAAAAAACG
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
451 TATCGTGACG AAACCGCCAA GGAATACCGT GAGCGCAAAG ACGATTTTGT
501 TAAAAACCGT TTCGATAATA CTGCTTTCGA GCAGTACCGC AGCCGCCGTG
551 CCGCAGAACG CAAAGCCGGT TTTGACGAGT GTATGAGTGC CCCTTTTGCG
601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGTG TTGATGCCGA
651 CAAGTCGGAA TTTGTGATA AAGCCCTTGC GAAGGAAGGC ATCTTTAATA
701 ATGCGGCACA ACGTTTTCCT AACAGCCTGT ATGACTCTTC CTTTAATCGG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTGTC GGCATACCAA
801 AGACGACCGC CAATGGGGAA TTAACTTGA CCTGACCGGC ACATATGGGC
851 TGTTCGGGCG GGAGCATGAT TTCTTTGTCG GCTATGCCTA CCGCGATGAA
901 AAGATACGTT CCGAATATCT GGAATCTAC GAACGCCGCC ACAGAGTACG
951 TCCGAATACA GGGGCAACGC ACGGCGTGTA TCGGGGAAGT TGTCAGGGGG
1001 AGCCGGACCG TGATTGTGCT TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAT GCCAAGAAAA TAAAACCGA GCCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAGCCG GACGCCAGTA

```

1201 TATGTCGATG TATATGAACT GGATGAAAAA GGCAATAAGA TTCAGGAGAC  
1251 CAATCCCGAC GGCACGCGTG CCTTTACCGG TTTTCCCGT ACGGTGCCGG  
1301 TTTGGAAAAC CGTCAAAGTG GCCGACGACC ATGTTCTCTG GCTGTATAAC  
1351 TACGCCAAAT ACCTCAACAC CAACAAAACC CATTGCTGA CTGCCGGCAC  
1401 GCGTTTCAAC GTAACCGGCC GACTGCATCT TTTGGGCGGG CTGCACTACA  
1451 CGCGCTATGA AACCTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG  
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAAGGCGG ATCAGGACCA  
1551 TTATACGGCC AAGATGCAAG GTCATAAAT GACGCCCTAT GCAGGCATTA  
1601 CCTATGATT GACACCGCAA CAGAGTATT ACGGAAGTTA TACCAAAATC  
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC  
1701 TTTGGTCCGG ACAAACTATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG  
1751 GACGGCTGAA TGCTTCGTTT GCATGTTTT ACCTCGAACA GAAAAACCGC  
1801 ACGGTCGTCG ATTTTGGCTA TGTCCCAGGA GCAGGCGGCA AGCAGGGGTC  
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG  
1901 AATTCGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAGT CTTTGCGGGT  
1951 TACACCTACA ACAAGAGCCG CTACAAAAC GCCGCCGAAG TCAACGCCGA  
2001 ACGCCTCGCC AAAAACACAG GCGCAGACCC GTACAACTT AGCAATTTCA  
2051 CACCCGTGCA CATATTCCGT TTCGGAACGA GCTTCCATAT ACCGAATACG  
2101 GGGCTGACCG TCGGCGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT  
2151 GTATAACATC AGGAGGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT  
2201 ACGAATTGGG CAAACACGCT AAATTGAGCC TCATCGGTAC GAACTTAAAC  
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAACAA  
2301 CTTCTATGGA GAGCCGCGCA CTGTCAGCAT GAACTGGAT TGGCAGTTTT  
2351 AA

This corresponds to the amino acid sequence <SEQ ID 2542; ORF 742.a>:

a742.pep  
1 MVGIAEADA GDSSVLTLLG MYQKSREVPD FSGIILSCEN QKTAPFSSTP  
51 ACNRPLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFNDGW QLNAEVSYTK  
101 NESDAKVQGF FLKNEHAAGL SDEDAVGFLT EKNEVIPFEP KDKALEKLKA  
151 YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAERKAG FDECMASAPFA  
201 LDFICQGSWG DPGVDADKSE FVDKALAKEG IFNNAQRFP NSLYDSSFNR  
251 KATANRRYSY MPLRHTKDDR QWGIKDLTG TYGLFGREHD FVGYAYGDE  
301 KIRSEYLEIY ERRHRVRPNT GATHGVYAGS CQGEFDGDL SPLVRGHKEP  
351 DWQAYDEKGN RTVYAEERN AKKIKTEPKL DAEGKQVYYY DEYSGSRTPV  
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKTVKV ADDHVPALYN  
451 YAKYLNTNKT HSLTAGTRFN VTGRLHLLGG LHYTRYETSQ TKDMPVRYGQ  
501 PASDFQTASS IKADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI  
551 FKQQDNVDVS AKTVLPPLVG TNYEVGWKGA FLQGRNLASF ALFYLEQKNR  
601 TVVDFGYVPG AGGKQGSFQT VAKPIGVVS RGAEFELSGE LNEDWKVFAG  
651 YTYNKSRYKN AAEVNAERLA KNTGADPNF SNFTPVHIFR FGTSFHIPNT  
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN  
751 GRTYFENNYN RTRGANNFYG EPRTVSMKLD WQF\*

a742/m742 98.5% identity in 783 aa overlap

a742.pep	10	20	30	40	50	60
	MVGIAEADAGDSSVLTLLGMYQKSREVPDFSGIILSCENQKTAPFSSTPACNRPLQLPR					
m742	10	20	30	40	50	60
	MVGIAEADAGDSSVLTLLGMYQKSREVPDFSGIILPCENQKTAPFSSTPACNRPLQLPR					
a742.pep	70	80	90	100	110	120
	NTYLGEDWSRSLSDKYNLFSGFKHVFNDGWQLNAEVSYTKNESDAKVQGFLLKNEHAAGL					
m742	70	80	90	100	110	120
	NTYLGEDWSRSLSDKYNLFSGFKHVFNDGWQLNAEVSYTKNESDAKVQGFLLKNEHAAGL					
a742.pep	130	140	150	160	170	180
	SDEDAVGFLTTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR					
m742	130	140	150	160	170	180
	SGEDAVGFLTTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR					
a742.pep	190	200	210	220	230	240
	SRRAERKAGFDECMASAPFALDFICQGSWGDGPGVDADKSEFVDKALAKEGIFNNAQRFP					

1210

```
|||||:|||||:|||||:|||||:|||||:|||||:
m742      SRRAERKAGFDKMSDPFALDFICQGSWGDPGVDADKAEFVDKALAKEGIFNNAQRFP
          190      200      210      220      230      240

          250      260      270      280      290      300
a742.pep  NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKDLTGTYGLFGREHDFVGYAYGDE
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      NSLYDSSFNRKATANRRYSYMLRHTKDDRQWGIKDLTGTYGLFGREHDFVGYAYGDE
          250      260      270      280      290      300

          310      320      330      340      350      360
a742.pep  KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGEPDGDLSSPLVRGHKEPDWQAYDEKGN
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      KIRSEYLEIYERRVRPNTGATHGVYAGSCQGEPDGDLSSPLVRGHKEPDWQAYDEKGN
          310      320      330      340      350      360

          370      380      390      400      410      420
a742.pep  RTVYAEECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTFVYVDVYELDEKGNKIQTNP
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      RTVYAEECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTFVYVDVYELDEKGNKIQTNP
          370      380      390      400      410      420

          430      440      450      460      470      480
a742.pep  GTPAFTGFSGTVPVWKTVKVADHDHPALYNYAKYLNTNKTSLTAGTRFNVGTGRLHLLGG
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      GTPAFTGFSGTVPVWKTVKVADHDHPALYNYAKYLNTNKTSLTAGTRFNVGTGRLHLLGG
          430      440      450      460      470      480

          490      500      510      520      530      540
a742.pep  LHYTRYETSQTKDMPVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLTPQ
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      LHYTRYETSQTKDMPVRYGQPASDFQTASSIRADQDHYTAKMQGHKLTPYAGITYDLTPQ
          490      500      510      520      530      540

          550      560      570      580      590      600
a742.pep  QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLQGRNLNASFALFYLEQKNR
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLQGRNLNASFALFYLEQKNR
          550      560      570      580      590      600

          610      620      630      640      650      660
a742.pep  TVVDFGYVPGAGGKQGSFQTVAKPIGKVVSARGAEFELSGELNEDWKVFAGYTYNKSRYKN
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      TVVDFGYVPGAGGKQGSFQTVAKPIGKVVSARGAEFELSGELNEDWKVFAGYTYNKSRYKN
          610      620      630      640      650      660

          670      680      690      700      710      720
a742.pep  AAEVNAERLAKNTGADPYNFSNFTPVHIFREGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      AAEVNAERLAKNSSADPYNFSNFTPVHIFREGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
          670      680      690      700      710      720

          730      740      750      760      770      780
a742.pep  RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD
          |||||:|||||:|||||:|||||:|||||:|||||:
m742      RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD
          730      740      750      760      770      780

a742.pep  WQFX
          |||
m742      WQFX
```

a742/ p25184

sp|P25184|PUPA\_PSEPU

FERRIC-PSEUDOBACTIN

358

RECEPTOR

PRECURSOR

&gt;gi|94923|pir||S15169

1211

ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi|45723 (X56605)  
 pseudobactin uptake protein [*Pseudomonas putida*] Length = 819  
 Score = 152 bits (381), Expect = 6e-36  
 Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADHDV-PALYNYAKYLNTNKTHTSLTAGTRFNVVTGRLHLLGGLHYTRYETSQTKDM 494  
 +T K DD + P + +Y +N+ +RFN+T LHL+ G + Y

Sbjct: 511 QTPKPGDDEIIPGI----QYNISNRQSGYFVASRFNLTDLHLLILGARASNYRFDYAL-- 564

Query: 495 PVRVYQGPASDFQTASSIKADQDHYTAKMQGHKLTTPYAGITYDLTPQQSIYGSYTKIFKQQ 554  
 R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q

Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPQ 609

Query: 555 DNVDVSAKTVLPPLVGTNYEVGWKGAFLLQGRNLNASFALFYLEQKNRTVVDFGYVPGAGGK 614  
 +NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG

Sbjct: 610 NNVDITGKP-LDPEVGKKNYELGWKGEFLEGRNLNANIALYMKRDNLAESTNEVVPDGGGL 668

Query: 615 QGSFQTVAKPIGVVSRGAEFELSGELNEDWKVFAGYTYNKSRYKNAEVAERLAKNTG 674  
 S + + +G + ELSGE+ W VF GY++ ++

Sbjct: 669 IAS-----RAVDGAETKGVDELSEVLPGWNVFTGYSHTRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFRFGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IROGGYGL 727  
 AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +

Sbjct: 708 ADGKRLTPQLPMDTFRFWNTYRLPGEWELTLGGGVNWNKSTLNFARYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTGANNFYGEPRTVSMKLDWQF 783  
 RY + + +L N+ + Y Y G+ YG PR ++ L + F

Sbjct: 768 TSLMARYRINESLAATLNVNIFDKKY----YAGMAGSYGHYGAPRNATVTLRDYF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq  
 1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC  
 51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA  
 101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTTGTTG  
 151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCCGC  
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA  
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA  
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTTCAG GCTTGCAGAC  
 351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA  
 401 TGACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG  
 451 TCTCCGAGTA CCGATTGGC GGTATTATGAC CATATTGAAG TTGTACGGGG  
 501 TGCAACGGGG TTGACCAAT CCAATTCAGA GCCGGGAGGA ACCGTCAATT  
 551 TGATCCGTAA GTGA

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep  
 1 MNQNHFSLSKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL  
 51 GKTEKTRSYT IDRMSTATGM RIAGKDTFQS VSVITRSRLD DKAHVHLEEA  
 101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGMTVNVAG RSGYTAKIDV  
 151 SPSTD LAVYD HIEVVRGATG LTQSNSEPGG TVNLIRK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq  
 1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC  
 51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA  
 101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTGCG  
 151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCCGC  
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA  
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA  
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTTCAG GCTTGCAGAC

1212

```

351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TTACCGTCAA TGTGTCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGGC GGTATTGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGTGGA ACCGTCAATT
551 TGATCCGTAA GCGA

```

This corresponds to the amino acid sequence <SEQ ID 2546; ORF 743.a>:

```

a743.pep
  1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALS
  51 GKTEKTRSYT IDRMSTATGM RIAGKDTPOS VSVITRSLD DKAVHTLEEA
 101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGITVNVAG RSGYTAKIDV
 151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRKR

```

a743/m743 98.9% identity in 187 aa overlap

a743.pep	10	20	30	40	50	60
	MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALS	SGKTEKTRSYT				
m743	10	20	30	40	50	60
	MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALLGKTEKTRSYT					
a743.pep	70	80	90	100	110	120
	IDRMSTATGMRIAGKDTPOSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRDSGLQTRFL					
m743	70	80	90	100	110	120
	IDRMSTATGMRIAGKDTPOSVSVITRSLDDKAVHTLEEAMKNTTGVNVVRDSGLQTRFL					
a743.pep	130	140	150	160	170	180
	SRGFYIDQIGEDGITVNVVAGRSGYTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG					
m743	130	140	150	160	170	180
	SRGFYIDQIGEDGMTVNVVAGRSGYTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG					
a743.pep						TVNLIRKR
m743						TVNLIRKX

g744.seq not found yet

g744.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2547>:

```

m744.seq
  1 ATGAAACCGT TAAAAACATT AGAATTTGGA TTTGTGGATG CTGCAAACTA
  51 CAGAAGAAGA GAAAATAAAG ATTTATTAA CCGAATATTT GTAAAAGGAG
 101 AATATTTGGA TGAATTATGT GAACCAAATA TTTCTTTTT AATCGGAGAA
 151 AAGGGAAGTG GAAAGACAGC ATATGCTGTT TATTTAAC TAACCTCTA
 201 TAAAAACATA CATGCCACTA CTAAGTTTGT TCGTGAAACC GATTATTCAT
 251 AATTTATTCA GCTAAAGAAA GCAAGACACT TAACTGTTTC AGATTTTACA
 301 AGTATTTGGA AAGTCATTTT ATATCTGTTG ATATCAAATC AAATCAAATG
 351 TAAAGAAAAC GGAATATTAT CTTCATATTT TAATAAATTT AAAGCCTTAG
 401 ATGAGGCTAT AAATGAATAT TATTATGGCG CTTTGTATCC GGAAATTGTA
 451 CAAGCAATAA CTTTAATAGA AAATTCAAAA GAAGCTGCGG AAATGATTTT
 501 TGGAAAAATTT GTTAAACTAG GTGAAGAGGA ATCCCAACAA ATAACCTTTA
 551 CAGAAAGTAA ATTCCAAGCA AATTTAGGTT TTATTGAAAG AAAATTTAAA
 601 GATGCTTTAT CTCAGTTAAA GCTAAAAGAT AATCATATTT TGTTTATTGA
 651 TGGGATAGAT ATTAGACCAT CACAGATTCC ATTTGATGAA TATCATGAGT
 701 GTGTAAAAGG TCTTGCTAAC GCCATATGGA TGTAAATAA TGATATCTTC
 751 CCTTCCATTA AAGATAGTAA GGAAGAGGAT AGAGTTGTGT TATTGATTAG
 801 ACCTGATATC TTTGATTCAT TAGGTTTACA AAATCAAAT ACCAACTTC
 851 AAGATAATTC AGTATTTTGA GACTGGAGGA CGGATTATAA ATCTTATAGA
 901 AGTTCAAAGA TTTTGGCGT TTTTGTATCT CTTTGTAGAA CCCAGCAAGA
 951 AAAACAAAGAT AGTTTAGAAA AAGGCAACTC ATGGGATTAT TATTTTCCAT
 1001 GGAATGCTCC TAATTTACAT GATGAGTATA AAAATTTAAC TTCATTTATT
 1051 AGCTTCCATA GAAAATCGTA TTATCGACCT CGCGATATTC TTCAGATGCT
 1101 TACTTTGCTA CAAAAAATA AGAAAAGTAA GGAAGATTAT GTCGTAGCAG
 1151 AAGATTTTGA TAATACTTCT TTTCAAAGAG AATACTCGAT ATATTACTT
 1201 GGTGAAATCA AAGATCATCT TTTGTTTTAT TATAGTCAA GTGATTATCA
 1251 AAATTCCTG AAATTTTGT AATTTTAAA CGGGAAGAT AGATTTAAT

```



1213

```

1301 ATAGTGATTT TTTAAAAGCA TTTGAACGTT TGAAAAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTATTTT GACTTGAATG TTATTGCTTA TTTAGATAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCTTTA AAGATAGAAA TTATGCAAAAT
1501 ATTTCTCCTA AAATAAAAC TGAACTGAA TATTTAATAT TTTCAGGATT
1551 ATCAAAAGCC CTTGATGTTG GTACTCCATT TAAGAACAAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

```

m744.pep
1  MKPLKTLEFG FVDAANYRRR ENKDLFNRIK VKGEYLDELK EPNISFLIGE
51  KGTGKTAYAV YLTNNFYKNI HATTKFVRET DYSKFIQLKK ARHLTVSDFT
101 SIWKVILYLL ISNQIKCKEN GILSSIFNKF KALDEAINEY YGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEESQQ ITFTESKFOA NLGFIERKFK
201 DALSQLKLKD NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVVLLIRPDI FDSLGLQNNQ TKLQDNSVFL DWRTDYKSYR
301 SSKIFGVFDH LLRTQQEKQD SLEKGNWDY YFPWNAPNLH DEYKNLTSFI
351 SFLRKSYYRP RDILQMLTLL QKNKSKEDY VVAEDFDNTS FQREYSIYLL
401 GEIKDHLLFY YSQSDYQNF LKFEFLNGKD RFKYSDFLKA FERLKKHLQT
451 TSVEIPKFMS TANEFLQFLF DLNVIAAYLDN PEDETKPYIH WCFKDRNYAN
501 ISPKIKTETE YLIFSGLSKA LDVGTPEKNK Q*

```

g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

```

m745.seq
1  ATGTTTTGGC AACTGACCGT TGTTCAGTA ACCGCCGTCA TGCACTGGG
51  GACAATATTC ATCAATAAGA AAACCTCAAA GCAAAAGGCG ACATTAGATG
101 TTATTTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
151 ATTCGCCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAAGAGA
251 GAGGGCATT ACTTACCGTA ATCAATCGGC ACGAGTTTGA TCGTGCGCA
301 ATCAACTCGG GAGTATTGGA TGAGGATTGG TTAAACGGC TGCATTGCAC
351 CAACCTCATA AAATTGTGGA ATGCAGTTTC GCCTCTTGTT ATGAAAATAC
401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTGGTT
451 GCATTATGGA AAGCAAACCC CCTAAAGGCA TCTGATTGTG GA

```

This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

```

m745.pep
1  MFQQLTVVSV TAVIALGTIF INKKTSKOKA TLDVILNDYQ DAQFVEADNH
51  ISPYIRGTAV DDNNARIDLY EIYQNKGGQW EKERGHLLTV INRHEFYACA
101 INSGVLDEDL FKRLHCTNFI KLWNAVSPV MKIREEERKD TIFRELEILV
151 ALWKANPLKA SDL*

```

a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

```

g746.seq
1  ATGTCCGAAA ACAACAAAA CGAAGTCCTG ACCGGTTACG AACAGCTGAA
51  ACGGCGCAAC CGCCGCCGCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCACTCAGTT CCGATCCTGC CGACAGCAAT
151 CCCGCACCGC AGGCCGGCGA AACCAGCGCA ACGGAAAGCC AAACGGCAAA
201 CACGGCAACA ACCCTGCCT TGAATCCGC CGCGAAAAC GGGGAAACCG
251 CCGCCGACAA ACCGCAGGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
301 GACAGCGAAA TCAGCGAGCC TGAACACGTA GCGCGCCGC TGGTGCTGAT
351 TAACGACCGG CTCGAAGACA GCAACATCAA AGGTTTGGA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAAACCG AACCAGAGCA GGCAAAACAA
451 CGCGCTGCCG AAAAAGTGTG GGCAACTGCC GACAGTACGG ATACGGTAGC
501 GGTGAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACTGCCGA AGCCAAGCCC AAAGCCAAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACCAGAAAC TGCTGCCGAA AAAACCAAAC CGGATACGGC
651 AAAATCCGAC AGCGCGGTAA AAGAAGCGAA AAAAGCCGAC AAGGCTGAAG
701 GCAAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAAA ACACGAAACG

```

1214

```

751 GCGCAAAAA CCGACAAAGC GGACAAAACC AAAACCGCCG AGAAGGAAAA
801 ATCCGGCAAG GCGGGCAAAA AAGCCGCCAT TCAGGCAGGT TATGCCGAAA
851 AAGAACGCGC CTTGAGCCTC CAGCGCAAAA TGAAGCGCGC GGGTATCGAT
901 TCGACCATCA CCGAAATCAT GACCGACAAC GGCAAGTTT ACCGCGTCAA
951 ATCAAGCAAC TATAAAACG CAAGGGATGC CGAACGCGAT TTGAACAAAC
1001 TCGCGTGCA CCGCATCGCC GGCCAGGTAA CGAATGAATA G

```

This corresponds to the amino acid sequence <SEQ ID 2552; ORF 746.ng>:

```

g746.pep
1 MSENKQNEVL TGYEQLKRRN RRLVTASSL VAASCILLAA ALSSDPADSN
51 PAPQAGETGA TESQTANTAQ TPALKSAAEN GETAADKPQD LAGEDKPSAA
101 DSEISEPENV GAPLVLINDR LEDSNIKGLE ESEKLQQAET AKTEPKQAKQ
151 RAAEKVSATA DSTDTVAVEK PKRTAEKPKQ KAERTAEAKP KAKETKTAEK
201 VADKPKTAEE KTKPDTAKSD SAVKEAKKAD KAEGKKTAEK DRSDGKKHET
251 AQTKDKADKT KTAKEKESGK AGKKAATQAG YAEKERALS LQRKMKAAAGID
301 STITEIMTDN GKVYRVKSSN YKNARDAERD LNKLRVHGIA GQVTNE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2553>:

```

m746.seq
1 ATGTCGGAAA ACAAAACAAA CGAAGTCCTG AGCGGTTACG AACAACCTCAA
51 ACGGCGCAAC CGCCGCCGCC TCCTAACGGC AAGTTGCCGT GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCCCTCAGTT CCGGCCCTGC CGAACAGACT
151 GCCGGCGGAA CAAGCGGCGT AGAAAACAAA GCGGCAGGTG CGGCACAAAC
201 CCCTGCCTTG AAATCCGCGC CCGACAAACC GCAGGACTTG GCAGGCGAAG
251 ACAAGCCTTC TGCCGCCGAC AGCGAAATCA GCGAGCCTGA AAACGTAGGC
301 GCGCCGCTGG TGCTGATTAA CGAGCGCCTC GAAGACAGCA ACATCAAAGG
351 TTTGGAAGCA TCCGAGAAAC TGCAACAGGC AGAAACCGCC AAAACCGCAC
401 CGAAGCAGGC AAAACAACGC GCTGCCGAAA AAGTGCCGGC AACTGCCGAC
451 AGTACGGATA CGGTAGCGGT TGAAAAACCG AAACGCACTG CCGAAACAAA
501 ACCGCAAAAA GCGGAACGCA CTGCCAAAGC CAAGCCCAAA GCCAAAGAAA
551 CCAAAACCGC CGAAAAAGTT GCCGACAAAC CGAAAACCTG CGCCGAAAAA
601 ACCAAACCGG ATACGGCAAA ATCCGACAGC GCGGTAAAG AAGCGAAAAA
651 AGCCGACAAG GCTGAAAGCA AAAAAACAGC CGAAAAAGAC CGTTCGGACG
701 GCAAAAAACA CGAAACGGCA CAAAAACCG ACARAAGCGGA CAAGACCAAA
751 ACCGCCGAGA AGGAAAAATC CGGTAAAAA GCCGCCATTC AGGCAGGTTA
801 TGCCGAAAAA GAACGCGCCT TAAGCCTCCA GCGCAAAATG AAGCGCGCGG
851 GTATCGATTG GACCATCACC GAAATTATGA CCGACAACGG CAAAGTTTAC
901 CGCGTCAAAAT CAAGCAACTA TAAAAACGCA AGGGATGCCG AACGCGATT
951 GAACAAATTG CGGTACACG GTATCGCCGG TCAGGTAACG AATGAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2554; ORF 746>:

```

m746.pep
1 MSENKQNEVL SGYEQLKRRN RRLVTASCL VAASCILLAA ALSSGPAEQT
51 AGETSGVENK AAGAAQTPAL KSAADKPQDL AGEDKPSAAD SEISEPENVG
101 APLVLINERL EDSNIGLEA SEKLQQAETA KTAPEKQAKR AAEKVPATAD
151 STDTVAVEKP KRTAETKPKQ AERTAKAKPK AKETKTAEKV ADKPKTAAEK
201 TKPDTAKSDS AVKEAKKADK AESKKTAEKD RSDGKKHETA QKTDKADKTK
251 TAEKEKSGKK AAIQAGYAEK ERALSQKRM KAAGIDSTIT EIMTDNGKVV
301 RVKSSNYKNA RDAERDLNKL RVHGIAGQVT NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 746 shows 89.9% identity over a 346 aa overlap with a predicted ORF (ORF 746) from *N. gonorrhoeae*:

```

m746/g746 89.9% identity in 346 aa overlap

          10      20      30      40      50
m746.pep  MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQT----AGETSG
          |||
g746       MSENKQNEVL TGYEQLKRRNRRRLVTASSLVAASCILLAAALSSDPADSNPAPQAGETGA
          10      20      30      40      50      60

          60      70      80      90     100     109
m746.pep  VENKAAGAAQTPALKSAA-----DKPQDLAGEDKPSAADSEISEPENVGAPLVLINER
          :|
g746       TESQTANTAQTPALKSAAENGETAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDR
          70      80      90     100     110     120

```

1215

```

      110      120      130      140      150      160      169
m746.pep  LEDSNIKGLEASEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPQ
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
g746      LEDSNIKGLEESEKLQQAETAKTEPKQAKQRAAEKVSATADSTDTVAVEKPKRTAEFPKPQ
          130      140      150      160      170      180

      170      180      190      200      210      220      229
m746.pep  KAERTAKAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEK
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
g746      KAERTAEAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAEGKKTAEK
          190      200      210      220      230      240

      230      240      250      260      270      280
m746.pep  DRSDGKKHETAQKTDKADKTKTAEKEKSGK---KAAIQAGYAEKERALS LQRMKAAGID
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
g746      DRSDGKKHETAQKTDKADKTKTAEKEKSGKAGKAAIQAGYAEKERALS LQRMKAAGID
          250      260      270      280      290      300

      290      300      310      320      330
m746.pep  STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
g746      STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          310      320      330      340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2555>:

```

a746.seq
1  ATGTCCGAAA ACAAACAAAA CGAAGTCCTG AGCGGTTACG AACAACTCAA
51  ACGGCGCAAC CGCGCCCGCC TCGTAACGGC AAGTTGCCTG GTTGCCCGCT
101 CCTGCATCCT GCTGGCAGCC GCCCTCAGTT CCGGCCCTGC CGAACAGACT
151 GCCGGCGAAA CAAGCGGCGT AGAAAAACAA GCGGCAGGTG CGGCACAAAC
201 CCCTGCCTTG AAATCCGCGC CGGACAAACC GCAGGACTTG GCAGGCGAAG
251 ACAAGCCTTC TGCCGCCGAC AGCGAAATCA GCGAGCCTGA AAACGTAGGC
301 GCGCCGCTGG TGCTGATTAA CGACCGCCTC GAAGACAGCA ACATCAAAGG
351 TTTGGAAGCA TCCGAGAAAC TGCAACAGGC AGAAACCGCC AAAACCGCAC
401 CGAAGCAGGC AAAACAACGC GGTGCCGAAA AAGTGCCGGC AACTGCCGAC
451 AGTACGGATA CGGTAGCGGT TGAAAAACCG AAACGCACTG CCGAAACAAA
501 ACCGCAAAAA GCGGAACGCA CTGCCAAAGC CAAGCCCAAA GCCAAAGAAA
551 CCAAAACCGC CGAAAAAGTT GCCGACAAAC CGAAAACGTC CGCCGAAAAA
601 ACCAAACCGG ATACGGCAAA ATCCGACAGC GCGGTAAAAG AAGCGAAAAA
651 AGCCGACAAG GCTGAAAGCA AAAAAACAGC CGAAAAAGAC CGTTCGGACG
701 CCAAAAAACA CGAAACGGCA CAAAAACCGC ACAAAGCGGA CAAGACCAAA
751 ACCGCCGAGA AGGAAAAATC CGGTAAAAAA GCCGCCATTG AGGCAGGTTA
801 TGCCGAAAAA GAACGCGCCT TAAGCCTCCA GCGCAAAATG AAGGCGGCGG
851 GTATCGATTG GACCATCACC GAAATTATGA CCGACAACGG CAAAGTTTAC
901 CGCGTCAAAT CAAGCAACTA TAAAAACGCA AGGGATGCCG AACGCGATTG
951 GAACAAATTG CGCGTACACG GTATCGCCGG TCAGGTAACG AATGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2556; ORF 746.a>:

```

a746.pep
1  MSENKQNEVL SGYEQLKRRN RRLVTASCL VAASCILLAA ALSSGPAEQT
51  AGETSGVENK AAGAAQTPAL KSAADKPQDL AGEDKPSAAD SEISEPENVG
101 APLVLINDRL EDSNIKGLEA SEKLQQAETA KTA PKQAKOR AAEKVPATAD
151 STD TVAVEKP KRTAETKPQK AERTAKAKPK AKETKTAEKV ADKPKTAAEK
201 TKPDTAKSDS AVKEAKKADK AESKKTAEKD RSDGKKHETA QTKDKADKTK
251 TAEKEKSGKK AAIQAGYAEK ERALS LQRM KAAGIDSTIT EIMTDNGKVY
301 RVKSSNYKNA RDAERDLNKL RVHGIAGQVT NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 746 shows 99.7% identity over a 332 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a746/m746: 99.7% identity in 332 aa overlap

```

      10      20      30      40      50      60
a746.pep  MSENKQNEVL SGYEQLKRRN RRLVTASCL VAASCILLAAALSSGPAEQTAGETSGVENK
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
m746      MSENKQNEVL SGYEQLKRRN RRLVTASCL VAASCILLAAALSSGPAEQTAGETSGVENK
          10      20      30      40      50      60

```

1216

	70	80	90	100	110	120
a746.pep	AAGAAQT PALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEA					
m746	AAGAAQT PALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINERLEDSNIKGLEA					
	70	80	90	100	110	120
a746.pep	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPKQAERTAKAKPK					
m746	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPKQAERTAKAKPK					
	130	140	150	160	170	180
a746.pep	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPKQAERTAKAKPK					
m746	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPKQAERTAKAKPK					
	130	140	150	160	170	180
a746.pep	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
m746	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
	190	200	210	220	230	240
a746.pep	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
m746	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
	190	200	210	220	230	240
a746.pep	QKTDKADTKTAEKEKSGKAAIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY					
m746	QKTDKADTKTAEKEKSGKAAIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY					
	250	260	270	280	290	300
a746.pep	QKTDKADTKTAEKEKSGKAAIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY					
m746	QKTDKADTKTAEKEKSGKAAIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY					
	250	260	270	280	290	300
a746.pep	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
m746	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
	310	320	330			
a746.pep	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
m746	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
	310	320	330			

g747.seq not found yet

g747.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2557>:

```

m747.seq
1   CTGACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGGGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTACAAACC
201 CCGTGAGATT GTCTTGACG GTGACAAAAC CAAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAGCCGCAA CGTTCATAG TCAATTAAAA
301 TCAAAATAG

```

This corresponds to the amino acid sequence &lt;SEQ ID 2558; ORF 747&gt;:

```

m747.pep
1   LTPWADAYAD LRKTKVMTT QMGASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYR HKTIIKPREI VLDGDKTMG RSKSNEYGFR VAATFYSQLK
101 SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2559>:

```

a747.seq
1   CTAACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGTGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTGCAAAACC
201 CCGTGAGATT GTTTTGACG GCGACAAAAC CAAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAACCGCAA CGTTCATAG TCAATTAAAA
301 TCAAGTAG

```

This corresponds to the amino acid sequence &lt;SEQ ID 2560; ORF 747.a&gt;:

```

a747.pep
1   LTPWADAYAD LRKTKVMTT QMCASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYR HKTICKPREI VLDGDKTMG RSKSNEYGFR VTATFYSQLK
101 SK*

```

Computer analysis of this amino acid sequence gave the following results:

1217

Homology with a predicted ORF from *N. meningitidis*

ORF 747 shows 97.1% identity over a 102 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a747/m747 97.1% identity in 102 aa overlap

```

              10      20      30      40      50      60
a747.pep      LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLVGKQLTDSVGLFDPYYR
              |||||
m747          LTPWADAYADLRGKTKVMTTQMGASRDVSKSAKGWSVGIGLVGKQLTDSVGLFDPYYR
              10      20      30      40      50      60

              70      80      90      100
a747.pep      HKTICKPREIVLDGDKTKMGRSKSNEYGFRVTATFYSQLKSKX
              |||||
m747          HKTIIKPREIVLDGDKTKMGRSKSNEYGFRVAATFYSQLKSKX
              70      80      90      100

```

a747/m80195

gi|150271 (M80195) outer membrane protein [*Neisseria meningitidis*] Length = 272

Score = 59.3 bits (141), Expect = 6e-09

Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)

Query: 1 LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLVGKQLTDSVGLFDPYYR 60  
 + PW++ DL + K+ T +D+++ GW G+G N+GK+L +S +E P+Y+  
 Sbjct: 174 INPWSEVKKFDLNSRYKLNTGVNTLKKDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233

Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95  
 +T + E + GD + ++ EYG RV F  
 Sbjct: 234 QRTYKESGEFSVTTKSGDVSLTIPKTSIREYGLRVGIKF 272

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2561>:

g748.seq

```

1  ATGAGTCAAA ACCAACCCGC ACAACCGACC AAACGCAATC TGTTCAAAAC
51  CGCCCTTGCC GTCGGCGCAA TCGGCGCAAT CGGAGGTTAT TTCGGCGGCA
101  AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACTCGCCC
151  CAAGCCTATC CTTGCTACGG CGAACATCAG GCAGGTATCG TTACGCCCGG
201  GCAGGCGTTT TCCATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251  AGCAGCTGGA AAACCTGTTC CGCACACTGA CGCCCGCAT CGAGTTTCTC
301  ACCCAAGGCG GAGAATACCA AGACGGCGAC GACAACTCC CGTCAGCCGG
351  CAGCGGCATT TTGGGTAAAG CCTTCAACCC CGACGGATTG ACCGTTACCG
401  TGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451  AAAACGGTTC ATTTGCAGGA AATGCGCGAC TTCCCAACG ATAAGCTGCA
501  AAAAAGCTGG TGGGACGGCG ATTTGAGCCT GCAAACTGCG GCCTTACCCC
551  CCGAAACCTG CCAAACCGCC CTGCGCGACA TCATCAACA CACCGCCCAA
601  ACCGCGTCA TCCGCTGGAG TATCGACGGG TGGCAGCCTA AATCCGAACC
651  CGCGCGGATG GCGCGCGCA ACCTGTTGGG CTTCCGAGAC GGCACGGGCA
701  ACCCAAGGT TTCCGATCCC AAAACCGCCG ACGAGGTTT ATGGACGGGC
751  GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGGCGAAAA ACGGCAGCTA
801  TCAGGCAGTC CGCCTTATCC GCCGCTTTGT CGAGTTTGG GACAGGACGC
851  CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GCGGAAAAA CAGCGGGGCG
901  CCGATGGACG GCAAAAAAGA AGCCGACCAA CCGGATTTCG CCAAAGACCC
951  CGAGGGTGAT ATCAGCCTCA AAGACAGCCA TATGCGCCTG GCGAATCCGC
1001 GCGATCCCGA ATTCCTCAA AAACACTGCC TCTTCCGCG CGCCTACAGC
1051 TATTCTCGCG GACCCGCTC AAGCGGACAG CTTGATGTCG GGCTGGTGT
1101 CGTCTGCTAT CAGGCAAAAT TTGCCGACGG TTTCACTTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCCTG GAAGAATACA TCAGCCCTT CCGCGGCGGC
1201 TATTCTTCG TCTTGCCCG CGTGGGAAAA GGCGGATTCT TGGGACAAGG
1251 GCTGCCGGGC GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

g748.pep

```

1  MSQNQPAQPT KRNLFKTLA VGAIGAIGGY FGGKKQGETA ERTAESQHSP
51  QAYPCYGEHQ AGIVTPROAF SIMCAFDVTA QSAQLENLF RTLTARIEFL
101  TQGGEYQDGD DKLPSAGSGI LGKAFNPDGL TVTVGVGSSL FDGRFLGKDK
151  KTVHLQEMRD FPNKLQKSW CDGDLQLQIC AFTPETCQTA LRDIKHATAQ
201  TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLWTG
251  VAANSLDEPE WAKNGSYQAV RLIRRFVEFW DRTPLQEQTD IFGRRKYSGA
301  PMDGGKEADG PDFAKDPEGD ITPKDSHMLR ANPRDPEFLK KHCLFRRAYS
351  YSRGPASSGQ LDVGLVFVCY QANLADGFIF VQNLNGEPL EEYISPFGGG

```

401 YFFVLPGVGK GGFLGQGLPG V\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2563>:

m748.seq  
 1 ATGAGCAAAA AACAAACCCGC ACAACCGACC AGGCGCACTC TTTTAAAAAC  
 51 CGCGATCGCA GCCGGAGCAG TCGGCGCAAT CGGAGGTTAT CTCGGCGGCA  
 101 AAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACTCGCCC  
 151 CAAGCCTATC CCTGCTACGG CGAATCATAG GCAGGCATCG TTACGCCGCA  
 201 GCAGGCGTTT TCGATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA  
 251 AGCAGCTGGA AAACCTGTTC CGCACGCTGA CCGCCCGCAT CGAGTTTCTC  
 301 ACCCAAGGCG GCGAATACCA AGACGGCGAC GACAAACTTC CGCCAGCCGG  
 351 CAGCGGCATT TTGGGCAAAG CCTTCAACCC CGACGGGTTG ACCGTTACCG  
 401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA  
 451 AAACCGATTG ATTTGCAGGA AATGCGCGAC TTCTCCAACG ATAAGCTGCA  
 501 AAAAAGCTGG TGGACGGCG ATTTGAGCCT GCAAATCTGT GCCTTCACCC  
 551 CCGAAACCTG CCAAGCCGCC CTGCGCGACA TCATCAAACA CACCGTCCAA  
 601 ACCGCCGTTA TCCGTTGGAG TATCGACGGG TGGCAGCCCA AATCCGAACC  
 651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTGAGGAC GGCACGGGCA  
 701 ACCCCAAAGT TTCCGATCCC AAAACTGCCG ACGAGGTTT GTGGACGGGG  
 751 GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGCGCAAAA ACGGCAGCTA  
 801 TCAGGCAGTC CGCCTTATCC GCCACTTTGT CGAGTTTGG GACAGGACGC  
 851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GGCGCAAATA CAGCGGTGCG  
 901 CCGATGGACG GCAAAAAGA AGCCGACCAA CCGGATTTG CCAAAGACCC  
 951 CGAGGGTGAT ATCAGCCCA AAGACAGCCA TATACGCTG GCGAATCCGC  
 1001 GCGATCCCGA ATTCTCAAA AAACACCGCC TCTTCGCCG CGCCTACAGC  
 1051 TATTGCGCGG GACTCGCCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT  
 1101 CGTCTGCTAT CAGGCAAAAC TTGCCGACGG ATTCATCTTC GTGCAAAACC  
 1151 TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC  
 1201 TATTCTTCG TCTTCCCGG CGTGGAAAA GCGGCTTTT TGGGGCAAGG  
 1251 GCTGCTGGG GTATAA

This corresponds to the amino acid sequence <SEQ ID 2564; ORF 748>:

m748.pep  
 1 MSKKQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKQGETA ERTAESQHSP  
 51 QAYPCYGEHQ AGIVTPQQAQ SIMCAFDVTA QSAKQLENLF RLTARIEFL  
 101 TQGEYQDGD DKLFPAGSGI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK  
 151 KPIHLQEMRD FSNDKLQKSW CDGDLQLQIC AFTPETCQAA LRDIKHTVQ  
 201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLTWG  
 251 VAANSLDEPE WAKNGSYQAV RLIRHFVEFW DRTPLOEQTD IFGRKRYSGA  
 301 PMDGKKEADQ PDFAKDPEGD ITPKDSHRL ANPRDPEFLK KHRLFRRAYS  
 351 YSRGLASSGQ LDVGLVFVCY QANLADGFIF VQNLNGEPL EEYISPFGGG  
 401 YFFVLPGVEK GGFLGQGLLG V\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 748 shows 95.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. gonorrhoeae*

m748/g748 95.0% identity in 421 aa overlap

	10	20	30	40	50	60
m748.pep	MSKKQPAQPT RRTLFKTAIAAGAVGAIGGYLGGKKQGETAERTAESQHSPOAYPCYGEHQ					
g748	MSQNQPAQPTKRNLFTALAVGAIGAIGGYFGGKKQGETAERTAESQHSPOAYPCYGEHQ					
	10	20	30	40	50	60
m748.pep	AGIVTPQQAQSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGEYQDGD DKLFPAGSGI					
g748	AGIVTPROAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGEYQDGD DKLPSAGSGI					
	70	80	90	100	110	120
m748.pep	LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLQLQIC					
g748	LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKTVHLQEMRDFPNLQKSWCDGDLQLQIC					
	130	140	150	160	170	180
m748.pep	AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAAARNLLGFRDGTGNPKVSDP					
g748	AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAAARNLLGFRDGTGNPKVSDP					
	190	200	210	220	230	240
m748.pep						
g748						

		190	200	210	220	230	240
g748	AFTPETCQTALRDI IKHTAQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP						
m748.pep	KTAEVLWTGVAA NSLDEPEWAKNGSYQAVRLIRHFVEFWDRTP LQEQTDFGRRKYSGA	250	260	270	280	290	300
g748	KTAEVLWTGVAA NSLDEPEWAKNGSYQAVRLIRRFVEFWDRTP LQEQTDFGRRKYSGA	250	260	270	280	290	300
m748.pep	PMDGKKEADQPDFAKDPEGDITPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ	310	320	330	340	350	360
g748	PMDGKKEADQPDFAKDPEGDITPKDSHMRLANPRDPEFLKKHCLFRRAYSYSRGPASSGQ	310	320	330	340	350	360
m748.pep	LDVGLVFVCYQANLADGFFIVQNLLNGEPL E EYISPFGGGYFFVLPGVGKGGFLQGQLLG	370	380	390	400	410	420
g748	LDVGLVFVCYQANLADGFFIVQNLLNGEPL E EYISPFGGGYFFVLPGVGKGGFLQGQLPG	370	380	390	400	410	420
m748.pep	VX						
g748	VX						

```

a748.seq
1  ATGAGCAAAA ACCAACCCGC ACAACCCGACC AGGCGCACTC TTTTAAAAAC
51  CGCGATCGCA GCTGGAGCAG TCGCGCGCAAT CGGAGGTTAT CTCGCGCGCA
101  AAAAACGGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACTCGCCC
151  CAAGCGCTATC GCTGCTACGG CGAACATCGA CGAGGACTCG TTACGCCGCA
201  GCAGGCGGTT TCGATTATGT TGGCGTTCGA CGTAAACCGCG CAAAGTGCCA
251  AGCAGCTGGA AAACCTGTTC CGCAGCGTGA CCGCCCGCAT CGAGTTTCTC
301  ACCAAGAGCG CGGATATACA AGACCGCGCAC GACAAACTTC CGCCAGCGCG
351  CAGCGGATCT TTGGGCAAGC CTTTCAACCG CGACGGGTTG ACCGTATCCG
401  TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451  AAACCGATTG ATTTGCAAGA AATGCGCGCAC TTCTCCAAGC ATAAGCTGCA
501  AAAAAGCTGG TGCAGCGCGC ATTTAGCGCT GCAAATCTGT GCCTTACCC
551  CCGAAACCTG CCAAGCGGCC CTGCGCGACA TCATCAAACA CACCGTCCAA
601  ACCGCGGTTA TTCGCTGGAG TATCGACGGG TGGCGAGCTA AATCCGAACC
651  CGCGCGGATG GCGCGCGGCA ACCTGTTGGG CTTCCGCGAC GGCACGGGCA
701  ACCCCAAAGT TTCCGACCCC AAAACTGCCG ACGAGGTTTT GTGACCGGGG
751  GTGGCGCGCA ACAGCGCTCGA CGAACCGGAG TGGCGGAAAA ACGCGAGCTA
801  TCAGGCAAGC GCCTTATCTG GCCACTTTGT TGAGTTTTGG GACAGGACGC
851  CGCTTCAAGA GCAAACCGAC ATTTTCTGGG GCGCAAAATA CAGCGGCGCG
901  CCGATGCGAG GCAAAAAAGA AGCCGACCAA CCGGATTTTG CCAAGAACCC
951  CGAGGGGAAT ACCACGCCCA AAGACAGCCA TATACGCTTC GGAATATCCG
1001  GCGATCCCGA GTTCCTTAAA AAACACCGCC TCTTCCGCGC CGCCTACAGC
1051  TATTCGCGCG GACTCGGCTC AAGCGGACAG CTTGATGTGC GGCTGTGGTT
1101  CGTCTGCTAT GACCAAAACC TTGCGCAGCG ATTCATCTTC GTGCAAAACC
1151  TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCTTT CGGCGGCGGC
1201  TATTTTCTTC TCTTCCCGCG CGTGAAAAAA GCGCGCTTTT TGGGCAAAAG
1251  GCTGCTGGGC GTATAA

```

```
a748.pep
1  MSKNQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKRGETA ERTAESQHSP
51  QAYPCYGEHQ AGIVTPQQA F SIMCAFDVTA QSAKQLENLF RLTARIEFKL
101 TOGGEYQDGD DKLPAPAGSGI LGKAFNPDL TVTVGVGSSL FDGFRGLKDL
151 KPIHQLQEMRD FSNDKLQKSW CDGDLSLQIC AFTPETCQAA LRDIKHTVQ
201 TAVIRWSIDG WQKSPSEGM AARNLLGFRD GTGNPKVSDP KTADEVMLTK
251 VAANSLEDEP WAKNGSYQAV RLRIHFVEVF DRTPLOEQTD IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEG TTPKDSHIRL ANPRDPEFLK KHLRFRRAYS
351 YSRGLASSQG LDVLGVFVCY QANLADGFIF VQNLNLEPL EEEYISPFGGG
401 YFFVLPGVEK GGFGLGGLLG V*
```

Computer analysis of this amino acid sequence gave the following results:

1220

Homology with a predicted ORF from *N meningitidis*

ORF 748 shows 99.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. meningitidis*:

a748/m748 99.0% identity in 421 aa overlap

```

a748.pep      10      20      30      40      50      60
MSKNQPAQPTRRRLFKTAIAAGAVGAIGGYLGKKRGETAERTAESQHSPPQAYPCYGEHQ
|||||
m748          10      20      30      40      50      60
MSKKQPAQPTRRRLFKTAIAAGAVGAIGGYLGKKQGETAERTAESQHSPPQAYPCYGEHQ
|||||

a748.pep      70      80      90     100     110     120
AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLRTARIEFLTQGGEYQDGGDKLPPAGSGI
|||||
m748          70      80      90     100     110     120
AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLRTARIEFLTQGGEYQDGGDKLPPAGSGI
|||||

a748.pep     130     140     150     160     170     180
LGKAFNPDGLTIVTVGVGSSLFDGRFGLKDKKPIHLQEMRDFSNDKLOKSWCDGDLSQLIC
|||||
m748        130     140     150     160     170     180
LGKAFNPDGLTIVTVGVGSSLFDGRFGLKDKKPIHLQEMRDFSNDKLOKSWCDGDLSQLIC
|||||

a748.pep     190     200     210     220     230     240
AFTPETCQAALRDI IKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
|||||
m748        190     200     210     220     230     240
AFTPETCQAALRDI IKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
|||||

a748.pep     250     260     270     280     290     300
KTADEVLWLTGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLEQETDIFGRRKYSGA
|||||
m748        250     260     270     280     290     300
KTADEVLWLTGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLEQETDIFGRRKYSGA
|||||

a748.pep     310     320     330     340     350     360
PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ
|||||
m748        310     320     330     340     350     360
PMDGKKEADQPDFAKDPEGDITPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ
|||||

a748.pep     370     380     390     400     410     420
LDVGLVFCYQANLADGFIFVQNLLNGEPL E EYISPFGGGYFFVLPGVKGGFLGQGLLG
|||||
m748        370     380     390     400     410     420
LDVGLVFCYQANLADGFIFVQNLLNGEPL E EYISPFGGGYFFVLPGVKGGFLGQGLLG
|||||

a748.pep      VX
||
m748          VX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2567>:

```

g749.seq
1  ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTGGGTTT
51  GACCGCGTGC CAGCCGCCGG AGCCGGAGAA AGCCGCGCCG GCCCGCTCCG
101 GTGAGACCCA ATCCGCCAAC GAAGCGGTT CGGTCGGTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCAGT GAATCTGACC GTGCCGAGCG GACAGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AGGGCGTGAT GGTGGTGGAC GAACGCGAAA ATATCGCCCC GGGGCTTTCC
301 GACAAAATGA CCGTAACcct GCTGCCGGGC GAATACGAAA TGACCTGCGG
351 CCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAGCCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGCCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTC AAGCGAGGTT AAAGAGCTGG CGGCGAAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAT
551 CCCTGTTTGC CGCCACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGTGTG AAGACGACTT
651 CAAAGACGGT GCGAAAGATG CCGGGTTTAC CGGCTTCCAC CGTATCGAAC
701 ACGCCCTTTG GGTGGAAAAA GACGTATCCG GCGTGAAGGA AACCGCGGCC
751 AAAGTATGTA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC

```



1221

```

801 GttccctCCG GGCAGAGTGG TCGCGGCGCG GTCCGAAGT ATTGAAGAAG
851 CGGCGGGCAG TAAATCAGC GCGGAAGAAG ACCgttaCAG CCACACCGAT
901 TTGAGCGACT TCCAAGCTAA TCGGACGGA TCTAAAAAAA TCGTCGATT
951 GTTCCGTCGG TTGATTGAGG CCAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATC TGGCGAAATA CCGACCAAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGAGC GAAGCCGACC GCAAGCATT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2568; ORF 749.ng>:

```

g749.pep
1 MRKFNLIALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIIVN
51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGMVVD ERENIAPLS
101 DKMTVTLPLG EYEMTCGLLT NPRGKLVVD SGFKDTANEA DLEKLPQPLA
151 DYKAYVQGEV KELAAKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
201 ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRGILGLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2569>:

```

m749.seq
1 ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51 GACCGCGTGC CAGCCGCCCG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCAGTAT CGCGTCAAC
151 GACAAATGCTT GCGAACCGAT GGAAGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAATGA CCGTCACCTT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAAACGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAC
501 CAAACTTTT ACCGAAGCCG TCAAGCAGG CGACATTGAA AAGCGGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTTTAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAATGATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTCTCTCCG GGCAGAGTGG TCGGCGGCGC GTCCGAAGT ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GCGGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATT
951 GTTCCGTCGG CTGATCGAGG CCAAAAACAA AGCCTTGTG GAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAGCGTT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2570; ORF 749>:

```

m749.pep
1 MRKFNLIALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIIVN
51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVD ERENIAPLS
101 DKMTVTLPLG EYEMTCGLLT NPRGKLVVD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. gonorrhoeae*

m749/g749 96.1% identity in 388 aa overlap

```

          10      20      30      40      50      60
m749.pep MRKFNLIALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSIIVNDNACEPMELT
          |||
g749      MRKFNLIALSVMLALGLTACQPPEAEKAAPASGETQSANEGGSVGIIVNDNACEPMNLT
          10      20      30      40      50      60

```

1222

	70	80	90	100	110	120
m749.pep	VPSGQVVFNIKNN	SGRKLEWEILK	GVMMVDERENI	APGLSDKMTVT	LLPGEYEMTCGL	LLT
g749	VPSGQVVFNIKNN	SGRKLEWEILK	GVMMVDERENI	APGLSDKMTVT	LLPGEYEMTCGL	LLT
	130	140	150	160	170	180
m749.pep	NPRGKLVVTD	SGFKDTANEAD	LEKLSQPLADY	KAYVQGEVKEL	VAKTKTFTTEAV	KAGDIE
g749	NPRGKLVVTD	SGFKDTANEAD	LEKLPQPLADY	KAYVQGEVKEL	AAKTKTFTTEAV	KAGDIE
	190	200	210	220	230	240
m749.pep	KAKSLFADTRV	HYERIEPIAE	LFSELDPVDA	REDDFKDGAK	DAGFTGFHRIE	YALWVEK
g749	KAKSLFAATR	VHYERIEPI	AESELDPVDA	CEDDFKDGAK	DAGFTGFHRIE	HALWVEK
	250	260	270	280	290	300
m749.pep	DVSGVKEIAA	KLMTDVEALQ	KEIDALAFPP	GVVGGASELIE	EVAGSKISGEED	DRYSHTD
g749	DVSGVKETA	AKLMTDVEAL	QKEIDALAF	PPGVVGGASEL	IEEAGSKISGEED	DRYSHTD
	310	320	330	340	350	360
m749.pep	LSDFQANVDG	SKKIVDLFR	PLIEAKNKAL	LEKTDNTNFQ	VNEILAKYRTK	DGFETYDKLG
g749	LSDFQANADG	SKKIVDLFR	PLIEAKNKAL	LEKTDNTNFQ	VNEILAKYRTK	DGFETYDKLS
	370	380	389			
m749.pep	EADRKALQAS	INALAEDLAQ	LRGILGLKX			
g749	EADRKALQAP	INALAEDLAQ	LRGILGLKX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2571>:

```

a749.seq
1  ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51  GACCCGCTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCAGTAT CGCCGTCAAC
151 GACAATGCCT CGGAACCGAT GGAAC TGACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGC GG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTCA AGGCGAAGTC AAAGAGCTGG TGGCGAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGCGGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGA AAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTGTGTA CCGATGTGCA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GCGAAGGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAAA TCGTCGATTT
951 GTTCCGTCCT TTGATCGAGA CCAAAAACAA AGCCTTGTGT GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGTTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGCGA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2572; ORF 749.a>:

```

a749.pep
1  MRKFNLTAIS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSI AVN
51  DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMMVVD ERENIAPLGS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVVGGASEL IEEVAGSKIS GEEDRYSHTD

```

1223

301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK  
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGLGLKX\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

a749/m749 99.7% identity in 388 aa overlap

a749.pep	MRKFNLTALSVMLALGLTACQPPEAEKAPAAASGEAQTANEGGSVSI	10	20	30	40	50	60
m749	MRKFNLTALSVMLALGLTACQPPEAEKAPAAASGEAQTANEGGSVSI	10	20	30	40	50	60
a749.pep	VPSGQVVFNIKNNSGRKLEWEILKGVVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT	70	80	90	100	110	120
m749	VPSGQVVFNIKNNSGRKLEWEILKGVVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT	70	80	90	100	110	120
a749.pep	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE	130	140	150	160	170	180
m749	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE	130	140	150	160	170	180
a749.pep	KAKSLFADTRVHYERIEPIAELEFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK	190	200	210	220	230	240
m749	KAKSLFADTRVHYERIEPIAELEFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK	190	200	210	220	230	240
a749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGAELIEEVAGSKISGEEDRYSHTD	250	260	270	280	290	300
m749	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGAELIEEVAGSKISGEEDRYSHTD	250	260	270	280	290	300
a749.pep	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG	310	320	330	340	350	360
m749	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG	310	320	330	340	350	360
a749.pep	EADRKALQASINALAEDLAQLRGLGLKX	370	380	389			
m749	EADRKALQASINALAEDLAQLRGLGLKX	370	380	389			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

g750.seq  
 1 GTGAAACCGC GTTTTTATTG GGCAGcctGC GCCGTCCTGC CGGCCGCTG  
 51 TTCGCCCCGAA CCTGCCGCCG AAAAACTGT ATccgCCGCA TCCCAAGCCG  
 101 CATCCACACC TGTCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC  
 151 GTTGTGCCGA AGAATCCCGA ACgcgtegcc gtgtAcgaCt ggCGGCGTt  
 201 ggaTACGCTG ACCGAGCCGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG  
 251 TGGCGGTGGA CTATTGCGAG CCTGCATTG ACAAGGCGGC AACGGTGGGG  
 301 ACGCTGTTTG AGCCCGATTG CGAATCCCTG CACCGCCACA ATCCGCAGTT  
 351 TGTCATTACC GGCAGGCCGG GTGCGGAAGC GTATGAACAG TTGGCGAAAA  
 401 ACGCGACCAC CATAGATTG ACGGTGGACA ACGGCAATAT CCGCACCAGC  
 451 GCGGAGAAGC AGATGGAGAC CCTGTCGCGG ATTTTCGCTA AGGAAGCGCG  
 501 CGTGGCGGAA TTGAATGCGC AGATTGACGC GCTGTTCCGC CAAAAGCGCG  
 551 AAGCGCCCAA AGGCAAAGGA CGCGGGCTGG TGCTGTCCGT TACAGGCAAC  
 601 AAGGTGTCCG CCTTCGGCAC GCAATCGCGG TTGGCAAGT GGATACACGG  
 651 CGACATCGGC CTGCCGCCG TGGACGAATC TTTACGCAAC GAAGGGCACG  
 701 GGCAGCCCGT TTCCTTCGAA TACATCAAAG AGAAAAACCC CGGCTGGATT  
 751 TTCATCATCG ACCGCACCGC CGCATCGGG CAGGAAGGGC CGGCTGCCGT

g750.pap

1	VKPRFYWAAC	AVLPAACSPE	PAAEKTVSAA	SQAASTPVAT	LTVPTARGDA
51	VVPKNPEEVA	HYDNDADLT	TEPGNVGAT	TAPVRVDYLQ	PAFDKAAVTG
101	TLFEPDCESL	HRHNPQFVIT	GGPGAIEYEQ	LAKNNATIDL	TVDNGNIRTS
151	GEKQMETLSR	IFGKEARVAE	LNAQIDALFA	CKREAAGKG	RGLVLSVTGN
201	KVSFAFGTQR	LASWIGHDIG	LPPVDECSLRN	EGHGQPVSE	YIKEKNPGWI
251	FIIDRTAAIG	QEGPAAEVL	DNDVLCGTNA	WKRKQIIVMP	AANYIVAGGA
301	ROLIQAAEQL	KAAFEKAEPV	AAQ*		

**m750.seq**

1	GTGAAACCGC	GTTTTTATTG	GGCAGCCTGC	GCCGTCCTGC	TGACCGCCTG
51	TTCCGCGCGA	CTCCGCCGCG	AAAAAATCTG	ATCCGCCGCA	TCCGCACTCG
101	CCGCGCCGGA	GACGTGCGCG	ACCGGACGTT	GCATATCCGT	TGTGCCGAAG
151	AATCCCGAAC	CGCTCGCCGT	GTACGACTGG	CGGGCGTTGG	ATACGCTGAC
201	CGAATTGGGC	GTGAATTGGG	AGCGCAACAC	CGCGCGCGTG	CGCGTGGATT
251	ATTGTCAGCG	TGCATTTGAC	AAGCGGCGCA	CGGTGGGACG	CTGTTCTGAG
301	CCCGATTACG	AAGCGCTGCA	CCGCTACAAT	CCTCAGCTTG	TCATTACCGG
351	CGGGCCGGCG	CGCGAAGCGT	ATGACACAGT	ACCGAAAAAC	CGCCACACCA
401	TGATCTCGAC	GGTGGACAGT	GGCAATATCC	AGCGACGGCG	GAAAAGACGA
451	ATGGAGACCT	TGGCGCGGAT	TTTCGCGAAG	GAAAGCGCGG	CGCGGGAATT
501	GAAAGCGCGA	ATTGACGCGC	TGTTTCGCCA	AACGCGCGAA	CGCGCGAAGG
551	CGAAGGACGC	CGGGCTGTGT	GTCTCGGTTA	CGGGCAACAA	GGTGTCCGCG
601	TTCCGACACG	AGTCGCGGTT	TGCAAGTTGG	ATACACGCGG	ACATCGGCCCT
651	ACCGCCTGTA	GACGAATCTT	TGCGACCAAC	GGGGCAGCGG	CAGCCTGTTT
701	CCTTCGAATA	CATCAAGAGG	AAAAACCCCG	ATTGATATTT	CATCATCGAC
751	CGTACGCGCG	CCATCGGGCA	GGAAGGGCGG	CGGGCTGTGC	AGATATTGGA
801	TAACGCGGTG	GTACGCGGCA	CGAACGCTTG	GAAAGCGAAG	CAAAATCATG
851	TCATGCCTGC	CGCGAACTAC	ATTGTGCGCG	CGGGCGCGCG	CGAGTTGATT
901	CAGCGCGGCG	AGCAGTTGAA	GGCGGCGTTT	AAAAAGGCAG	AACCCGTTCG
951	GGCGGGGAAA	AGATAG			

m750.pgp

1	VKPRFYWAAC	AVLLLTACSPE	PAAEKTVSAA	SASAATLTVP	TARGDAVVPK
1	NPERVAAYAD	AADLTLTGEL	VNUGGATAPV	RDVYLQAFAD	KAATVGTLFE
101	PDYEAHLRYN	PQLVITGGPG	AEAYEQLAKN	ATTIDLTVDN	GNIRTSGEKQ
151	METLARIIFCK	EAASAEELKA	IDALFAQTRE	AANKGKRGVL	LSVTGNKVSAA
201	FTGTQSLRAS	IHGGDILPPV	DESILRNHGK	QPVSFYIEIK	KNPDVFIID
251	RTAAITQGEQG	AAVEVDLVAN	VRGTNAWKRR	QIIVMPAANY	IVAGGARQLI
301	QAEEOLKKA	KKAEVPAAGK	K*		

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 750 shows 93.8% identity over a 322 aa overlap with a predicted ORF (ORF 750) from *N. gonorrhoeae*

m750/g750 93.8% identity in 322 aa overlap

	10	20	30	40	50	
m750.pep	VKPRFYWAACAVLLTACSEPEAAEKTVSAASASA----	ATLTVPTARGDAVVPKNPERVA				
g750	VKPRFYWAACAVLPACSEPEAAEKTVSAASQAASTPVATLTVPTARGDAVVPKNPERVA					
	10	20	30	40	50	60
	60	70	80	90	100	110
m750.pep	VYDWAALDRTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYNPQLVIT					
g750	VYDWAALDRTLTEPGNVVGATTAPVRVDYLQPAFDKAATVGTLFEPDCESLRHNPQFVIT					
	70	80	90	100	110	120
	120	130	140	150	160	170
m750.pep	GGPGAEEYEQLAKNATTIDLTVDNGNIIRTSGEKOMETLARIFGKEARAALKAQIDALFA					

1225

```

g750      GGFGAEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLSRIFGKEARVAELNAQIDALFA
           130      140      150      160      170      180

m750.pep  180      190      200      210      220      230
QTREAAKKGKRGVLVSVTGNKVSFAFGTQSRLASWIHGDIPLPPVDESLRNEGHGQPVVSFE
g750      QKREAAKKGKRGVLVSVTGNKVSFAFGTQSRLASWIHGDIPLPPVDESLRNEGHGQPVVSFE
           190      200      210      220      230      240

m750.pep  240      250      260      270      280      290
YIKEKNPDWIFIIDRTAAIGQEGPAAVEVDNALVRGTNAWKRKQIIVMPAANYIVAGGA
g750      YIKEKNPDWIFIIDRTAAIGQEGPAAVEVDNALVCGTNAWKRKQIIVMPAANYIVAGGA
           250      260      270      280      290      300

m750.pep  300      310      320
RQLIQAAEQLKAAFKKAEFPVAAAGKKX
g750      RQLIQAAEQLKAAFEKAEFPVAAQX
           310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2577>:

```

a750.seq
1   GTGAAACCGC GTTTTATTG GGCAGCCTGC GCCGTCCTGC TGACCGCCTG
51  TTCGCCCGAA CCTGCCGCGG AAAAACTGT ATCCGCCGCA TCCGCATCTG
101 CCGCCACACT GACCGTGCCG ACCGCGCGGG GCGATGCCGT TGTGCCGAAG
151 AATCCCGAAC GCGTCGCCGT GTACGACTGG GCGGCGTTGG ATACGCTGAC
201 CGAATTGGGT GTGAATGTGG GCGCAACCAC CGCGCCGGTG CGCGTGGATT
251 ATTTGCAGCC TGCATTGTAC AAGCGGGCAA CGGTGGGGAC GCTGTTCCAG
301 CCCGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
351 CGGGCCGGGC GCGGAAGCGT ATGAACAGTT GCGGAAAAAC GCGACCAACA
401 TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCAGCGG CGAAAAGCAG
451 ATGGAGACCT TGGCGCGGAT TTTCGGCAAG GAAGCGCGCG CGGCGGAATT
501 GAAGGCGCAG ATTGACGCGC TGTTGCGCCA AACGCGCGAA GCCGCCAAG
551 GCAAAGGACG CGGGCTGGTG CTGTCGGTTA CGGGCAACAA GGTGTCCGCC
601 TTCGCACGCG AGTCGCGGTT GGCAAGTTGG ATACACGGCG ACATCGGCCT
651 ACCGCCTGTA GACGAATCTT TACGCAACGA GGGGCACGGG CAGCCTGTTT
701 CCTTCGAATA CATCAAAGAG AAAAACCCCG ATTGGATTTT CATCATCGAC
751 CGTACCGCCG CCATCGGGCA GGAAGGGCCG GCGGCTGTGC AAGTATTGGA
801 TAACGCGCTG GTACGCGGCA CGAACGCTTG GAAGCGCAAG CAATCATCG
851 TCATGCCTGC CGCGAATAC ATTGTCGCGG GCGGCTCGCG GCAGTTGATT
901 CAGGCGGCGG AGCAGTTGAA GGAGGCGTTT GAAAAGCAG AACCCGTTGC
951 GGCGGGGAAA GAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2578; ORF 750.a>:

```

a750.pep
1   VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
51  NPERVAVDW AALDTLTELG VNVGATTAPV RVDYLQPAFD KAATVGTLFE
101 PDYEALHRYN POLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ
151 METLARIFGK EARAELKAQ IDALFAQTRE AAKGKRGVLV LSVTGNKVSA
201 FGTQSRLASW IHGDIPLPPV DESLRNEGHG QPVVSFEYKE KNPDWIFIID
251 RTAAIGQEGP AAVEVDNAL VRGTNAWKRK QIIVMPAANY IVAGGSRQLI
301 QAAEQLKEAF EKAEPVAAAGK E*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from *N. meningitidis*:

a750/m750 98.8% identity in 321 aa overlap

```

a750.pep  10      20      30      40      50      60
VKPRFYWAACAVLLTACSPEPAAEKTVSAAASASAATLTVP TARGDAVVPKNPERVAVDW
|||||
m750      VKPRFYWAACAVLLTACSPEPAAEKTVSAAASASAATLTVP TARGDAVVPKNPERVAVDW
           10      20      30      40      50      60

a750.pep  70      80      90      100     110     120
AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYN POLVITGGPG
|||||
m750      AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYN POLVITGGPG

```

1226

	70	80	90	100	110	120
a750.pep	130	140	150	160	170	180
	AEAYEQLAKNATTIDLTVDNGNI RTSGEKOMETLARIFGKEARAAELKAQIDALFAQTRE					
m750	AEAYEQLAKNATTIDLTVDNGNI RTSGEKOMETLARIFGKEARAAELKAQIDALFAQTRE					
	130	140	150	160	170	180
a750.pep	190	200	210	220	230	240
	AAKGKGRGLVLSVTGNKVSFAFGTQSRLASWINGDIGLPPVDES LRNEGHGQPVSF EYIKE					
m750	AAKGKGRGLVLSVTGNKVSFAFGTQSRLASWINGDIGLPPVDES LRNEGHGQPVSF EYIKE					
	190	200	210	220	230	240
a750.pep	250	260	270	280	290	300
	KNPDWIFIIDRTAAIGQEGPAAVEVL DNALVRGTNAWK RKQIIVMPAANYIVAGGS RQLI					
m750	KNPDWIFIIDRTAAIGQEGPAAVEVL DNALVRGTNAWK RKQIIVMPAANYIVAGG ARQLI					
	250	260	270	280	290	300
a750.pep	310	320				
	QAAEQLKEAF EKAEPVAAGKEX					
m750	QAAEQLKAAFEK AEPVAAGKKX					
	310	320				

g751.seq not found yet

g751.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2579>:

```
m751.seq..
1  ATGGCTTGA  GTATGTTTGC  CACAACCCAA  GCCGATAGAG  CGGTAAGGTC
51  TGCAACTGCA  CCTAAAGAAA  TGTGGTTCCA  TAAGAAGATA  ATAGATGAAA
101 AAACAGGTAA  AGTATCCTTT  GATACCAGAC  AAATTTGGTC  ATTGAATGAT
151 TTAAGCAAGG  AAGAACTGGC  AAGCATTCAA  GACACAAATG  GCAAAGTTAT
201 TACTGTGTCT  AATCCTGGTA  TTTTCAATAA  TCGAGAAGAT  TCATTAAGCA
251 ACGCAGCAAA  ACAAATCGT  AATAGTACAA  ACGGTAGTGG  TGTATTGCA
301 GTCATGAATC  CTCCAACAGG  GAAATATAAA  TCTGATTCTA  ATAACAAAAT
351 AAAAGATTIT  TTATGGCTCG  GTTCAAGTCT  TGTTCCTGAA  CTGATGTATG
401 TCGGTTACGA  CCAATTAAAT  AATAAAGTGT  TCCAAGGCTA  TTTACCCAAA
451 ACCAATTCAG  AAAAACTGAA  TCAAGATATT  TATCGAGAGG  TTCAAAAAAT
501 GGGTAACGGC  TGGTCGGTTG  ATACCAGTAA  TCACAGTCGT  GGGGGAATTA
551 CAGCAAGCGT  TTCCTTAAAA  GATTGGGTAA  ACAATCAAAA  ACAAATGGC
601 ATTGCCCAA  TCAGAAAAGC  ACGTTTCTAT  GGTACAGCCA  CAAATGTGCA
651 GAATGATTAC  GCCGATGTTT  TACAGAAAAA  CGGCTATACC  TATACGGGTG
701 CAGACGGCAA  AACTTATAAC  AGCGATCCT  ACTCAATCGT  GCATGATAAA
751 GATTTTGTGG  GGAACAAATG  GATACCTTTC  TTGCTAGGAA  CCAATGACAC
801 CACACAAGGT  ACATGTAAGG  GGTGTGCTA  TTGCTAGAGC  AGTTATTTTG
851 CGGAGGTGCC  AAAAGCAGGT  ACAAAGAAT  TTGATGACTA  TGTAAAAATA
901 TGGGGTGAAG  TTGAATATGA  CGCTCAAGGT  AAGCCAATTA  ACAAATCTAA
951 ACCCTACTG  GTAGAACCAA  ACAAACAAA  AGATAATGAA  AAATATGAAA
1001 AAGAAGCTTT  CTAA
```

This corresponds to the amino acid sequence <SEQ ID 2580; ORF 751>:

```
m751.pep..
1  MAWSMFATTQ  ADRAVRSATA  PKEMWFHKKI  IDEKTGKVSF  DTRQIWSLND
51  LSKEELASIQ  DTNGKVITVS  NPGIFNNRED  SLSNAAKQNR  NSTNGSGVIA
101 VMNPPTGKYK  SDSNNKIKDF  LWLGSSLVSE  LMYVGVDQLN  NKVFQGYLPK
151 TNSEKLQNDI  YREVQKMGNG  WSVDTSNHSR  GGITASVSLK  DWVNNQKQNG
201 IAPIRKARFY  GTATNVQNDY  ADVLQKNGYT  YTGADGKTYN  SGSYSIVHDK
251 DFGVGNKWIPF  LLGTNDTTQG  TCKGLCYSHS  SYFAEVPKAG  TKEFDDYVKI
301 WGEVEYDAQG  KPINKSKPIL  VEPNKT KDNE  KYEKEAF*
```

a751.seq not found yet

a751.pep not found yet

1227

g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

m752.seq..

```

1 ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51 GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCCT
101 CCGCAAACAA TCCTGATATA GACATTCCTG ATTTTCTTAC TGAAATCAAA
151 GATTATTTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCTGAC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAGC GGTAGAATTG
601 AAAAAATACG CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC
651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGACAG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTGCAATTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GCCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTTCATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTG GAGCACTACA TTTCCGACAA ACAAACACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAAACTG GGAGAATATA GATTCTTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTAT TGGAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

m752.pep

```

1 MKISRPEFT LLQEYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFFP
101 EHQFWFCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSAQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAILLHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLTYFIYYQC DIIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPEK
451 SGNALFYVAP QDLLERLEKK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

m752-1.seq

```

1 ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51 GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCCT
101 CCGCAAACAA TCCTGATATA GACATTCCTG ATTTTCTTAC TGAAATCAAA
151 GATTATTTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCTGAC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAGC GGTAGAATTG
601 AAAAAATACG CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC

```

1228

```

651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTCACTTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTG GAGCACTACA TTTCCGACAA AAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 TAGCGGATTG GAGTAAACTG GGAGAATATA GATTCTAGT GCCGTTCAA
1351 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTAT TGAAAGGTT
1401 AAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2584; ORF 752-1>:

m752-1.pep

```

1 MKISRPPEFT LLQEQMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EQQWFNCPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSQALE GAATTRKVK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAILLHF LIGYIHFPD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPQYAK SYLYAETDDL
351 DLTYFIYYQC DIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVFPK
451 SGNALFYVAP QDLEERLEK *

```

a752.seq not found yet

a752.pep not found yet

g753.seq not found yet

g753.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2585>:

m753.seq

```

1 ATGCCCCATCA CTCCACCCTT AAACATCATC TCTCCTAAAC TCTACCCCAA
51 TGAACAATGG AACGAAAGCG AAGCACTCGG TGCCATCACT TGGCTATGGT
101 ATCAGTCGCC TACGCATCGC CAAGTACCTA TTGTGGAGAT GATGACGTAT
151 ATATTGCCTG TGTAAAAAAA CGGGCAGTTC GCTTTGTTTT GCAAGGGTAC
201 CCAACCAATC GGTATATCT CATGGGCTTA TTTTGATGAA GTGGCGCAGG
251 CGCATTATTT AGAATCTGAC CGCCATTTGC GTGACAACAG CGATTGGAAC
301 TGTGGCGACA ATATTGGCT GATTCAATGG TTTGCGCCAT TGGGACACAG
351 TCATCAAATG CGCTCAGCTG TGCGCCAGTT ATTTCTAGT ACGACAGTAC
401 GCGCCTTGTA TCATAAAGGG AGCGATAAGG GTTTGAGAAAT TTTAACTTTT
451 AAAACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2586; ORF 753>:

m753.pep

```

1 MPITPPLNII SPKLYPNEQW NESEALGAIT WLWYQSPTHR QVPIVEMMTY
51 ILPVLKNGQF ALFCKGTQPI GYISWAYFDE VAQAHYLED RHLRDNSDWN
101 CGDNIWLIQW FAPLGHSQOM RSAVRQLFPS TTVRALYHKG SDKGLRILTF
151 KT*

```

a753.seq not found yet

a753.pep not found yet

g754.seq not found yet



1229

g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```

m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
201 GCCGCATATC TTTGCACAGT ATTTTCCGGA AGGCTTTTGT GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCGC CTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTTA ATGAATGGAT TGACGGGTTG GAGATGAAAA
401 ATCCAAGAAT ATTGACTGAA CGGGATTTCG TGGGCATAAA TGCCCGACAG
451 GTTTTTCAGC AATATATGGC AGAAATCTTC CATCACGGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCAAGCAAAC TGCCTCATAT ATTGCCAAAG GTTTTGATGC ATCCGAATAT
601 CCTTGCTTGG CTGCCAATGA ATTTTATGCG ATGCAGACCA TCAAACAAGC
651 CGGCATTGCC GTTGACACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTTGATGTC AGTGAACAGG GTTATTTTAT AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATTCCGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATTGCACAGA TTATCCGACA GATATCCGGC AGACCAGATG
851 AAGATTTAAT CCATTTCTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGGCGATG CACACCTCAA AAATTTTTCG TACTCTATC ATGACGAATA
951 CGATGTTTCG CTGACACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATTG
1051 AACCTGACTA ACCACGGTAA GAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCTTGT TAAATACTCG
1201 GATGTATTGC GTGAGAATGA ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAT GAAGAAGGTC TACCGTTTAC ATTCCGGTAG

```

This corresponds to the amino acid sequence &lt;SEQ ID 2588; ORF 754&gt;:

```

m754.pep
1  MMKSILTVSG NRMKPRITY LDVWANDERI GTLEKGAMYP FAYDNPNSSL
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
101 LRLAILCRET LGRIHVROND PLFNEWIDGL EMKNPRILTE RDLLGINARQ
151 VFQQYMAEIF HHGRFVSVSG IQQKMSLDAI RRNTKQTASY IAKGFDASEY
201 PCLAANEFLC MQTIKQAGIA VAQTSLSSEDS SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQIIRQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLDT SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKTTY PSKNTLLDFA EKYCDLGRED ASFMIDTIVQ AKEQVLVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*

```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```

m755.seq..
1  ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTAATCCGAT ATTAACCA
101 TCTTGGCTAG ACATGGATTT GAGAACATTC AGGGCAGTGT TTATCTAGGC
151 CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAACTGAC
201 CGCTCGGTTT GATTGGTTTT ACTCCTGTAT TTCAAACATT AAGTTTACC
251 GCCTTGAAAG TGATTGTAAC GCACAATTTA TCGCTGATGG TGTGTATCAA
301 GCCAAACAGG CTTTCCTTCA ACGTGTGTA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGCTGATG AGCAATCAA TCAGGTTCTG GAAAACAGA
401 AATTTGAATT GGAAAGTCCT AACCTGAAAT TAAATTAA

```

1230

This corresponds to the amino acid sequence <SEQ ID 2590; ORF 755>:

```
m755.pep..
  1 MSRYLITFDM DTNCLKDNYH GNNYTNAYSD IKTILARHGF ENIQGSVYLG
 51 REGISEAHGT IAIQELTARF DWFYSCISNI KFYRLESDLN AQFIADGVYQ
101 AKQAFLOQVE QLRISLTEAG LSDEQINQVL EKQKFELESP NLKLN*
```

a755.seq not found yet

a755.pep not found yet

g756.seq not found yet

g756.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2591>:

```
m756.seq
  1 ATGACCGCCA ACTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
 51 CAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGCA AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2592; ORF 756>:

```
m756.pep
  1 MTANFAQTLV EIQDSLVRV STVQYGGDNL KRLTADKRKQ YELNFKISEG
 51 STRVESDFKE TLVRFGDML QDMPPKIRSA TLVALTTLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DVFQIGRRSY
151 SREDISEANR RAERVYPYGA LVSDGNFTAV LSDIGD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2593>:

```
a756.seq
  1 ATGACCGCCA ACTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
 51 NAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGCA AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2594; ORF 756.a>:

```
a756.pep
  1 MTANFAQTLV EIQDSLXRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
 51 STRVESDFKE TLVRFGDML QDMPPKIRSA TLVALTTLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DVFQIGRRSY
151 SREDISEANR RAERVYPYGA LVSDGNFTAV LSDIGD*
```

m756 / a756 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
m756.pep	MTANFAQTLVEIQDSLVRVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
a756	MTANFAQTLVEIQDSLXRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
	10	20	30	40	50	60

1231

```

              70      80      90      100      110      120
m756.pep      TLVRFGRDMLQDMPPKIRSATLVALTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD
              |||||
a756          TLVRFGRDMLQDMPPKIRSATLVALTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD
              70      80      90      100      110      120

              130      140      150      160      170      180
m756.pep      RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV
              |||||
a756          RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVYPYGAELVSDGNFTAV
              130      140      150      160      170      180

m756.pep      LSDIGDX
              |||||
a756          LSDIGDX

```

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

```

m757.seq
1  ATGAAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51  TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTAAAAACC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCAATA AAGGGCTGAA TGACCAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCGGAAGG AAAGAATCTG CTGCATGACT
251 TTTGAGACGG CCTCACAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAAGC
351 GGAAAACTG TCCAAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
401 AAGACCGCAC AATGCTGCGT GATACCGCGC ACCAAATCGA AATGGCGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGAATGGG CGCGTGGTGG
501 GATTGCTTAT AAAGTCACTG TTACCAATTT ACCGAGCGTG GTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2596; ORF 757>:

```

m757.pep (lipoprotein)
1  MKILALLIAA TCALSACGSQ SEEQPASAQP QEQAQSELKT MPVSYTDYQS
51  AANKGLNDQK TGLTLPEHVV PIDNAEGKNL LHDFSGLTI LTVDTDKADK
101 ITAVRVVWNT DAMPQKAEL SKAAAALIAA TAPEDRTMLR DTGDQIEMAI
151 DSHNAQKEPT REWARGGIAY KVTVTNLPSV VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

```

m758.seq
1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAAC TGGTGAATTT CCGTCTGCT ACGGCGGCGA ATACGGCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTCGGTGC GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGCGGCG TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTGTA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGCAAAA GGATTGAGCC
501 ATGA

```

1232

This corresponds to the amino acid sequence <SEQ ID 2598; ORF 758>:

```
m758.pep
  1 MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51 DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101 RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPT
151 LLAAGDQVRF VAERIEP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2599>:

```
a758.seq
  1 ATGAACAATC TGACCGTGTT CACCCGTTTC GATACCGATT TGGCGACGCT
 51 TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAACCT GGTGGAAATT CCCGCTCTGCT ACGGCGGCGA ATACGGCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CTGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCCG
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGACAGAA GGATTGAGCC
501 ATGA
```

This corresponds to the amino acid sequence <SEQ ID 2600; ORF 758.a>:

```
a758.pep..
  1 MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51 DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101 RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPT
151 LLAAGDQVRF VAERIEP*
```

m758 / a758 100.0% identity in 167 aa overlap

m758.pep	10	20	30	40	50	60
	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGGEYGPDLAEVAAFHQ					
a758						
	10	20	30	40	50	60
	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGGEYGPDLAEVAAFHQ					
m758.pep	70	80	90	100	110	120
	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPAGSVGIGGSQT					
a758						
	70	80	90	100	110	120
	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPAGSVGIGGSQT					
m758.pep	130	140	150	160		
	GVYPFASPGGWQIIGRTELPFRADLNPPTLLAAGDQVRFVAERIEPX					
a758						
	130	140	150	160		
	GVYPFASPGGWQIIGRTELPFRADLNPPTLLAAGDQVRFVAERIEPX					

g759.seq not found yet

g759.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2601>:

```
m759.seq
  1 ATGCGCTTCA CACACACCAC CCCATTTTGT TCCGTATTGT CCACCCTCGG
 51 TCTTTTGGCC GTTCCCTG CTTACTCATC CATGTGCCG AACGATGTCG
101 ATTACCAATA TTTTCGCGAC TTTGCCGAAA ATAAAGCGC GTTCACCGTA
151 GGTGCAAGCA ATATTTCCAT CCAAGACAAG CAAGGCAAAA TATTAGGCAG
201 GGTCTCAAC GGCATCCCA TGCCCGACTT CCGCGTCAGC AACCGCCAAA
251 CCGCCATCGC CACCCTGGTT CACCCCAAT ACGTCAACAG TGTCAAACAC
301 AACGTCGGCT ACGTTCCAT ACAATTCGGC AACGACACCC AAAATCCAGA
351 AGAACAAGCC TATACCTACC GCCTCGTATC ACGCAACCCG CACCCGACT
401 ACGACTACCA CTTCCCGC CTCAACAAAC TGGTTACCGA AATCTCACCT
```

451 ACCGCACTCA GCAGCGTACC CTTGCTTGGA AACGGCCAGC CAAAGGCCAA  
 501 TGCCTACCTC GATACCGACC GCTTCCCCTA CTTTGTACGA CTCGGCTCAG  
 551 GCACGCAACA AGTCCGCAAA GCAGACGGCA CGCGTACACG AACCGCCCCG  
 601 GCATACCAAT ACCTGACCGG CGGCACGCCG CTGAAAGTAT TGGGGTTCCA  
 651 AAACCCACGGC TTACTCGTCG GCGGCAGCCT GACCGACCAA CCCCTTAACA  
 701 CCTACGCAAT CGCCGGAGAC AGCGGTTCCC CCCTGTTTGC CTCGACAAG  
 751 CATGAAAACC GCTGGGTGCT TCGGGGCGTA CTCAGCACCT ACGCCGGCTT  
 801 CGATAATTTC TTCAACAAAT ACATCGTCAC GCAACCCGAA TTCATCCGTT  
 851 CCACCATCCG CCAATACGAA ACCCGGCTGG ATGTCGGGCT GACCACCAAC  
 901 GAACTCATAT GGC CGCAGCAA CGGTAATGGC AACAGCACCC TGCAAGGGCT  
 951 CAACGAACGC ATCACCCTGC CCATTGCAA CCCTTCGCTT GCCCCACAAA  
 1001 ACGACAGCAG GCACATGCCG TCTGAAGATG CCGGCAAAAC GCTCATCCTA  
 1051 TCCAGCAGGT TCGACAACAA AACACTGATG CTGGCAGACA ATATCAACCA  
 1101 AGGCGCAGGC GCATTGCACT TCGACAGCAA CTTACCCGTC GTCGGTAAAA  
 1151 ACCACACATG GCAAGGTGCA GCGGTTATCG TAGCCGACGG CAAACGCGTC  
 1201 TTCTGGCAAG TCAGCAACCC CAAAGGCGAC CGGCTCTCCA AACTGGGCGC  
 1251 AGGCACGCTT ATCGCCAACG GACAAGGCAT CAACCAGGGC GACATCAGCA  
 1301 TCGGGGAAGG CACTGTCGTA CTCGCCCAA AAGCTGCTTC AGACGGCAGC  
 1351 AAACAAGCAT TCAACCAAGT CGGCATCACC AGCGGCAGGG GCACGGCCGT  
 1401 CCTCGCCGAC AGCCAGCAAA TCAAACCCGA AAACCTCTAT TTCGGCTTCA  
 1451 GGGGCGGACG GCTCGACCTC AACGGCAACA ACCTTGCTT TACCCATATC  
 1501 CGCCATGCGG ACGGCGGCGC GCAAATCGTC AATCACAACC CTGACCAAGC  
 1551 CGCGACACTG ACGCTGACCG GCAACCCCGT CCTCAGTCCC GAGCATGTGCG  
 1601 AGTGGGTGCA ATGGGGCAAC CGTCCGCAAG GCAACGCGGC GGTTTACGAA  
 1651 TACATCAACC CGCACCGBAA CCGTCGGACC GACTACTTCA TACTCAAACC  
 1701 CGGCGGCAAC CCGCGCGAAT TTTTCCGTT AAATATGAAA AACTCAACAA  
 1751 GCTGGCAATT TATCGGCAAC AACAGGCAAC AGGCCGCGA ACAAGTCGCC  
 1801 CAAGCCGAAA ATGCCCGCCC CGACCTGATT ACCTTCGGCG GATACTTGGG  
 1851 TGAAAACGCG CAAACGGGCA AAGCCGCGCC GAGTTACAGC AAAACCAATG  
 1901 AAGCAGCCAT AGAAAAAACC CGCCATATCG CAAATGCCGC CGTATACGGC  
 1951 CGGCCCGAAT ACCGTTACAA CGGCGCACTC AACCTGCACT ATCGTCCCAA  
 2001 ACGCACCGAC AGCACGCTGT TGCTCAACGG CGGCATGAAC CTTAACGGGG  
 2051 AAGTCTTGAT TGAGGGCGGC AATATGATTG TGTCAGGCAG GCCGTACCC  
 2101 CATGCTACG ACCACCAGGC CAAACGCGAA CCCGTTCTTG AAAACGAATG  
 2151 CACCGACGGC AGCTTCAAGG CTGCACGGTT CACCCTGCGA AACCATGCC  
 2201 GACTGACGGC AGGGCGCAAT ACCGCGCATC TGGACGGCGA CATAACCGCA  
 2251 TACGATCTGT CCGGCATCGA CCTCGGCTTT ACCCAAGGCA AAACACCGGA  
 2301 ATGCTACCGC TCCTACCATA GCGGCAGCAC CCACTGCACA CCCAACGCCG  
 2351 TTTTAAAAGC CGAAAACATAT CGTGCACTAC CTGCAACGCA AGTACGCGGC  
 2401 GACATTACCC TTAACGACCG TTCAGAGCTC CGCCTGGGCA AAGCACACCT  
 2451 GTACGGCAGC ATCCGTGCCG GCAAAGACAC CGCAGTCCGC ATGGAAGCAG  
 2501 ACAGCAACTG GACACTTTCC CAGTCCAGCC ACACCGGGCC ACTGACGCTT  
 2551 GACGGCGCAC AAATTACCTT GAACCCCGAT TTCGCCAATA ATACACACAA  
 2601 CAACCGCTTC AACACACTGA CCGTCAACGG CACACTTGAC GGGTTCGGCA  
 2651 CATTCCGATT CCTGACCGGC ATCGTCCGAA AACAAAATGC CCCCCCCTC  
 2701 AAAGTGAAG GGGACAGCCG CGGCGCATTC CAAATCCAGC TCAAAAACAC  
 2751 CGGACAAGAA CCTCAAACAA CCGAATCGCT TGCACTTGTC AGCCTCAATC  
 2801 CGAAACACAG CCACCAAGCC CGATTACCC TCCAAAACGG CTATGCCGAT  
 2851 TTGGGTGCCT ACCGCTACAT CCTCCGCAA AACAAACACG GATACAGCCT  
 2901 GTACAACCCG CTCAAAGAGG CCGAATTCA AATTGAAGCC ACGCGTGC GG  
 2951 AACATGAGCG CAACCAACAG GCATACAACC AATTACAGGC AACCGACATC  
 3001 AGCAGACAGG TTCAACATGA CTCTGACGCG ACCAGGCAGG CACTACAGGC  
 3051 CTGGCAGAAC AGTCAAACCG AACTTGCCCG CATCGACAGC CAAGTCCAAT  
 3101 ATCTGTCCGC CCAATTGAAA CAGACAGACC CGCTGACCGG CATTCTGACG  
 3151 CGTGCCCAAA ACCTGTGTGC CGCACAAGGA TACAGTGCCG ATATCTGCCG  
 3201 TCAGGTTGCC AAAGCCGCCG ACACGAACGA CCTGACACTC TTCGAAACCG  
 3251 AACTGGATAC GTATATAGAA CGTGTAGAAA TGGCCGAATC CGAACTTGAC  
 3301 AAAGCACGGC AAGGCGGGCA TGCGCAAGCC GTCGAAACAG CCCGGCAGGC  
 3351 CTACCTGAAC GCACTCAACC GTCTGTCCCG ACAAATCCAC AGTTTGAAAA  
 3401 CCGGCGTTGC CGGCATCCGT ATGCCGAACC TGGCCGAAT GATCAGCCGG  
 3451 TCGGCCAACA CGCCGTTTC CGAACAGGCC GCCTACAATA CCGGCCGGCA  
 3501 ACAGGCGGGA CGCCGCATCG ACCGCCACCT TACCGATCCG CAGCAGCAAA  
 3551 ACATCTGGCT GGAACCCGGT ACGCAACAAA CCGACTACCA TAGCGGCACA  
 3601 CACCGTCCCT ACCAACAAC TACCAACTAT GCACATATCG GCATCCAAAC  
 3651 CGGCATCACC GACCGTCTCA GTGTCGGTAC GATTTTAACC GATGAGCGCA  
 3701 CAAACAACCG TTTTGATGAA GCGGTATCCG CCCGAAACCG CAGCAACGGC

1234

```

3751 GCACATCTGT TCGTCAAAGG GGAAAACGGC GCACTCTTTG CCGCGGCAGA
3801 TTTAGGCTAC AGCAACAGCC GTACCCGATT TACCGATTAT GACGGGGCTG
3851 CCGTCCGCGG CCACGCATGG GATGCAGGCA TCAACACCGG CATCAAATC
3901 GATACCGGCA TCAACCTCAG ACCCTATGCC GGCATCCGTA TAAACCGCAG
3951 CAACGGCAAC CGGTACGTAC TCGACGGCGC AGAGATAAAC AGCCCGGCGC
4001 AAATCCAAAC CACATGGCAT GCCGGCATCC GTCTCGATAA AACCCTCGAA
4051 CTGGGTCAAG CCAAGCTGAC CCCCGCCTTC AGCAGCGATT ACTACCATAC
4101 CCGCCAAAC AGCGGTTCG CCCTCAGCGT CAACGACCGT ACCTTACTGC
4151 AGCAAGCCGC CCACGGCACA CTGCATACCC TGCAAATCGA CGCCGGATAC
4201 AAAGGCTGGA ACGCCAAACT TCATGCCGCT TACGGCAAAG ACAGCAACAC
4251 CGCCCGCCAC AAACAGGCAG GAATCAAAT AGGCTACAAC TGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2602; ORF 759>:

```

m759.pep
1 MRFTHTPFC SVLSTLGLFA VSPAYSSIVR NDVDYQYFRD FAENKGAFTV
51 GASNISIQDK QGKILGRVLN GIPMPDFRVS NRQTAIATLV HPQVNSVVKH
101 NVGYGSIQFG NDTQNPEEQ A YTYRLVSRNP HPDYDYHLPR LNKLVTEISP
151 TALSSVPLLG NGQPKANAYL DTRFPYFVR LSGSTQQVRK ADGTRTRTAP
201 AYQYLTGGTP LKVLGFQNHG LLVGGSLTDQ PLNTYAIAGD SGSPLFAFDK
251 HENRWVLAGV LSTYAGFDNF FNKYIVTQPE FIRSTIRQYE TRLDVGLTTN
301 ELIWRDNGNG NSTLQGLNER ITLPIANPSL APQND SRHMP SEDAGKTLIL
351 SSRFDNKTLM LADNINQGAG ALQFDSNFTV VGKNHTWQGA GVIVADGKRV
401 FQVSNPKGD RLSKLGAAGT IANGQGINQG DISIGEGTVV LAQKAASDGS
451 KQAFNQVGIT SGRGTAVLAD SQQIKPENLY FGFRGGRLDL NGNNLAFTHI
501 RHADGGAQIV NHPDQAATL TLTGNPVLSP EHVEWVQWGN RPOGNAAVYE
551 YINPHRNRRT DYFILKPGGN PREFPLNMK NSTSWQFIGN NRQQAEEQVA
601 QAENARPDLI TFGGYLGENA QTGKAAPSYS KTNEAAIEKT RHIANAAYVG
651 RPEYRYNGAL NLHYRPKRTD STLLNGGMN LNGEVLIIEG NMIVSGRPVE
701 HAYDHOAKRE PVLENEWTDG SFKAARFTLR NHARLTAGRN TAHL DGDITA
751 YDLSGIDLGF TQGKTPECYR SYHSGSTHCT PNAVLKAENY RALPATQVRG
801 DITLNRSEL RLGKAHLYGS IRAGKDTAVR MEADSNWTL S QSHTGALTL
851 DGAQITLNP FANNTHNNRF NTLTVNGTLD GFGTFRFLTG IVRKQNPAPL
901 KLEGDSRGAF QIHVKNTGQE PQTTESLALV SLNPKHSHQA RFTLQNGYAD
951 LGAYRYILRK NNGYSLYNP LKEAELQIEA TRAEHERNQQ AYNQLQATDI
1001 SRQVQHSDA TRQALQAWQN SQTELARIDS QVQYLSAQLK QTDPLTGILT
1051 RAQNLCAAQG YSADICRQVA KAADTNDLTL FETELDTYIE RVMAESEL D
1101 KARQGGDAQA VETARHAYLN ALNRLSRQIH SLKTGVAGIR MPNLAE LISR
1151 SANTAVSEQA AYNTGRQQAG RRIDRHLTDP QQQNIWLETG TQQTDYHSGT
1201 HRPYQQTNNY AHIGIQTGIT DRLSVGTILT DERTNNRFE GVSARNRSNG
1251 AHLFVKGENG ALFAAADLGY SNSRTRFTDY DGAAVRRHAW DAGINTGIKI
1301 DTGINLRPYA GIRINRSNGN RYVLDGAEIN SPAQIQTTWH AGIRLDKTVE
1351 LGQAKLT PAF SSDYYHTRQN SGSALSVNDR TLLQQA AHGT LHTLQIDAGY
1401 KGWNAKLHAA YGKDSNTARH KQAGIKIGYN W*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2603>:

```

g760.seq (partial)
1 AACAAACGCA ACACCCGTTA CGCCGCATTG GGCAAACGGC TGATGGAAGG
51 CGTTGAGACC GAAATCAGCG GTGCGATTAC ACCGAAATGG CAAATCCATG
101 CAGGTTACAG CTATCTGCAC AGCCAAATCA AAACCGCCGC CAATCCACGC
151 GACGACGGCA TCTTCTGCT GGTGCCCAA CACAGCGCAA ACCTGTGGAC
201 GACTTACCAA GTTACGCCCG GGCTGACCGT CGGCGGCGGC GTGAACGCGA
251 TGAGCGGCAT TACTTCATCT GCAGGATGTC ATGCAGGCGG TTATGCCACG
301 TTCGATGCGA TGGCGGCATA CCGCTTCACG CCCAAGCTGA AGCTGCAAAAT
351 CAATGCCGAC AACATCTTCA ACCGCCATTA CTACGCCCGC GTCGGCGGCA
401 CGAACACCTT TAACATTCCC GGTTCGGAGC GCAGCCTGAC GGCAAACCTG
451 CGTTACAGTT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2604; ORF 760.ng>:

```

g760.pep (partial)
1 NNRNTRYAAL GKRVMIEGVE EISGAITPKW QIHAGYSYLH SQIKTAANPR
51 DDGIFLLVFK HSNLWTTYQ VTPGLTVGGG VNAMSGITSS AGMHAGGYAT
101 FDAMAAYRFT PKLKLQINAD NIFNRHYEAR VGGTNTFNIP GSERSLTANL
151 RYSF*

```

1235

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

```
m760.seq
1  ATGGGACAGT TTATGTCACT TTTCCGCATC AATATGACCG CCGCCACGGT
51  TTTGGCAGCA CTCTCGTCTT CGGTTTTTGC CGCACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCTT ACAACGCGAT TGCCACCGAG
151 AAAAACGGCG ATTACAGCTC GTTTGCGGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCAGC
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCCGGCCTGC GCGTGTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTAC GAATACAGCG AATACAACAT CGACGGCCTG CCCGCGCAGA
401 TGCAGAGTAT CAACGGCACG CTGCCCAACC TGTTGCGCTT CGACCGCGTG
451 GAAGTGATGC GCGGGCCGAG CGGACTGTTT GACAGCAGCG GCGAGATGGG
501 CGGCATCGTG AATCTGGTGC GCAAACGCCC GACCAAAGCG TTCCAAGGTC
551 ATGCGGCGGC AGGGTTCGGT ACGCACAAAC AATATAAAGC CGAGGCGGAC
601 GATCGGGCA GCCTCAATTC AGACGGCAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GCGCGCTCTC CGCGTCCC GCAGAAAAAC AACCGGCGCG
701 AAACCTTCTA CGCGGCGGCG GATTGGGACA TCAACCCCGA TACGGTTTTG
751 GCGCGGGCT ATCTTTACCA GCAACGCGCG CTCGCGCGGT ACAACGGCCT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCGCA CACGTATTTG
851 TCGGCGCGGA TTGGAACAAA TTTAAATGCG ACAGCCACGA CGTGTTCGCC
901 GATTTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG
951 CTATTCCGAT CGGAAAGCCG ATTCCAATTA TACGTTTGGC GGCAGCAAAC
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAAGCCT TTGCGGTTGA CGCAAGTTAC AGCGTCCGT TTGCTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCGCA
1151 GTACTAATGA ACAAGGGCGT TCGACTTTGT CAAAAAGCGT CGCTTTAGAT
1201 GGTTCGCGG CTTTGCCCTTA TAACGGCATA CTTCAGAACG CCCGCGCCGG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAACCTC GACGAAACCG
1301 GTTTGTATGC CAAGACGGTG TTCCGTCCTC TGGAGGTTT GTCGTTGATT
1351 GCAGGCGGAC GTGTAGGACA TCACAAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAATTTTAC AAGCTACGCC GCGCGGTTT
1451 ACGATATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCTC CCAACTCTAC
1501 ACACCGCAAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACCGCGCGA
1551 AGGCAACCG TTTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC
1601 TCAATACCCG GGTTCGTTT TACCGCATGA AGGATAAAAA CGCCGCCGCA
1651 CCGCTGGACT CAAACAACAA AAAAACCCGT TACGCCGCGT TGGGCAACG
1701 CGTGATGGAA GGTGTTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAAT
1751 GGCAAATCCA TGCAGGTTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC
1801 TCTCAATTCG GCGACGAAGG CATCTTCTG CTGATGCCCA AACACAGCGC
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG
1901 GCGTGAACGC GATGAGCGGC ATTACTTCAT CTGCAGGGAT ACATGCAGGC
1951 GGTATATGCCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAAACT
2001 GAAGCTGCAA ATCAACGCCG ACAACATCTT CAACCGCCAT TACTACGCCC
2051 GCGTCGGCAG CGAGAGCACC TTTAACATTC CCGGTTGCGA GCGCAGCCTG
2101 ACGGCAAACC TGCCTTACAG TTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

```
m760.pep
1  MGQFMSVFRI NMTAATVLAA LSSSVFAAQT EGLETVHIKG QRSYNAIATE
51  KNGDYSSFAA TVGTKIPASL REIPQSVSII TNQQVKDRNV DTFDQLARKT
101 PGLRVLSNDD GRSSVYARGY EYSEYNIDGL PAQMQSINGT LPNLFADFDRV
151 EVMRGPSGLF DSSGEMGGIV NLVRKRPTKA FQGHAAAGFG THKQYKAEAD
201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDTVL
251 GAGYLYQQR LAPYNGLPAD ANNKLPSLPQ HVFVGADWNK FKMHSADVFA
301 DLKHYFGNGG YGKVGMRYSR RKADSNYTF GSKLNNTGQA DVAGLGTDIK
351 QKAFAVDASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLKSVVALD
401 GFRLPYNGI LQNRAGNKG FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGHKKI ESGDGKTLHK ASKTFTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA
551 PLDSNNKKTR YAALGKRVME GVETEISGAM TPKWQIHAGY SYLHSQIKTA
601 SNSRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAA YRFTPCLKLQ INADNIFNRH YYARVGSEST FNIPGSERSL
701 TANLRYSF*
```

1236

m760 / g760 91.6% identity in 154 aa overlap

	530	540	550	560	570	580
m760.pep	YKGSYMDRLNTRVSYRMKDKNAAAPLDSNNKTRYAALGKRVMEGVETEISGAMTPKW					
				:		
g760				NNRNTRYAALGKRVMEGVETEISGAITPKW		
				10	20	30
	590	600	610	620	630	640
m760.pep	QIHAGYSYLHSQIKTASNSRDEGIFLLMPKHSANLWTTYQVTSGLTIGGGVNAMSGITSS					
g760	QIHAGYSYLHSQIKTAAANPRDDGIFLLVPKHSANLWTTYQVTPGLTVGGGVNAMSGITSS					
	40	50	60	70	80	90
	650	660	670	680	690	700
m760.pep	AGIHAGGYATFDAMAAAYRFTPKLKLQINADNIFNRHYARVGSESTFNIPGSERSLTANL					
g760	AGMHAGGYATFDAMAAAYRFTPKLKLQINADNIFNRHYARVGSTNTFNIPGSERSLTANL					
	100	110	120	130	140	150
	709					
m760.pep	RYSEFX					
g760	RYSEFX					

g761.seq not found yet

g761.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2607>:

```

m761.seq
1  ATGAAATAT  CATTTCATTT  AGCTTTATTA  CCCACGCTGA  TTATTGCTTC
51  CTTCCTGTT  GCTGCCGCCG  ATACGCAGGA  CAATGGTGAA  CATTACACCG
101 CCACTCTGCC  CACCGTTTCC  GTGGTCGGAC  AGTCCGACAC  CAGCGTACTC
151 AAAGGCTACA  TCAACTACGA  CGAAGCCGCC  GTTACCCGCA  ACGGACAGCT
201 CATCAAGAA  ACGCCGCAAA  CCATCGATAC  GCTCAATATC  CAGAAAAACA
251 AAAATTACGG  TACGAACGAT  TTGAGTTCCA  TCCTCGAAGG  CAATGCCGGC
301 ATCGACGCTG  CCTACGATAT  GCGCGGTGAA  AGCATTTTTC  TGCGCGGTTT
351 TCAAGCCGAC  GCATCCGATA  TTTACCGCGA  CGGCGTGCGC  GAAAGCCGAC
401 AAGTGCGCCG  CAGTACTGCC  AACATCGAGC  GCGTGGAAAT  CCTGAAAGGC
451 CCGTCTTCCG  TGCTTTACGG  CCGCACCAAC  GGCGGCGGCG  TCATCAACAT
501 GGTCAGCAAA  TACGCCAACT  TCAAAACAAAG  CCGCAACATC  GGAGCGGTTT
551 ACGGCTCATG  GGCAAACCGC  AGCCTGAATA  TGGACATTAA  CGAAGTGCTG
601 AACAAAAACG  TCGCCATCCG  TCTCACCAGC  GAAGTCGGGC  GCGCAATTC
651 GTTCCGCAGC  GGCATAGACA  GCAAAATGT  CATGGTTTCG  CCCAGCATT
701 CCGTCAAAC  CGACAACGGC  TTGAAGTGGA  CGGGGCAATA  CACCTACGAC
751 AATGTGGAGC  GCACGCCCGA  CCGCAGTCCG  ACCAAGTCCG  TGTACGACCG
801 CTTCCGACTG  CCTTACCGCA  TGGGGTTCGC  CCACCGGAAC  GATTTTGTCA
851 AAGACAAGCT  GCAAGTTTGG  CGTTCGAC  TTGAATACGC  CTCAACGAC
901 AAATGGCGTG  CCCAATGGCA  GCTCGCCAC  CGCACGGCGG  CGCAGGATTT
951 TGATCATTT  TATGCAGGCA  GCGAAAATGG  CAACTTAATC  AAACGTAATC
1001 ACGCCTGGCA  GCAGACCGAC  AACAAAACCC  TGTCGTCCAA  CTTAACGCTC
1051 AACGGCGACT  ACACCATCGG  CCGTTTGTAA  AACCACCTGA  CCGTAGGCAT
1101 GGATTACAGC  CGCGAACACC  GCAACCCGAC  ATTGGGTTTC  AGCAGCGCCT
1151 TTTCCGCCTC  CATCAACCCC  TACGACCGCG  CAAGCTGGCC  GGCTTCGGGC
1201 AGATTGCAGC  CTATTCTGAC  CCAAAACCGC  CACAAAGCCG  ACTCCTACGG
1251 CATCTTTGTG  CAAAACATCT  TCTCCGCCAC  GCCCGATTG  AAATTCGTCC
1301 TCGGCGGCCG  TTACGACAAA  TACACCTTTA  ATTCCGAAAA  CAAACTCACC
1351 GGCAGCAGCC  GCCAATACAG  CGGACACTCG  TTCAGCCCCA  ACATCGGCGC
1401 AGTGTGGAAC  ATCAATCCCG  TCCACACACT  TTACGCCTCG  TATAACAAAG
1451 GCTTCGCGCC  TTATGGCGGA  CGCGGCGGCT  ATTTGAGCAT  CGATACGTTG
1501 TCTTCCGCCG  TGTTCACGCG  CGACCCCGAG  TACACCCGCC  AATACGAAAC
1551 CGGCGTGAAA  AGCAGTTGGC  TGGACGACCG  CCTCAGCACT  ACGTTGTCTG
1601 CCTACCAAT  CGAACGCTTC  AATATCCGCT  ACCGCCCGCA  TCCAAAAAAC
1651 AACCTTATA  TTTATGCGGT  TAGCGGCAAA  CACCGTTCGC  GCGGCGTGGA

```



1237

```

1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT
1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCGTAACCG
1901 GTACAGGCAA ACGCTACGGT TACAACCTAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

m761.pep

```

1 MKISFHLALL PTLIIASFPV AAADTDNGE HYTATLPTVS VVGQSDTSVL
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSX YANFKQSRNI GAVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDFGL PYRMGFARHN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQT D NKTLSNLTL
351 NGDYITIGREF NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFLVGGRYDK YTFNSNKLTL
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFAFYGG RGGYLSIDTL
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRDPKPN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRSLGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT
651 LPGAARVDAM LGWNHKNVNV TFAANLLNQ KYWRSDSMPG NPGYTARVN
701 YRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

a761.seq

```

1 ATGAAAATAT CATTTTATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51 CTTCCCTGTT GCTGCCGCGG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCGG CCTACGATAT GCGCGGCGAA AGCATTTTCC TGCGCGGCTT
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC
401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAAT CCTGAAAGGT
451 CCGTCTCTCG TGCTTTATGG GCGTACCAAC GCGGCGGGTG TCATCAACAT
501 GGTACAGCAA TACGCCAACT TCAACAAAG CCGTAATATC GGTACGGTTT
551 ATGGTTCTGT GGCAAACCGC AGCCTGAATA TGGACATCAA CGAAGTGCTG
601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC
651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATT
701 CCGTCAAAC TACGACCGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC
751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG GTTACGACCG
801 CTTCCGACTG CCTTACCGCA TGGGGTTTCG CCACCGGAAC GATTTTGTCA
851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC
901 AAATGGCGTG CCCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT
951 TGATCATTTC TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAATC
1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCA CTTAACGCTC
1051 AACGGCGACT ACACCATCGG CCGTTTGTGA AACCACTGA CCGTAGGCAT
1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT
1151 TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
1201 AGATTGCAGC CTATTCTGAC CCAAAACCGC CACAAAGCCG ACTCCTACGG
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTG AAATTCTGTC
1301 TCGGCGGCGG TTACGACAAA TACACCTTTA ATTCCGAAA CAAACTCACC
1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC
1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCTCG TATAACAAAG
1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTAGCAT CGATACGTTG
1501 TCTTCGCGCG GTTCAACGC CGACCCGAG TACACCCGCC AATACGAAAC
1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CTCAGCACT ACGTTGTCTG
1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCGA TCCAAAAAAC
1651 AACCCCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCG CGGCGGTGGA
1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

```

1238

```

1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCCTAACCG
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2610; ORF 761.a>:

```

a761.pep
1  MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
51  KGYINYDEAA VTRNGQLIKE TPQTIIDLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GTVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNMVVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDFGL PYRMGFARHN DFKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAQQTND NKTLSNLT
351 NGDYTIGRFE NHTLVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFLVGGRYDK YTFENSENKL
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL
501 SSAVENADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
551 NPYYIYAVSGK HSRGVELSA IGQIIPKKLY LRSLGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT
651 LPGFARVDAM LGWNHKNVNV TFAAANLFNQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

m761 / a761 99.6% identity in 703 aa overlap

m761.pep	10	20	30	40	50	60
	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
a761	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
	10	20	30	40	50	60
m761.pep	70	80	90	100	110	120
	VTRNGQLIKETPQTIIDLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
a761	VTRNGQLIKETPQTIIDLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
	70	80	90	100	110	120
m761.pep	130	140	150	160	170	180
	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRNNGGGVINMVSKYANFKQSRNI					
a761	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRNNGGGVINMVSKYANFKQSRNI					
	130	140	150	160	170	180
m761.pep	190	200	210	220	230	240
	GAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNMVSPSITVKLDNG					
a761	GTVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNMVSPSITVKLDNG					
	190	200	210	220	230	240
m761.pep	250	260	270	280	290	300
	LKWTGQYTYDNVERTPDRSPTKSVYDFGLPYRMGFARHNDFKDKLQVWRSLEYAFND					
a761	LKWTGQYTYDNVERTPDRSPTKSVYDFGLPYRMGFARHNDFKDKLQVWRSLEYAFND					
	250	260	270	280	290	300
m761.pep	310	320	330	340	350	360
	KWRAQWQLAHRRTAAQDFDHFYAGSENGNLIKRNAYAQQTNDKTLSSNLTNGDYTIGRFE					
a761	KWRAQWQLAHRRTAAQDFDHFYAGSENGNLIKRNAYAQQTNDKTLSSNLTNGDYTIGRFE					
	310	320	330	340	350	360
	370	380	390	400	410	420

1239

```

m761.pep  NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
|||||
a761      NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
          370      380      390      400      410      420

          430      440      450      460      470      480
m761.pep  QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
|||||
a761      QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
          430      440      450      460      470      480

          490      500      510      520      530      540
m761.pep  YNKGFAFYGGRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDLRLSTTSLAYQIERF
|||||
a761      YNKGFAFYGGRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDLRLSTTSLAYQIERF
          490      500      510      520      530      540

          550      560      570      580      590      600
m761.pep  NIRYRPDPKNNPYIYAVSGKHSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
|||||
a761      NIRYRPDPKNNPYIYAVSGKHSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
          550      560      570      580      590      600

          610      620      630      640      650      660
m761.pep  RVGIHLNNTSNVTGNLFFRYTPPTENLYGEIGVTGTGKRYGYSRNEKVTTLPGFARVDAM
|||||
a761      RVGIHLNNTSNVTGNLFFRYTPPTENLYGEIGVTGTGKRYGYSRNEKVTTLPGFARVDAM
          610      620      630      640      650      660

          670      680      690      700
m761.pep  LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
|||||
a761      LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
          670      680      690      700

```

g762.seq Not yet found

g762.pep Not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

```

m762.seq
1   ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT
301 AGTTTATGAG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
351 TGAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTCTT
401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

```

m762.pep
1   MKWLLNMIMR PIKFSMVNTL LFIVICSFF DLLVQLCTIL FHSQKIYFIT
51  LFLLEFIENFV TKSIIYMAIIY PILYFFTICK YYPYSRKVII LLSLALSIYF
101 SFMDFYFFSI YSDNLSYTE PLHLYIPIII NFFSLLSNF ILSFINK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

```

a762.seq
1   ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT

```

1240

301 AGTTTATG ACTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA  
351 TGAACGGAG CCTTACATT TATACATCCC TATTATTATT AATTTTCT  
401 CACTTTTAGT TTCTAATTT ATTTATCTT TTATCAACAA GTAA

This corresponds to the amino acid sequence <SEQ ID 2614; ORF 762.a>:

a762.pap  
1 MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT  
51 LFLLFIFNFV TKSIIYMAIIY PIIYFFTIKK YYPYSRKVII LLSLALSIYF  
101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NEFSLVSNF ILSFINK\*

m762 / a762 100.0% identity in 147 aa overlap

m762.pap	10	20	30	40	50	60
	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
a762	10	20	30	40	50	60
	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
m762.pap	70	80	90	100	110	120
	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
a762	70	80	90	100	110	120
	TKSIYMAIIYPILYFFTIKKYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
m762.pap	130	140				
	PLHLYIPIIINFSLVSNFILSFINKX					
a762	130	140				
	PLHLYIPIIINFSLVSNFILSFINKX					

g763.seq not yet found

g763.pap not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2615>:

m763.seq  
1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG  
51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT  
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA  
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC  
201 GCGCGAGCAA CATTGCGCTG ATTTTCAAGC GTCCCATTA CAGCGTGATG  
251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA  
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATT CTTCCACCCG  
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAACCTTA TTTGACGCTG  
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA  
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG  
501 TTATTTC AAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG  
551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT  
601 AAAGGTGCTG CCACCGCGCT GGATATTAC GAAGCCAAAG CCGGTTACGA  
651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG  
701 AAAACAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC  
751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA  
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC  
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA  
901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTGCGCT ATCAGAATAA  
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG  
1001 GGATGAGCGT CGGCGTACAG TTGAATTGCG CGCTTTATAC CGGCGGAGAA  
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC  
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT  
1151 ATACCGAAAG CCGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT  
1201 TTGGAAGCA GCCGTTTGA ACTGAAATCG ACCGAAACCG GCCAACATAA  
1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCGAG GAAGTCGCC  
1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT  
1351 TTGCGCTTGG TGAAAGAGAG CGGTTAGGG TTGGAACGG TATTTGCGGA  
1401 ATAA

1241

This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

```
m763.pep
1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFAQSHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDVTAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE
351 LSGKIHEAEA QYGAAEAQLT ATERHIKLA V RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQYGYR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

```
a763.seq
1  ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGCTA TTTCCGTTTG
51  CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTTCG CTTGCCACTA
151 TCCTTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG
251 CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATT TTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
551 AAAAAGAGGC TTATGCCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTACG GAAGCCAAAG CCGGTACGCA
651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACCAAGT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
1251 CGGCATCCCG AACCGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC
1301 AAGCAGAACA GAACTGGCT CAAGCAGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGG TTGGAAACGG TATTGCGGA
1401 ATAA
```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

```
a763.pep
1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFAQSHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDVTAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE
351 LSGKIHEAEA QYGAAEAQLT ATERHIKLA V RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQYGYR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*
```

m763 / a763 99.8% identity in 467 aa overlap

	10	20	30	40	50	60
m763.pep	MTLLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT					
a763	MTLLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT					
	10	20	30	40	50	60

1242

	70	80	90	100	110	120
m763.pep	LPEAWRAAQHSADFQASHYQ	ORDAVRARQQQAKAAFLPHV	SANASYQRQPPSISSTRETQ			
a763	LPEAWRAAQHSADFQASHYQ	ORDAVRARQQQAKAAFLPHV	SANASYQRQPPSISSTRETQ			
	70	80	90	100	110	120
	130	140	150	160	170	180
m763.pep	GWSVQVGQTLFDAAKFAQYRQ	SFRDTQAAEQRFDAAREELLK	VAESYFNVLLSRDTVAA			
a763	GWSVQVGQTLFDAAKFAQYRQ	SFRDTQAAEQRFDAAREELLK	VAESYFNVLLSRDTVAA			
	130	140	150	160	170	180
	190	200	210	220	230	240
m763.pep	HAAEKEAYAQQVRQAQALFNK	GAATALDIHEAKAGYDNALAQ	EIAVLAEKQTYENQLNDY			
a763	HAAEKEAYAQQVRQAQALFNK	GAATALDIHEAKAGYDNALAQ	EIAVLAEKQTYENQLNDY			
	190	200	210	220	230	240
	250	260	270	280	290	300
m763.pep	TDLDSKQIEAIDTANLLARYL	PKLERYSLDEWQRIALSNNHE	YRMQQLALQSSGQALRAA			
a763	TGLDSKQIEAIDTANLLARYL	PKLERYSLDEWQRIALSNNHE	YRMQQLALQSSGQALRAA			
	250	260	270	280	290	300
	310	320	330	340	350	360
m763.pep	QNSRYPTVSAHVGYNQNNLYT	SSAQNNDYHYRGKMSVGVQ	LNPLTYGGELSGKIHEAEA			
a763	QNSRYPTVSAHVGYNQNNLYT	SSAQNNDYHYRGKMSVGVQ	LNPLTYGGELSGKIHEAEA			
	310	320	330	340	350	360
	370	380	390	400	410	420
m763.pep	QYGAAEAQLTATERHIKLAVR	QAYTESGAARYQIMAQERVLE	SSRLKLKSTETGQQYGIR			
a763	QYGAAEAQLTATERHIKLAVR	QAYTESGAARYQIMAQERVLE	SSRLKLKSTETGQQYGIR			
	370	380	390	400	410	420
	430	440	450	460		
m763.pep	NRLEVIRARQEVAAEQKLAQ	ARYKFMLAYLRLVKESGLGL	ETVFAEX			
a763	NRLEVIRARQEVAAEQKLAQ	ARYKFMLAYLRLVKESGLGL	ETVFAEX			
	430	440	450	460		

1243

g764.seq not found yet

g764.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

```
m764.seq
1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTACTGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAATT GAAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCCGCGCATT TGGAAGTACG CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCCTG
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GCGGCGCGCA GCAAAACCAT CCAGCCGCTG
301 GAAACGGCGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCGAGGAG CAGAAGCTGG TTTCGGTGGG GCGGATCGAG CAGCAGAAAA
701 CAGCAGACTA CCGCCGTTTG CCGGCGGACA ATTTTATTTC GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGTCAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG GCGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCTACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGATTGC GCCCGATGAC GACAAAATGG ACGTGGAAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGCTTT CCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG CCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAAGCAGT GAATCTGACG GCGGGCATGA ATGTCACGGC GGAGATTAAA
1351 ACGGGTAAAC GCGGGGTGCT GGATTATCTG TTAAGCCCGC TGCAAACCAA
1401 ATTGGACGAA AGCTTTAGGG AGCGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2620; ORF 764>:

```
m764.pep
1  MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAEQAFLL PAHLELTDTP
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETAVVKAVHV RDQHVHKQGE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPFHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE QKLVSVAIE QOKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRQOTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVIAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVDHDAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTAIEIK
451 TGKRRVLDYL LSPLQTKLDE SFRER*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

```
a764.seq (partial)
1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCCCCTACAC TTACCGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCAATT GGAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCCGCGCATT TGGAAGTACG CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCCTG
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GCGGCGCGCA GCAAAACCAT CCAGCCGCTG
301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCGAGGAG CAGAAGCTGG TTTCGGTGGG GCGGATCGAG CAGCAGAAAA
```

1244

```

701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTGAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CCGTGCAGGA ATTGGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGGAAAT
1101 TTTGGTATTG AACAAAGACA TCGGTTTGTG GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

```

a764.pep (partial)
1  MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEQAF LPAHLELTDTP
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETVVVKAVHV RDGQHVKGGE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSAALRGHQ AELQSAKAQE QKLVSVGAIE QOKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVVAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVDHDAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

m764 / a764 99.3% identity in 435 aa overlap

	10	20	30	40	50	60
m764.pep	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAF LPAHLELTDTPVSAAPKWAAR					
a764	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAF LPAHLELTDTPVSAAPKWAAR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m764.pep	FIMAFALLALLWSWFGKIDIVAAASGKTVS GGRSKTIQPLETAVVKAVHV RDGQHVKGGE					
a764	FIMAFALLALLWSWFGKIDIVAAASGKTVS GGRSKTIQPLETAVVKAVHV RDGQHVKGGE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m764.pep	TLAELEAVGTDSDVVQSEQALQAAQLSKLRYEAVLAALESRTVPHIDMAQARSLGLSDAD					
a764	TLAELEAVGTDSDVVQSEQALQAAQLSKLRYEAVLAALESRTVPHIDMAQARSLGLSDAD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m764.pep	VQSAQVLAQH QYQAWAAQDAQLQSAALRGHQ AELQSAKAQE QKLVSVGAIE QOKTADYRRL					
a764	VQSAQVLAQH QYQAWAAQDAQLQSAALRGHQ AELQSAKAQE QKLVSVGAIE QOKTADYRRL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m764.pep	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA					
a764	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m764.pep	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVIAPDD					
a764	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVVAPDD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m764.pep	DKMDVEVLVLNKDIGFVEQQDAVVKIESFPYTRYGYLTGKVKSVDHDAVSHEQLGLVYT					



1245

```
|||||
a764      DKMDVEVLVLNKGIDGFEVQGDVAVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT
           370      380      390      400      410      420

           430      440      450      460      470
m764.pep  AVVSLDKHTLNIDGKAVNLTAGMNVTAIEIKTGKRRVLDYLLSPLQTKLDESFRERX
           |||||
a764      AVVSLDKHTLNIDGK
           430
```

g765.seq not yet found

g765.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```
m765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTGG GATTCAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCTTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTCGGG TCGTTGCTGA TGTTCACGGT CATGATTCGG CCACAATGAA
201 CGCTGCGGCT GCCAAAGATT ATATGAAAAC GGTGAGTTA AACAACTCTG
251 CCGGCAATGT CGATACACCA TCCAGAACAG CCCGACGGGT GCAGGCAGTA
301 TTTGACGCTA TGCTGCCTTA TGCCGATGCG GCAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCCG TGGAAAATG GCGTTTATA CGGGGATAGT CGACAACTC
451 AAGCTGACCG ATGACGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 CGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGCAA ATCTTGACCA
551 ATACGCGCGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAT
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGACGTACGG
651 TCTTACCTTG CCTTATAGCC GCAGCTTGGG AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCGGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAACACGAC CAAACGGCT TATTATATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCAAAGTGT CAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA
```

This corresponds to the amino acid sequence &lt;SEQ ID 2624; ORF 765&gt;:

```
m765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKEI SFLPSFKRIL CLSAVISVLG
51  ACAVVADVYG HDSATMNAAA AKDYMKTVEL NKSAGNVDTT SRTARRVQAV
101 FRRMLPYADA ANNTSHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDDEIAAI MGHMETHALH EHGKNKVGQQ ILTNTAAQIG TQIILDKKPD
201 TNPELVGLGM DILGTYGLTL PYRSLEEAA DEGGMMLMAQ AGYHPAAAVR
251 VWEKNQENDR QNGFIYATTS THPTNNARIE NLKRLLEPTVM PVYEQSVRNR
301 GRVNRKRRR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```
a765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTGG GATTCAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCTTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGACGGG TCGTTGCTGA TGTTCACGGT CAGGATTCGG CCACAATGAA
201 TGCTGCGGCT GCCAAAGATT ATATGAAAAC GGTGAGTTG AACAACTCTG
251 CCGGCAATGT CGATACTACA TCCAAAACAG CCCGTAGGGT GCAGGCAGTA
301 TTTGACGCTA TGTTGCCTTA TGCCGATGCG GCAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCCG CGGAAAATG GCGTTTATA CGGGGATAGT CGATAAACTT
451 AAGCTGACCG ATGGCGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 TGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGAAA ATCTTGACTA
551 ATATGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAC
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGATGTACGG
651 CATTACCTTG CCTTATAGCC GCAGCTTGGG AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCAGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAACACGAC CAAACGGCT TATTATATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCACAGTGT TAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA
```

This corresponds to the amino acid sequence &lt;SEQ ID 2626; ORF 765.a&gt;:

```
a765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKEI SFLPSFKRIL CLSAVISVLG
```

1246

```

51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FRRLPYADA ANNTGHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTGGEIAAI MGHEMTHALH EHGNKVGQK ILTNMAAQIG TQIILDKKPD
201 TNPELVGLGM DILGMYGITL PYSRSLLEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAITS THPTNNARIE NLKRLPTVM PVYEHVSRNK
301 GRVKNRRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

	10	20	30	40	50	60
m765.pep	MLRCRPKSVLDS	SDGIFLKFNF	LRSKPKYEIS	FLPSFKRILCL	SAVISVLGAC	AVVADVYG
a765	MLRCRPKSVLDS	SDGIFLKFNF	LRSKPKYEIS	FLPSFKRILCL	SAVISVLGAC	TVVADVYG
	10	20	30	40	50	60
m765.pep	70	80	90	100	110	120
	HDSATMNAAA	AKDYMKTVEL	NKSAGNVDTT	SRTARRVQAV	FRRLPYADA	ANNTSHKFDW
a765	QDSATMNAAA	AEDYMKTVEL	NKSAGNVDTT	SKTARRVQAV	FRRLPYADA	ANNTGHKFDW
	70	80	90	100	110	120
m765.pep	130	140	150	160	170	180
	KMTVFKNDEL	NAWAMPGGK	MAFYTGIVDK	LKLTDDEIA	AIMGHEMTH	ALHEHGKNGV
a765	KMTVFKNDEL	NAWAMPGGK	MAFYTGIVDK	LKLTDGEIA	AIMGHEMTH	ALHEHGKNGV
	130	140	150	160	170	180
m765.pep	190	200	210	220	230	240
	ILTNMAAQIG	TQIILDKKPD	TNPVLGMDIL	GTGLTPYSR	SLEEEADEG	GGMMLMAQ
a765	ILTNMAAQIG	TQIILDKKPD	TNPVLGMDIL	GTGLTPYSR	SLEEEADEG	GGMMLMAQ
	190	200	210	220	230	240
m765.pep	250	260	270	280	290	300
	AGYHPAAAVR	VWEKMNQEND	QNGFIYAITS	THPTNNARIE	NLKRLPTVM	PVYEQSVRNK
a765	AGYHPAAAVR	VWEKMNQEND	QNGFIYAITS	THPTNNARIE	NLKRLPTVM	PVYEHVSRNK
	250	260	270	280	290	300
m765.pep	310					
	GRVKNRRRX					
a765	GRVKNRRRX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

```

g767.seq
1  ATGAAGTTTA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTGTG TGGATAAAC
101 CCATTCTCTCA AGAACAGCCG GGAAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTTTGTGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAAACTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGTCTGGC
251 GGCCTGAAAT GCTCGGTCTG GCAAGAAATG CTGCTGCGGT CAAGCTGTCTG
301 GGTTTGAAAT ATCAGGCAAA CTCTGCTGTG TTTAAAGCAG TTTACGAACA
351 AAAAAATCCGT TTGGAACACA GGGCTGTTGC CGGGAATGG GCTTTATCTC
401 AAAAAGGTTT TGACGGCAAA AACTGATGCG GCGCCTATGA TTCCCCGAA
451 GCTGCCGCCG TCGCATTAAT AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCAGC CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAAGAATT GGTGCCCCAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

```

g767.pep
1  MKFKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQP GKIEVLEFFG
51  YFCVHCHHFD PLLLLKLGKAL PSDTYLRTEH VVWREMLGL ARMAAAVKLS

```

1247

101 GLKYQANSAV FKAVYEQKIR LENRAVAGKW ALSQKGFDDG KLMRAYDSPE  
 151 AAAVALKMQK LTEQYIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK  
 201 VREERKRQTP AVQK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2629>:

m767.seq  
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCCGCAG TGTGTCCGC  
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC  
 101 CCATTCCCTCA AGAACAGTCG GGTAAAATTG AGGTTTGGGA ATTTTCGGC  
 151 TATTCTCGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAACTGGG  
 201 CAAGGCATTG CCGTCTGATG CCTATTTGAG GACGGAGCAC GTGGTCTGGC  
 251 AGCCTGAAAT GCTCGGTTTG GCTAGGATGG CCGCTGCCGT CAATTTGTCG  
 301 GGTTTGAAAT ATCAGGCAAA CCCTGCTGTG TTTAAAGCAG TTTACGAACA  
 351 AAAAATCCGC TTGGAACA GGTGCGTTGC CGGAAATGG GCTTTGTCTC  
 401 AAAAAGGCTT TGACGGCAAA AACTGATGC GCGCTATGA TTCCCGCGAA  
 451 GGTGCGGCGG CCGCATTAAA AATGACGAAA CTGACGGAAC AATACCGCAT  
 501 CGACAGCAGC CCGACCGTTA TTGTCGGCGG AAAATACCGG GTTATCTTCA  
 551 ATAAACGGCT TGACGGCGGC GTTCATACGA TTAAGAATT GGTGCGCAAA  
 601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>:

m767.pep  
 1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQS GKIEVLEFFG  
 51 YFCVCHHFD PLLKLKAL PSDAYLRTEH VVWQPEMLGL ARMAAVNLS  
 101 GLKYQANPAV FKAVYEQKIR LENRSVAGKW ALSQKGFDDG KLMRAYDSPE  
 151 AAAAALKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK  
 201 VREERKRQTP AVQK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. gonorrhoeae*

m767/g767 95.8% identity in 214 aa overlap

	10	20	30	40	50	60
g767.pep	MKFKHLLPLL	LSAVLSAQAY	ALTEGEDYLV	LDKPIPQEQS	GKIEVLEFFG	YFCVCHHFD
m767	MKFKHLLPLL	LSAVLSAQAY	ALTEGEDYLV	LDKPIPQEQS	GKIEVLEFFG	YFCVCHHFD
	10	20	30	40	50	60
g767.pep	PLLLKLGKAL	PSDTYLRTEH	VVWRPEMLGL	ARMAAAVKLS	GLKYQANSAV	FKAVYEQKIR
m767	PLLLKLGKAL	PSDAYLRTEH	VVWQPEMLGL	ARMAAAVNLS	GLKYQANPAV	FKAVYEQKIR
	70	80	90	100	110	120
g767.pep	LENRAVAGKW	ALSQKGFDDG	KLMRAYDSPE	AAAAVALKMQ	KLTEQYIDST	PTVIVGGKYR
m767	LENRSVAGKW	ALSQKGFDDG	KLMRAYDSPE	AAAAALKMQK	LTEQYRIDST	PTVIVGGKYR
	130	140	150	160	170	180
g767.pep	VIFNNGFDGG	VHTIKELVAK	VREERKRQTP	AVQKX		
m767	VIFNNGFDGG	VHTIKELVAK	VREERKRQTP	AVQKX		
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2631>:

a767.seq  
 1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCCGCAG TGTGTCCGC  
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC  
 101 CCATTCCCTCA AAAACAGTCG GGCAAAATTG AGGTTTGGGA ATTTTCGGC  
 151 TATTCTCGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAAATGGG  
 201 CAAGGCATTG CCGTCTGATG CCTATTTAAG GACGGAGCAC GTGGTCTGGC  
 251 AGCCTGAAAT GCTCGGCTG GCAAGAATGG CTGCTGCCGT CAAGCTGTCA  
 301 GGTTTGAAAT ATCAGGCAAA CCCTGCCGTG TTTAAAGCAG TTTACGAACA  
 351 AAAAATCCGC TTGGAACA GGTGCGTTGC CGAATAATGG GCTTTGTCTC  
 401 AAAAAGGCTT TGACGGCAAA AACTGATGC GCGCTACGA CTCTCCTGCG

1248

```

451 GCAGCGGCTG CTGCATCAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGACGGCGGT GTTCATACGA TTAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

```

a767.pep
  1 MKLKHLPLLL LSAVLSAQAY ALTEGEDYLV LDKPIPKQKS GKIEVLEFFG
 51 YFCVCHHHFD PLLKLKGLAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
101 GLKYQANPAV FKAVYEQKIR LENRSVAEKW ALSQKGFDDG KLMRAYDSPA
151 AAAAASKMQQ LTEQYRIDST PTVVVGKYYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

```

m767/a767    96.7% identity in 214 aa overlap

      10      20      30      40      50      60
a767.pep    MKLKHLPLLLSAVLSAQAYALTEGEDYLVLDKPIPKQSGKIEVLEFFGYFCVCHHHFD
            |||
m767        MKLKHLPLLLSAVLSAQAYALTEGEDYLVLDKPIPEQSGKIEVLEFFGYFCVCHHHFD
      10      20      30      40      50      60

      70      80      90     100     110     120
a767.pep    PLLKLKGLALPSDAYLRTEHVWQPEMLGLARMAAAVKLSGLKYQANPAVFKAVYEQKIR
            |||
m767        PLLKLKGLALPSDAYLRTEHVWQPEMLGLARMAAAVNLSGLKYQANPAVFKAVYEQKIR
      70      80      90     100     110     120

      130     140     150     160     170     180
a767.pep    LENRSVAEKWALSQKGFDDGKLMRAYDSPAAAAASKMQQLTEQYRIDSTPTVVVGKYYR
            |||
m767        LENRSVAGKWALSQKGFDDGKLMRAYDSPEAAAAALKMQKLTQYRIDSTPTVIVGKYYR
      130     140     150     160     170     180

      190     200     210
a767.pep    VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
            |||
m767        VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX
      190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

```

g768.seq
  1 ATGAATATCA AACAAATTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCCGC AAAAACCCTG ATCCGCGCGC CAAACCGCGC
101 AACATTACAGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGTCATTTGC ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCGC
201 CATATACGAA GCCGCGCCCG ACAAGACAC GCCGCTCAAC CTCTACTGCC
251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
301 TATACAAATG TTGCAATCA CGGCGGTTAT GAAGACTGAC TCAAAAAGG
351 GATGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

```

g768.pep
  1 MNIKQLITAA LIASAAFATQ AAPQKPVSA QTAQHSVWVI DVRSEQEFSE
 51 GHLHNAVNIPI VDQIVRRIYE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
101 YTNVANHGGY EDLLKKGMK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

```

m768.seq
  1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCCGC AAAAACCCTG ATCCGCGCGC CAAACCGCGC
101 AACATCCGGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGGCATTTCG ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCGC
201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGCTCAAC CTCTACTGCC

```

1249

251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT  
 301 TATACAAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAGG  
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>:

m768.pep  
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE  
 51 GHLHNAVNI VQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG  
 101 YTNVANHGGY EDLLKGMK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. gonorrhoeae*

m768/g768 96.6% identity in 119 aa overlap

	10	20	30	40	50	60
g768.pep	MNIKQLITAALIASAFAAQAPQKPVSAQAQHSVWIDVRSEQEFSEGHNAVNIP					
m768	MNIKHLITAAALIASAFAAQAPQKPVSAQAQHSVWIDVRSEQEFSEGHNAVNIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g768.pep	VQIVRRIHEAAPDKDTPVNLVCRSGRRAEALQELKKAGYTNVANHGGYEDLLKGMKX					
m768	VQIVRRIHEAAPDKDTPVNLVCRSGRRAEALQELKKAGYTNVANHGGYEDLLKGMKX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2637>:

a768.seq  
 1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT  
 51 TGCCGCGCAG GCAGCCCGC AAAAACCCT ATCCGCGCC CAAACCGCGC  
 101 AACATTACAG CGTTTGGATC GATGTCCGCA GCGAACAGGA ATTTAGCGAA  
 151 GGTCATTGCG ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCGCGCG  
 201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC  
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAACTGAA AAAAGCAGGC  
 301 TATACGAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAGG  
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>:

a768.pep  
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSVWI DVRSEQEFSE  
 51 GHLHNAVNI VQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG  
 101 YTNVANHGGY EDLLKGMK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. meningitidis*:

m768/a768 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
a768.pep	MNIKHLITAAALIASAFAAQAPQKPVSAQAQHSVWIDVRSEQEFSEGHNAVNIP					
m768	MNIKHLITAAALIASAFAAQAPQKPVSAQAQHSVWIDVRSEQEFSEGHNAVNIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
a768.pep	VQIVRRIHEAAPDKDTPVNLVCRSGRRAEALQELKKAGYTNVANHGGYEDLLKGMKX					
m768	VQIVRRIHEAAPDKDTPVNLVCRSGRRAEALQELKKAGYTNVANHGGYEDLLKGMKX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

g769.seq  
 1 TTGATAATGG TTATTTTTTA TTTTATTTT TGTGGGAAGA CATTATATGCC  
 51 TGCACGAAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG  
 101 CCGAAGAaAC ACCgtgCGAA CCGGATTGA GAAGCCGTCC CGAGTTCAGG  
 151 CTTTCATGAAG CCGAGGTCAA ACCGATCGAC AGGGAGAAGG TACCGGGGCA  
 201 GGTGCGGGAA AAAGGAAAAG TTTTGCAGGT TGACGgcGAA ACCCTGCTGA  
 251 AAAATCCCGA ATTGTTGTCG CGTGCCATGT ATTCCGCAGT GGTCTCAAAC  
 301 AATATTGCCG GTATCCGCGT GATTTTGGCG ATTTACCTAC AACAGGCGCG  
 351 GCAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG  
 401 AGGGCAGGGT GAAGGAGGCG GTTCCCATTT ACCGGGAATT GATTGCCCGC  
 451 CAACCCGACG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATTGTTTGA  
 501 AGACAGGCAG AACGAGGCGG CGGCAGACCA GTTCGACCGC CTGAAAACAG  
 551 AAGATCTGCC GCCGCAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA  
 601 TTGCGCGAAG GCGATGCGTG GAAGGTAAAC GGCGGTTTCA GCGTTACCCG  
 651 CGAACACAAT ATCAACCAAG CCCCAGAAAC GCAGCAGTAC GGCAATTGGA  
 701 CTTTCCCGAA ACAGGTGGAC GGCACGGCAG TCAATTACCG GTTCGGCGCG  
 751 AGAAAAAAT GGTCCGTGAA AAACGGCTGG TACACGACGG CGGGCGGCGA  
 801 CGTGTCGGCG AGGGTTTATC CGGGGAATAA GAAATTC AAC GATATGACGG  
 851 CAGGTGTTTC CGGCGGCATC GGTTTTGCCG ACCGGCGTAA AGATGTCGGG  
 901 CTGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA  
 951 CGCCAACGGC GCACGCCTTT ATTTCAACCG TTGGCAAACC CCGAGATGGC  
 1001 AAACGCTGTC TTCGGCGGAG TGGGGCGGTT TGAAGAATAC GCGCCGGGCG  
 1051 CGTTCCGACA ATACCCATTG GCAAATTTCC AATTGCTGG TGTTTTACCG  
 1101 GAATGCGCGC CAATATTGGA CGGGCGGTTT GGATTTTAC CGCGAGCGCA  
 1151 ACCCGCGCGA CCGTGGCGAC AATTTC AAC GTTACGGCCT GCGCTTTGCC  
 1201 TGGGGCGCAGG AATGGGCGG CAGCGGCTG TCTTCGCTGT TCCGCTCGG  
 1251 CGTGGCGAAA CGGCATTATG AAAAACC CGTCTTCAGC AGTTTAAAG  
 1301 GGGAAAGCGC CAGGGATAAA GAATCGGACA CATCCTTGAG CCTTTGGCAC  
 1351 CGGGCATTGC ATTTCAAAG CATCACGCC CGCTGACGC TGTGCGACCG  
 1401 CGAAACGTGG AGCAACGATG TGTTTAACA ATACGAGAAA AACAGGCGT  
 1451 TTGTCGAGTT TAACAAAACG TTCTGA

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

g769.pep  
 1 LIMVIFYFYF CGKTFMPARN RWMLLP LLAS AAYAEETPCE PDLRSRPEFR  
 51 LHEAEVKPID REKVPQVRE KGKVLQVDGE TLLKNPELLS RAMYSAVVSN  
 101 NIAGIRVILP IYLQARQDK MLALYAQIL AQAEGRVKEA VSHYRELIAA  
 151 QPDAPAVRMR LAAALFEDRQ NEAADQFDR LKTEDLPPQL MEQVELYRKA  
 201 LRERDAWKVN GGFVSTREHN INQAPKQQQY GNWTFPKQVD GTAVNYRFGA  
 251 EKKWSLKNGW YTTAGDVSF RVYPGNKKFN DMTAGVSGGI GFADRRKDVG  
 301 LAVFHERRY GNDAYSANG ARLYFNWQT PRWQTLSSAE WGRKKNTRRA  
 351 RSDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRYLRFRA  
 401 WGQWGGSGSL SSFLRLGVAK RHYEKPGEFFS SFGERRRDK ESDTSLSLWH  
 451 RALHFKGITP RLTLSHRETW SNDVFNEYEK NRAVFEFNKT F\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

m769.seq  
 1 TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCTGCACG  
 51 AAACAGATGG ATGCTGCTGC TGCTTTTATT GGCAAGCGCG GCATATGCCG  
 101 AAGAAACACC GCGGAACCG GATTGAGAA GCCGTCCCGA GTTCAGGCTT  
 151 CATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGGAGGT  
 201 GCGGAAAAA GGAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA  
 251 ATCCCGAATT GTTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT  
 301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA  
 351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG  
 401 GTAGGGTGAA GGAGGCGATT TCCCATTAAC GGAATTGAT TGCCGCCCAA  
 451 CCCGACGCGC CGCCGTCGCG TATGCGTTTG CCGGCAGCAT TGTTTGAAAA  
 501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCCTG AAGGCGGAAA  
 551 ACCTGCCGCG CGAGCTGATG GAGCAGGTGC AGCTGTACCG CAAGGCATTG  
 601 CGCGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TCACCCGCGA  
 651 ACACAATATC AACCAGCCCG CGAAACGGCA GCAGTACGGC AAATGGACTT  
 701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG  
 751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGCG AGGCGCAGCT  
 801 GTCCGGCAGG GTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG  
 851 GCGTTTCCCG CGGCATCGGT TTTGCCGACC GCGCGAAAAG TGCCGGGCTG  
 901 CCAGTGTTCC ACGAACGCGC CACCTACGGC AACGACGCTT ATTCTTACAC  
 951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA  
 1001 CGTTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACCGC CCGGGCGCGT  
 1051 TCCGACAATA CCCATTGCA AATTTCCAAT TCGCTGGTGT TTTACCGGAA  
 1101 TCGCGGCCAA TATTGGATGG GCGGTTTGA TTTTACCAGC GAGCGCAACC  
 1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCCTGCG CTTTGCTGG  
 1201 GGGCAGGAAT GGGGCGGCG CCGCTGTCT TCGCTGTGCG GCCTCGGCGC

1251

```

1251 GCGGAAACGG CATTATGAAA AACCCGGCTT TTCAGCGGT TTTAAAGGGG
1301 AAAGGCGCAG GGATAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCAG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCCGGA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>:

m769.pep

```

1 LIMVIFYFCG KTFMPARNRW MLLPLLLASA AYAETPREP DLRSRPEFRL
51 HEAEVKPIDR EKVPGQVREK GKVLIQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQODKM LALYAQGILA QADGRVKEAI SHYRELIAAQ
151 PDAPAVRMRL AAALFENRQN EAAADQDFDL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTREHNI NOAPKQQYQ KWFPPKQVDG TAVNYRLGAE
251 KKWSLKNWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNRWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGDLFYR ERNPADRGDN FNRYGLRFAW
401 QEWGSGSLS SLLRLGAAKR HYEKPGFFSG FKGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

m769/g769 95.1% identity in 492 aa overlap

```

          10      20      30      40      50      59
g769.pep  LIMVIFYFCGKTFMPARNRWMLL-PLLASAAYAETPCEPDLSRPEFRLHEAEVKPI
          |||||
m769      LIMVIFY--FCGKTFMPARNRWMLLPLLASAAYAETPREPDLSRPEFRLHEAEVKPI
          10      20      30      40      50

          60      70      80      90     100     110     119
g769.pep  DREKVPQVREKGVQVLDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQD
          |||||
m769      DREKVPQVREKGVQVLDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQD
          60      70      80      90     100     110

          120     130     140     150     160     170     179
g769.pep  KMLALYAQGILAQAEGRVKEAVSHYRELIAAQPDAPAVRMRLAAALFEDRQNEAADQFD
          |||||
m769      KMLALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAADQFD
          120     130     140     150     160     170

          180     190     200     210     220     230     239
g769.pep  RLKTEDLPPQLMEQVELYRKALRERDAWKVNGGFSVTREHNIQAPKQQYGNWTFPKQV
          |||||
m769      RLKAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTREHNIQAPKQQYGNWTFPKQV
          180     190     200     210     220     230

          240     250     260     270     280     290     299
g769.pep  DGTAVNYRFGAEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDV
          |||||
m769      DGTAVNYRLGAEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDA
          240     250     260     270     280     290

          300     310     320     330     340     350     359
g769.pep  GLAVFHERRTYGNDAYSANGARLYFNWQTPRWQTLSSAEWGRLKNTRRARSNTHLQI
          |||||
m769      GLAVFHERRTYGNDAYSANGARLYFNWQTPRWQTLSSAEWGRLKNTRRARSNTHLQI
          300     310     320     330     340     350

          360     370     380     390     400     410     419
g769.pep  SNSLVFYRNARQYWTGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLRLGVA
          |||||
m769      SNSLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGLSLRLGAA
          360     370     380     390     400     410

          420     430     440     450     460     470     479
g769.pep  KRHYEKPGFFSSFKGERRRDKESDTLSLSLWHRALHFKGITPRLTLSHRETWSNDVFNEYE
          |||||

```

1252

```

m769      KRHYEKPFFSGFGKERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYE
          420      430      440      450      460      470

g769.pep   480      490
          KNRAVFVEFNKTFX
          |||||
m769      KNRAVFVEFNKTFX
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```

a769.seq
1  TTGATAATGG TTATTTT TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTGAGAA GCGGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGGCAGGT
201 GCGGGAAAAA GGAAGATTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAAACAAT
301 ATTCGCCGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTACC GGAATTGATG TGTCGCCCAA
451 CCCGACGCGC CCGCCGTCGG TATGCGTTTG GCGGCGGCAT TGTGTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCT AGCTGTACCG CAAGGCATTG
601 CCGCAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAATATC AACCAAGCCC CGAACGCGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGCG GCGGCGACGT
801 GTCCGCGCAG GTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CCGCATCGGT TTTGCCGACC GCGCGAAAGA TGCCGGGCTG
901 CCGATGTGTC ACGAACGCGG CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
1051 TCCGACAATA CCCATTGCA AATTTCGAAT TCGCTGTTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCGTTCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCAG CGGCTGTCT TCGCTGTTGC GCCTCGGCGC
1251 GGCGAAACGG CATTATGAAA AACCCGGCTT TTTACGCGGT TTTAAAGGGG
1301 AAAGGCGCAG GGATAAGAAA TTGAACACAT CCTTGAGCCT TTGGCACCAG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCAGCA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```

a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLLPLLASA AYAETPREP DLRSRPEFRL
51  HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVMRML AAALFENRQN EAAADQFDR LKAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTRHNI NQAPKRQYQ KWTFFKQVDG TAVNYRLGAE
251 KKWSLKNGWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401 GQEWGSGSL SLLRLGAAGR HYEKPGFFSG FKGERRRDEK LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

m769/a769 99.8% identity in 490 aa overlap

```

a769.pep      10      20      30      40      50      60
              LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR
              |||||
m769          10      20      30      40      50      60
              LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR

a769.pep      70      80      90     100     110     120
              EKVPQVREK GKVLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM

```



1253

m769						
	EKVP	QGVREK	GKVLQIDGET	LLKNPEL	LSRAMYS	AVVSNNIAGIRVILPIYLQQAQDKM
	70	80	90	100	110	120
a769.pep	130	140	150	160	170	180
	LALYAQ	GILAQADGRVKEA	ISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL			
m769	130	140	150	160	170	180
	LALYAQ	GILAQADGRVKEA	ISHYRELIAAQPDAVAVRMRLAAALFENRQNEAAADQFDRL			
a769.pep	190	200	210	220	230	240
	KAENLP	PQLMQVELYRKALRERDAWKVNGGFSVTREHNINQAPKQQYQKWTFFKQVDG				
m769	190	200	210	220	230	240
	KAENLP	PQLMQVELYRKALRERDAWKVNGGFSVTREHNINQAPKQQYQKWTFFKQVDG				
a769.pep	250	260	270	280	290	300
	TAVNYRL	GAEKKWSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL				
m769	250	260	270	280	290	300
	TAVNYRL	GAEKKWSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL				
a769.pep	310	320	330	340	350	360
	AVFHERR	TGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLKNTRRARSNDNTHLQISN				
m769	310	320	330	340	350	360
	AVFHERR	TGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLKNTRRARSNDNTHLQISN				
a769.pep	370	380	390	400	410	420
	SLVFYRN	ARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGGSLSSLLRLGAAGR				
m769	370	380	390	400	410	420
	SLVFYRN	ARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGGSLSSLLRLGAAGR				
a769.pep	430	440	450	460	470	480
	HYEKP	GFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYEKN				
m769	430	440	450	460	470	480
	HYEKP	GFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYEKN				
a769.pep	490					
	RAFVEFNKTFX					
m769	490					
	RAFVEFNKTFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

```

g770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCCGA CTGCCTGCCG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATGT
101 TGGGCAAAAA CGACCGTATC GAAGTGGGAG GATTGACGCA TCCCGACGTT
151 CAAGGGGTG CCTGTTATAT TTCGTATGCA AAAAAAGCGC GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTCA AGCGCGGTAC GGGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAGCCTT CGCCTATTG GTTTACAGCG
401 ATAAATCGT CCAAGGATCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCAGCG GCATACCGCA AACCGACGGG GTGCAAGCCG ATACTTCCGG
501 CAAACTGCTT GCCGGCGCCT GCATTATTTC CAACCCGATA AAAAATCCCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

```

g770.pep
1  MNRLLLLSAA VLPTACSGSE TDKIGRASTV FNMLGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKRGTGFA FKSRIQVRY DPKRKAFAYL VYSDKIVQGS PKNSLSAVSC
151 FGSGIPQTDG VQADTSGKLL AGACIIISNPI KNPDKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

```

m770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCCG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC

```

1254

```

101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCCTTC
251 AGACGGCATC TTCGATTTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAATCTCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2648; ORF 770>:

```

m770.pep
1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKSQIVRYY DPKRKTFAYL VYSDKIIQGS PKNSLSAVSC
151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENLDRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. gonorrhoeae*

```

m770/g770 93.5% identity in 186 aa overlap

g770.pep      10      20      30      40      50      60
MNRLLLLSAAVLPTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA
|||||
m770          10      20      30      40      50      60
MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA
|||||

g770.pep      70      80      90      100     110     120
KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKKEVFKRGTFAFKSRQIVRYY
|||||
m770          70      80      90      100     110     120
KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKKEVFKHGASFAFKSRQIVRYY
|||||

g770.pep      130     140     150     160     170     180
DPKRKFAYLVYSDKIVQSPKNSLSAVSCFGSGIPQTDGVQADTSGKLLAGACIISNPI
|||||
m770          130     140     150     160     170     180
DPKRKTFAVLVYSDKIIQSPKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI
|||||

g770.pep      KNPDKRX
               :| ||||
m770          ENLDRKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2649>:

```

a770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCCTTC
251 AGACGGCATC TTCGATTTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAATCCCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2650; ORF 770.a>:

```

a770.pep
1  MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKSQIVRYY DPKRKTFAYL VYSDKIIQGS PKNSLSAVSC

```

1255

151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPKR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

m770/a770 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
a770.pep	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIVEGFDPPDVQGVACYISYA					
m770	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIVEGFDPPDVQGVACYISYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a770.pep	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKEVFKHGASFAFKSRQIVRYY					
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKEVFKHGASFAFKSRQIVRYY					
	70	80	90	100	110	120
	130	140	150	160	170	180
a770.pep	DPKRKTFAYLVYSDKIIQGSFKNLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI					
m770	DPKRKTFAYLVYSDKIIQGSFKNLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI					
	130	140	150	160	170	180
a770.pep	ENPKRXX					
m770	ENLDKRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

g771.seq

```

1  ATGCGATTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51  GGTGCTGACG ATGCTGCTTT TGGCGGCAGT CGGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCCCGAA AACATCCGCA GCCGCCTCCA ACAAAAGCATT
151 GCCCATACCC ACCGAAAAT CTGTTTGAT GCGGATATAC GCGCAGGCT
201 TCTGCCCGCG CCGACCGTCA TCCTGAAAAA CTTGACCATT ACCGAACCCG
251 ACGCGCGCGG GGTGCGCGTT TCCGTCAAAG AAACCAAAAT CGGATTGAGC
301 TGGAAAAACC TGTGGTCGGA TCGGATACAG GTTGAAAAAT GGGTGGTTTC
351 GGGTGGCGAT CTTGCCCTGA CGCGCGACAG AACCGGCGCT TGGAAATCC
401 AAGACCTGTT CGACGGCGCG AAACACTCCG CCTCAGTCAA CCGCATTATC
451 GTCGAAAAAC GCACCGTCCG CCTCAATTTC CTGCAGCAAC AGCTTATCCT
501 GAAGGAAATC AGCCTCAACC TGCAATCCCC CGATTCTGTC GGGCAGCAGT
551 TTGAAAGTTC GGGCATACTG GTTTGGAGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGC TGTTCCTTTC AGACGGCATC GGCACGCCCG AAATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTGCTGGA CGGACACGGC ATCACCATT
701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
751 GCCGGCCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCGCAAATC CCCGCACTGG CACTCAAAAA CAACAGCATC AAAACCGGCA
851 CGGTCAACGG CACGTTTACC GCCGGCGGCG AATATGCCCG ATGGGACGGT
901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GTTTCAAAAC ACCGCGCCTT CAAACCAATT
1001 TCTCCCTCGG CTCGCCGTTG GTTTGGAGTC GGGACAACGG GCTGGACGCC
1051 CCGCGCCTGC ACATATCGAC CCTTCAGGAT ACCGTCGACC GCCTGCCGCA
1101 ACCCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCATA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA ACCCGTTGCC
1201 GCAAAATTCA AATATACGCG GGAAGGCGCA CCGCACCTGG AAGCCGCCGC
1251 CGCGCTGCAA AAATTAACCC TCGCCCCCTA TCTTGACGAA TTTCCGCAAC
1301 AAAACGGCAA AATATTCCCC GACATCCTCG GCAGGCTGTC CGGCAACGTC
1351 GAGGCACACC TCAAAATCGG CAGCATCCAA CTCCCGGGCT TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGACCATATC GCGCTCAGCC
1451 GTTTCAGATC AGGGCTTTAC GCGCGCCATA CCGAAGCGCG CATCAGCATC
1501 GCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGAATG CAAGCAACAT
1551 CCAAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA TCGGTCATC GACCTGACCG CAAGCGGCGA AAACGCGCAA
1651 CAGCTTATCC GCTCGCTGCA AGGCAGCCTG TCGCTGAATA TTTCCAACGG
1701 AGCGTGGCAC GGCATCGATA TGGACAGCAT TTTAAAAAAC GGCCTTTCCG

```

1256

```

1751 GGAAAAATCTC GGGCAGCACA CCCTTCTACC GATTACGCT CAACAGCGAA
1801 ATTTTCAGACG GCATCAGCCG CCACATCGAT ACCGAACCTCT TCTCCGACAG
1851 CCTCTATGTT ACCAGCAACG GCTATACCAA TCTGGATACG CAGGAATTGT
1901 CTGAAGATGT CCTTATCCGC AACGCCGTCC ATCCGAAAAA CAAACCGATT
1951 CCCCTGAAAA TCACCGGTAC GGTGGACAAG CCGTCCATTA CCGTCGATTA
2001 CCGCAGGCTG ACCGGCGGCA TCAATTCGCG CAAAGAGAAA CAGAAAAATCC
2051 TCGAAGACAC CCTGCTGGAA CAATGGCAGT GGCTCAAACC TAAAGAACCG
3051 TAA

```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

g771.pep

```

1 MDLLSVFHKY RLKYAVAVLT MLLLAAVGLH ASVYRTFTPE NIRSRLQOSI
51 AHTRKISFD ADIRRRLLPR PTVILKNLTI TEPDGGRVAV SVKETKIGES
101 WKNLWSDRIQ VEKVVVSGAD LALTRDRNGA WNIQDLFDGA KHSASVNRRI
151 VENSTVRLNF LQQQLILKEI SLNLQSPDSS GQOFESSGIL VWRKLSVPWK
201 SRGLFLSDGI GTPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALKNNIS KTGTVNGTFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRL QTNFSLGSPL VWSRDNLDA
351 PRLHISTLQD TVDRLPQPRF ISRLDGLSLI PNLQNWNAEL NGTFDRQPPA
401 AKFKYTREGA PHLEAAAAAQ KLNLAPLYDE FRQNGKIFP DILGRLSGNV
451 EAHLKIGSIQ LPGLQLDDME TYLHADKDHI ALSRFKSGLY GHTEGGISII
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFSNGDAVI DLTAASGENRK
551 QLIRSLQGS LSLNISNGAWH GIDMDSILKN GLSGKISGST PFYRFTLNSE
601 ISDGISRHD TELFSDSLYV TSNGYTNLDT QELSEDVLR NAVHPKNKPI
651 PLKITGTVDK PSITVDYGR L TGGINSRKEK QKILEDTLLE QWQWLKPKEP
701 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

m771.seq

```

1 ATGGATTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51 CGTGTGACG ATACTGCTTT TGCGCGCAGT CGGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCGTGAA AACATCCGCA GCCGCTACA ACAAAGCATT
151 GCACACACAC ACCGGAATAT CTCGTTTGAT GCGGACATTC AGCGCAGGCT
201 CTTGCCCCCG CCGACCGTCA TCCTGAAAAA CTTGACCATC ACCGAACCCG
251 GCGGCGACCA GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
301 TGGAAAAACC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
351 GAGTGGCGAA CTTGCCCTGA CGCGCGACGG GAAAGGTGTT TGGAAACATCC
401 AAGACCTGAT CGACAGCCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
451 GTCGAAAAA GCACCGTCCG CCTCAATTTT CTGACGGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTCTGCG GGGCAGCCGT
551 TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGC TGTTCCCTTC AAACGGCATC GGCCCGCCCG AAATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTGCTGGA CGGACACGGC ATTACATTT
701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCGGCGCG AGCGGATGCC
751 GCCCGCCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCCCAAAAT CCGCGGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CCGTCAACGG CGCATTTACC GCCGCGCGCG AATATGCCCG ATGGGACGGT
901 TCGTTCAAAC TCACAAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAAC ACCGCGCCAC CAGACCAACT
1001 TCTCCCTCAA TTCGCCGCTC GTATGGACGG AAAACAAAGG GCTGGACGCG
1051 CCGCGCCTGT ATGTATCGAC CTTTCAAGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCGGTTTC ATCAGCCGCG TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCGTTGCC
1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1251 CGCACTGCAA AAATTGAACC TGACCCCTTA TCTTGACGAC GTGGGGCAAC
1301 AAAACGGCAA AATATTTCCT GACACCCTCG CCAAGCTGTC CGGCGACATC
1351 GAGGCGCACC TGAATATCGG AAAAGTCCAA CTTCCCGGCC TGCAACTGGA
1401 CGATATGGA ACCTACCTCC ACGCGACAA AGGCCATATC GCGCTCAGCC
1451 GTTTCAGTGC AGGGCTTTAC GCGGCGCATA CCGAAGGCGG CATCAGCATC
1501 GCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGATG CAAGCAACAT
1551 CCAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA CGCGGTCATC GACCTGACCG CGGCGGCGCA AACCAGAAAA
1651 GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTTCCAACGG
1701 TGCATGGCAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
1751 GCAAAACTGC CGACAATGCC GCACCCAGCA CACCTTCCA CCGATTACAG
1801 CTAACAGCG AAATTTTACA CGGCATCAGC CGCCACATCG ATACCGAACT
1851 CTTCTCCGAC AGCCTCTATG TTACAGCAA CGGCTATACC AATCTGGATA
1901 CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCGCT CCATCCGAAA
1951 AACAAACCGA TTCCCTGAA AATCACCAGC ACGGTGGACA AACCGTCCAT
2001 TACCGTCGAT TACGGCAGGC TGACCGCGCG CATCAATTCG CGCAAGAGA
2051 AACAGAAAT CCTCGAAGAC ACCCTGCTGG AACATGGCA GTGGCTCAAA
2101 CCTAAGAAC CGTA

```

m771.pap

```

1 MDLLSVFHKY RLKYAVAVLT ILLAAVGLH ASVYRTFTPE NIRSRLQQSI
51 AHTHRKISFD AQDORLLPR PTVLKNLTI TEPGGDQTAV SVQETKIGLS
101 KWNKLWSSQD IEKWVSSSAE LATLRDGKV WNIQDLISQ KRQASVNRII
151 VENSTVRLNF LQEQLILKEI NLNLQSPDSS QGFESSIGL VWGKLSVPWK
201 SRGLFSLNGI FPNISPFHF EASTSLDGHG ITISTTGSFS VRFNAGGADA
251 AGLGLRADTS GRRLHLTAQI PALALRNNSI KIETVNGAFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNSLSNPL VTWENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRDLGSLV PNLQNWNAEL NGTFDRQTV
401 AKFRYTHEDA PHLEAAVALQ KLNLTPLYLD VRQONGKIFP DTLAKLSGDI
451 EAHLKIGKVQ LPLQLDDME TYLHADKGHI ALSRFKSGLY GGHTEGGSI
501 ANTRPATYRL QMASNIQIF PLQLQDFGH SFSNGDAVI DLTAGGETRK
551 ELIRSQQGSL LSNISNGAWH GIDMNLILKN GISGKTADNA APSTPFHFR
601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDQTQELSD VLRINAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGSIN RKEKQKILED TLEQOWWLK
701 PKEP*

```

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

m771/g771	90.3% identity in 704 aa overlap					
	10	20	30	40	50	60
g771.pep	MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLLQQSIAHTRKISFD					
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSRLLQQSIAHTRKISFD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g771.pep	ADIRRRLLPRPTVILKNLTITEPDGGRVAVSVKETKIGLSWKNLWSDRIQVEKWVVSAG					
m771	ADIQRLLPRPTVILKNLTITEPGDQTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
g771.pep	LALTRDRNGAWNIQDLFDGAKHSASVNRIIVENSTVRLNFLQQLILKEISLNLQSPDSS					
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQLILKEINLNLQSPDSS					
	130	140	150	160	170	180
	190	200	210	220	230	240
g771.pep	GQQFESSGILVWRKLSVPWKSRLFLSDGIGTPEISPFHFEASTSLDGHGIIISTTGSPS					
m771	GQQFESSGILVWGKLSVPWKSRLFLSNGIGPPEISPFHFEASTSLDGHGIIISTTGSPS					
	190	200	210	220	230	240
	250	260	270	280	290	300
g771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNISIKTGTVNGTFTAGGEYARWDG					
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG					
	250	260	270	280	290	300
	310	320	330	340	350	360
g771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPLVWSRONGLDAPRLHISTLQD					
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD					
	310	320	330	340	350	360
	370	380	390	400	410	420
g771.pep	TVDRLPQPRFISRLDGSLSPNLQNNWNAELNGTFFDRQPVAAKFYTRREGAPHLEAAAAALQ					
m771	TVNRLPQPRFISRLDGSLSPNLQNNWNAELNGTFFDRQTVAAKFYTHEDAPHLEAAVALQ					
	370	380	390	400	410	420
	430	440	450	460	470	480
g771.pep	KLNLAPYLDEFROQNGKIFPDILGRLSGNVEAHLKIGSIQLPGLQDDMETYLHADKDH					
m771	KLNLTPYLDVVRQNGKIFPDTLAKLSGDI EAHLKIGKVQLPGLQDDMETYLHADKGHT					

1258

	430	440	450	460	470	480
g771.pep	490	500	510	520	530	540
	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQONASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
g771.pep	550	560	570	580	590	
	DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMDSILKNGLSGKISG---STPFYRFT					
m771	DLTAGGETRKLIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
g771.pep	600	610	620	630	640	650
	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
g771.pep	660	670	680	690	700	
	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

a771.seq

```

1  ATGGATTAT  TATCGGTCTT  CCACAAATAC  CGTCTGAAAT  ATGCGGTAGC
51  CGTGCTGACG  ATACTGCTTT  TGGCGGCAAT  CGGGCTGCAC  GCTTCCGTAT
101 ATCGCATCTT  CACACCTGAA  AACATCCGAA  GCCGCCTCCA  ACAAGCATT
151 GCCCCATACG  ACCGGAATA  CTCGTTTGAT  GCGGATATAC  AGCGCAGGCT
201 TCTGCCCCGG  CCGACCGTCA  TCCTGAAAAA  CCTGACCAT  ACCGAACCCG
251 GCGGCGACCG  GACTGCCGTT  TCCGTCCAAG  AAACCAAAAT  CGGATTGAGC
301 TGGAAAAACC  TGTGGTCGGA  TCAGATACAG  ATTGAAAAAT  GGGTGGTTTC
351 GAGTGGCGAA  CTTGCCCTGA  CGCGCGACGG  GAAAGGTGTT  TGGAAATCC
401 AAGACCTGAT  CGACAGCCAA  AAACGCCAAG  CCTCAGTCAA  CCGCATTATC
451 GTCGAAAAAC  GCACCGTCCG  CCTCAATTTC  CTGCAGGAAC  AGCTTATCCT
501 GAAGGAAATC  AACCTCAACC  TGCAATCCCC  CGATTCTCGT  GGGCAGCCGT
551 TTGAAAGTTC  GGGCATACTG  GTTTGGGGAA  AGCTGTCCGT  CCCGTGAAA
601 AGCAGGGGGC  TGTTCCTTTC  AGACGGCATC  GGCACGCCCA  AAATCTCACC
651 GTTCCATTTT  GAAGCTTCCA  CTTGCTGGA  CGGACACGGC  ATTACCATTT
701 CCACACCCGG  CAGCCCTTCT  GTCCGCTTCA  ACGCCGGCGG  AGCGGATGCC
751 GCCGGCCTCG  GCCTGCGTGC  AGACACTTCC  TTCCGCAACC  TCCACCTGAC
801 CGCCCAAACT  CCTACGCTGG  CACTCAGGAA  CAACAGCATT  AAAATTGAAA
851 CCGTCAACGG  CGCATTATCC  GCCGGCGGCG  AATATGCCCA  ATGGGACGGT
901 TCGTTCAAAC  TCGACAAAGC  CAACCTGCAC  TCCGGCATCG  CCAACATCGG
951 CAACGCCGAA  ATCTCCGGCA  GCTTCAAAAC  ACCGCGCCAC  CAGACCAACT
1001 TCTCCCTCAA  TTCGCCGCTC  GTATGGACGG  AAAACAAAGG  GCTGGACGCG
1051 CCGCGCCTGT  ATGTATCGAC  CCTTCAGGAT  ACCGTCAACC  GCCTGCCGCA
1101 ACCCGGTTTC  ATCAGCCGGC  TCGACGGTTC  GCTGTCCGTA  CCGAATCTGC
1151 AAAATTGGAA  TGCCGAATTA  AACGGCACAT  TCGACCCGCA  AACCCTTGCC
1201 GCGAAATTCA  GATACACACA  TGAAGACGCA  CCGCATCTGG  AAGCCGCCGT
1251 CGCACTGCAA  AAATTGAACC  TGACCCCTTA  TCTTGACGAC  GTGCGGCAAC
1301 AAAACGGCAA  AATATTTCCT  GACACCTTCG  CCAAGCTGTC  CGCGACATC
1351 GAGGCGCACC  TGAATATCGG  AAAAGTCCAA  CTTCCCGGCC  TGCAACTGGA
1401 CGATATGGAA  ACCTACCTCC  ACGCGGACAA  AGGCCATATC  GCGCTCAGCC
1451 GTTTCAGTTC  AGGGCTTTAC  GGGCGCCATA  CCGAAGCGCG  CATCAGCATC
1501 GCCAACACCC  GTCCCGCCAC  TTACCGCTCG  CAACAGAATG  CAAGCAACAT
1551 CCAATATCAA  CCGCTGCTGC  AAGACCTGTT  CGGCTTCCAC  AGCTTCAGCG
1601 GCAACGGGCA  CGCGGTATC  GACCTGACCG  CGGGCGGCGA  AACCAGAAAA
1651 GAGCTTATCC  GCTCGCTTCA  GGGCAGCCTG  TCGCTAAATA  TTTCCAAACG
1701 TGCATGGGAC  GGTATCGACA  TGGACAATAT  CCTGAAAAAC  GGCATTTCGG
1751 GCAAACTGCG  CGACAATGCC  GCACCCAGCA  CACCCTTCCA  CCGATTACAG
1801 CTCAACAGCG  AAATTTCAGA  CGGCATCAGC  CGCCACATCG  ATACCGAACT
1851 CTTCTCCGAC  AGCCTCTATG  TTACCAGCAA  CGGCTATACC  AATCTGGATA
1901 CGCAGGAATT  GTCTGAAGAT  GTCCTTATCC  GCAACGCCGT  CCATCCGAAA
1951 AACAAACCGA  TTCCCTGAA  AATCACCGET  ACGGTGGACA  AACCCTCCAT
2001 TACCGTCCAT  TACGCGAGGC  TGACCGGCGG  CATCAATTCC  CGCAAAGAGA
2051 AACAGAAAAT  CCTCGAAGAC  ACCCTGCTGG  AACAATGGCA  GTGGCTCAAA
2101 CCTAAAGAAC  CGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

1259

a771.pep

```

1 MDLLSVFHKY RLKYAVAVLT ILLLAAGLH ASVYRIFTPE NIRSRLQQSI
51 ANTHRKISFD ADIQRRLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
101 WKNLWSDQIQ IEKVVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
151 VENSTVRLNF LQEQLILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTVA
401 AKFRYTHEDA PHLEAAVALQ KNLNTPYLD VRQNGKIFP DTLAKLSGDI
451 EAHKIGKVQ LPGLQDDME TYLHADKGHI ALSRFKSGLY GGHTGGGSI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
551 ELIRSLQGS SLNISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRT
601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLEQWQWLK
701 PKEP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

a771.pep	MDLLSVFHKYRLKYAVAVLTILLLAAIGLHASVYRIFTPE	NIRSRLQQSI	ANTHRKISFD
m771	MDLLSVFHKYRLKYAVAVLTILLLAAVGLHASVYRTFTPE	NIRSRLQQSI	ANTHRKISFD
a771.pep	ADIQRRLPRPTVILKNLTITEPGGDRTAVSVQETKIGLS	SWKNLWSDQIQIEKVVSSAE	
m771	ADIQRRLPRPTVILKNLTITEPGGDQTA	SVQETKIGLS	SWKNLWSDQIQIEKVVSSAE
a771.pep	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLN	FLQEQLILKEINLNLQSPDSS	
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLN	FLQEQLILKEINLNLQSPDSS	
a771.pep	GQPFESSGILVWGKLSVPWKS	RGFLSDGIGTPKISPFHFEASTSLDGHG	ITISTTGSPS
m771	GQPFESSGILVWGKLSVPWKS	RGFLSNGIGPPEISPFHFEASTSLDGHG	ITISTTGSPS
a771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPTLALRNNSI	KIETVNGAFTAGGEYAQWDG	
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSI	KIETVNGAFTAGGEYARWDG	
a771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPL	VWTENKGLDAPRLYVSTLQD	
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPL	VWTENKGLDAPRLYVSTLQD	
a771.pep	TVNRLPQPRFISRLDGSLSV	PNLQNWNAELNGTFDRQTVA	AKFRYTHEDAPHLEAAVALQ
m771	TVNRLPQPRFISRLDGSLSV	PNLQNWNAELNGTFDRQTVA	AKFRYTHEDAPHLEAAVALQ
a771.pep	KNLNTPYLDDVRQONGKIFP	DTLAKLSGDI	EAHLKIGKVQLPGLQDDMETYLHADKGHI
m771	KNLNTPYLDDVRQONGKIFP	DTLAKLSGDI	EAHLKIGKVQLPGLQDDMETYLHADKGHI

1260

	490	500	510	520	530	540
a771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	600
a771.pep	DLTAGGETRKEIIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
m771	DLTAGGETRKEIIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
	610	620	630	640	650	660
a771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	670	680	690	700		
a771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKPEX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKPEX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

g772.seq

1	GTGTTTCGGCA	CGGTCTTGCG	GACTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGTCGGCAAG	TTCTTTCAGG	TTGTTGCGTA	TGGTTTTCGCG	GCGTTGGCGG
101	AAGGCGAGTT	TCACCAAGTT	GGCGAAATGA	TCGAAATCGT	CCGCCTTGCC
151	GATACGGTGT	TTACCCGGAA	TCATGCGCAC	CACGCGGAA	TCGATTTTCG
201	GCGCGGATC	GAACGATTCG	GGCGGCACGT	CAATCAGCAG	CTCCATATCG
251	AAAAAATATT	GCAGCATCAC	ACCCAAGCGA	CCGTAGTCGT	TGCTTTTCGG
301	GCGCGCAACC	ATGCGCTCGA	CCACTTCTTT	TTGCAACATA	AAGTGCATAT
351	GCGCGACATC	GTCCGCCACC	TCCGCCAGTT	TGAACAAAAG	GCGCGTGGAG
401	ATGTTATACG	GCAGGTTGCC	GACGATTTTC	TTTTTGCTCG	AGATGCCGTT
451	GAATCAAAAC	TGCAACACGT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTCAGACGG	CATACGATGT	CGCGGTTCGAT	TTTCGACAACG
551	TGCAGGCGGT	TCAGCTTTTT	CGCCAAAGGT	TCGGTAATTC	CCGCCAAACC
601	GCGGCCGATT	TCAATCACGA	CATCATCCGC	CTGCGGGCGC	ACGGCGTTGA
651	CAATATCGCC	GATAATCCGC	GTGTCCTGCA	AAAAATTCTG	CCCGAAACGC
701	TTGCGGGGCT	TGTGTTCTTT	CATCGTGTTC	CCTCTTCGGT	TGAACCCCGG
751	CCCTTTAGGG	CGGCAGGATC	AGACTCTGTT	TGGCGGGGGC	GTAACCCCTT
801	CCAAATCAGG	ACGACACATA	GGGCGGTGCT	TTATGTGTCG	TCCTGTGTGT
851	TGGAACATAA	ATGTGTTTAC	AGTATCCGTT	TGATGTCGGC	ATTGTAA

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

g772.pep

1	VFGTVLRTDA	DCLQIIVVGK	FFQVVAYGFA	ALAEGEFHFQ	GEMIEIVRLA
51	DTVFHRNHAH	HCGIDFRRGI	ERFGRHVNQO	LHIEKILQHH	TQATVVVAFR
101	RGNHALDHFF	LQHKVHIGDI	VRHLRQFEQK	RRGDVIRQVA	DDFLFA*DAV
151	EIKLQHVAFV	NHQFIRKRQR	FQTAYDVAVD	FDNVQAVQLF	RQRFNGCRQT
201	RADFNHDIIR	LRAHGVNDIA	DNPRVLQKIL	PETLAGFVFF	HRVSSSVETP
251	PFRAAGSDSV	WAGRNPFQIR	TTHRAVLVYS	SCVLEHKCVY	SIRLMSAL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

m772.seq

1	ATGTTTCGGCG	CGGTCTTGCG	GATTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGCCTGCAAG	CTCTTTCAGA	TTGTTGCGTA	TGGTTTTCGCG	GCGTTGGTGG
101	AAGGCGAGTT	TCACCAAGTT	GGCAAAATGC	TCGAAATCGT	CCGCCTTGCC
151	GATGCGGTGT	TTACCCGGAA	TCATACGGAC	GACGGCGGAA	TCCACTTTTCG
201	GCGCAGGGTC	GAACGATTCG	GGCGGTACGT	CAATCAGCAT	TTCCATATCG
251	AAAAAATATT	GCAGCATCAC	GCCCAAGCGG	CCGTAGTCGT	TGCTTTTCGG
301	GCGCGCAACC	ATACGCTCGA	CCACTTCTTT	TTGCAGCATA	AAGTGCATAT
351	CGACGACATC	GTCCGCCACC	TCCGCCAGCT	TGAACAAAAG	CGGTGTGGAA
401	ATGTTGTACG	GGAGGTTGCC	GACGATTTTC	TTTTTGCTCG	CGATGCCGTT
451	GAATCAAAAC	TGCAATACAT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTCAGACGG	CATACGATGT	CGCGGTTCGAT	TTTCGACAACG
551	TGCAGGCGGT	TCAGCTTTTT	CGCCAAAGGT	TCGGTAATTC	CCGCCAAACC
601	GCGGCCGATT	TCAATCACGA	CATCATCCGC	CTGCGGGCGC	ACGGCGTTGA
651	CAATATCGCT	GATAATCCGC	GTGTCCTGCA	AAAAATTCTG	CCCGAAACGC



m772.pap

1	MFGAVLRIDA	DCLQIIIVACK	LFQIVAYGFA	ALVEGEFHEF	GKMLEIVRLA
51	DAVFHRNHTD	DGGIHFRRRV	ERFRGVNVQH	FHIEKILQHH	AQAQVAVAFR
101	RGNHTLDDHF	LQKHVVIDDI	VRLHRLQLEQK	RCGNVVREHA	DDFLACDAV
151	EIKLQYIAFV	NHQFTRKKOR	FQATYDVAVD	FDNVQAVOLF	RQRFGNRRQT
201	RADFNHDIIR	LHAGVNDNIA	DNPRVLQKIL	PETLAGVFVF	HRVFSNVRTP
251	PFRAVESDSI	WEGRNSFQIR	MAHRAVLVVS	SCVLKHKCVY	SIRLSMAI

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. gonorrhoeae*

g772.pep	10	20	30	40	50	60
	VFGTVLRTDADCLQIIVGVGKFFQVVAYGFAALAEGEFHQFGEMIEIVRLADTVFHRNHAAH					
m772	10	20	30	40	50	60
	MFGAVLRIDADCLQIIVACKLQIIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD					
g772.pep	70	80	90	100	110	120
	HCGIDFRRGIERFGRHVNQQLHIEKILQHHTQATVVVAFRRGNHALDHFFLQHKVHIGDI					
m772	70	80	90	100	110	120
	DGGIHFRRRVERFGRYVNQHFHIEKILQHAQAQVVVAFRRGNHTLDHFFLQHKVHIDDI					
g772.pep	130	140	150	160	170	180
	VRHLRQFEQKRRGDVIRQVADDFLFXADAVEIKLQHVAFVNHQFIRKQRQFTAYDVAVD					
m772	130	140	150	160	170	180
	VRHLRQLEQKRCGNVVREVADDFLFCADAVEIKLQYIAFVNHQFIRKQRQFTAYDVAVD					
g772.pep	190	200	210	220	230	240
	FDNVQAVQLFRQRFGNCRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
m772	190	200	210	220	230	240
	FDNVQAVQLFRQRFGNRRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
g772.pep	250	260	270	280	290	299
	HRVSSSVETPPFRAAGSDSVWAGRNPFQIRTHRAVLVYSSCVLEHKCVYSIRLSALX					
m772	250	260	270	280	290	
	HRVSFSVETPPFRAVESDSIWEGRNSQFIRMAHRAVLVYSSCVLKHKCVYSIRLSALX					

**a772.seq**

1	ATGTTCGGCG	CGGCTTTGCG	GATTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGCGTCGAAG	CTCTTTTCGA	TTGTTGGCTA	TGGTTTTGCG	CGGCTTGGTG
101	AAGCGGAGTT	TCACGAGTTT	GGCGAAGAATG	TCGAATCGAT	CGCGTTTGGC
151	GATACGGTGT	TTCACCGGAA	TCATGCGGAC	GACGGCCGAA	TCCACTTTCG
201	CGCGGGGGTC	GAACGATTCC	GGCGGCACGT	CAATCAGCAT	TTCATATTCG
251	AAGAAATATT	GACGACATCAC	GCCCAAGCCG	CCGTAGTCGT	TGCTTTTCGG
301	CGCGGCACAC	ATACGATCGA	CCACTTCTTT	TTGCAGCATA	AAGTGCATAT
351	CGACGCACAT	GTCGCGCCAC	TCCGCGCAGT	TGACAAAAGT	CGGCTGGGAA
401	ATGTTGTAGG	GCAAGTTGCC	GACGATTTTC	TTTTTTCGCT	CGATGTCGAT
451	GAAATCAACG	TGCAATACAT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTCAGACGG	CATACGATGT	CGCGGTCGAT	TTGCAGAACT
551	TGCAGGCGGT	TCAGCTTTTT	CGCCAAAGGT	TCGGTATATC	CCGCGCAACG
601	CGGACCCGAT	TCAATCACGA	CATATCCGCG	CTGCGGGCGC	ACGGCGTTGA
651	CAATATCGCT	GATAATCCCG	GTGTCCTGCA	AAAAATTTCT	CCCCGAACCG
701	TTCGGGGCTT	TGTGTTCTTT	CATCGTGTTT	CCTTTTCGGT	TGAACCCCGC
751	CCCTTTAGGG	CGGTAGAAAT	AGACTCTATT	TGGGAGGGGC	GTAACCTCCT
801	CCAAATCAGG	ACGGCACATA	GGGCGGTGCT	TTATGTCTGC	TCCTGTGTGT
851	TGAAACATAA	ATGTGTTTAC	AGTATCCGTT	TGATGTGCGC	ATTGTAA

1262

This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

```
a772.pep
1  MFGAVLRIDA DCLOIIVACK LFOIVAYGFA ALVEGEFHEF GEMLEIVRLA
51  DTVFHRNHAD DGRIHFRGV ERFGRHVNOH FHIEEILQHH AQAQVVVAFR
101 RGNHTIDHFF LQHKVHIDDI VRHLRQLEQK RRGNVVGQVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RTDFNHDII RLAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRVESDSI WEGRNSFQIR TAHRVLYVS SCVLKHKCVY SIRLMSAL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

```
m772/a772 95.6% identity in 298 aa overlap

a772.pep      10      20      30      40      50      60
MFGAVLRIDADCLQIIVACKLFOIVAYGFAALVEGEFHEFGEMLEIVRLADTVFHRNHAD
m772          10      20      30      40      50      60
MFGAVLRIDADCLQIIVACKLFOIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD

a772.pep      70      80      90     100     110     120
DGRIHFRGVERFGRHVNOHFHIEEILQHHAAQAAVVVAFRRGNHTIDHFFLQHKVHIDDI
m772          70      80      90     100     110     120
DGGIHFRRRVERFGRYVNOHFHIEKILQHHAAQAAVVVAFRRGNHTLDHFFLQHKVHIDDI

a772.pep     130     140     150     160     170     180
VRHLRQLEQKRRGNVVGQVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD
m772         130     140     150     160     170     180
VRHLRQLEQKRCGNVVGQVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD

a772.pep     190     200     210     220     230     240
FDNVQAVQLFRQRFGNRRQRTDFNHDIIRLAHGVNDIADNPRVLQKILPETLAGFVFF
m772         190     200     210     220     230     240
FDNVQAVQLFRQRFGNRRQRTDFNHDIIRLAHGVNDIADNPRVLQKILPETLAGFVFF

a772.pep     250     260     270     280     290     299
HRVSFSVETPPFRVESDSIWEGRNSFQIRTAHRVLYVSSCVLKHKCVYSIRLMSALX
m772         250     260     270     280     290
HRVSFSVETPPFRVESDSIWEGRNSFQIRMAHRVLYVSSCVLKHKCVYSIRLMSALX
```

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

```
m773.seq
1  ATGGGATTGG GTGCAACGAC TTTGTGCGGT TCGGGTGCTA TAGGCGGAGG
51  TCTGTGCACT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG
101 CAGGTATGAC CGGTGGTTAT ACACAGGCCT CAGAAGGAAG CCGGCAATTG
151 TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG
201 TACACCAATA GAATACGAAT CGCCGTTAGT ATCTGATGCG AAAAATCTAG
251 CCGTATGGGG ATTGGAACAG CTGATTACGC GCAAAATGGG AAACCTGGCA
301 ACGGGTGTGA AAACCTCCTT GACTCCGAAA ACTGCTGACG TACAGCGAAA
351 TATCCTGTCC CAATCCGAAG TCGGTATCAA GTGGGGCAAG GGGATTGAAG
401 GACAGGGAAT GCCTTGGGAG GATTATGTCG GTAAGGGCTT GTCTGCCAAT
451 GCAAGGTTAC CTAAAATT TAAAACATTT GATTATTTT ATCGTGGTAC
501 AGGCACGGCA ATCAGTGCCA AAACCTGGA TACGCAAACT ACGGCACGCC
551 TGTCCAAACC CGAACAGCTT TACAGTACCA TGAAAGGGTA CATCGATAAG
601 ACGGCAAAAT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGGCAGA
651 CATGATCAAA CAGCGCGAAA TCCATCTGGC CATACCCGCA CAAACTAATA
701 AGGAGCAAAG ATTGCAGTTG CAACGTGTGG TAGAGTATGG CAAAAGTCAA
751 AACATTACAG TCAAAATTAC GGAGATCGAA TAA
```

1263

This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

```
m773.pep
1  MGLGATTFVG SGAIGGGLCS TGIGCAAGGL IATAGMTGGY TQASEGSROL
51  FGTYQSDFGK KVVLSLGTPI EYESPLVSDA KNLAVWGLET LITRKLGNLA
101 TGVKTSLSLTPK TADVQRNLS QSEVGKWKWK GIEGQGMPEW DYVGRGLSAN
151 ARLPKNFKTF DYFDRGTGTA ISAKTLDTQT TARLSKPEQL YSTMKGIDK
201 TANFKSYELS EVPLRADMIK QREIHLAIPA QTNKEORLQL QRVVEYKSKQ
251 NITVKITEIE *
```

a773.seq not found yet

-- a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

```
g774.seq
1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCTGCCTC
51  CTGTGCTTCC GTTTTACCCG TTCCGGAGGG CAGCCGAACC GAAATGCCGA
101 CACAGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC CACTCTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201 GGAATGTGTA AACGGGAAAG TCAAAGCATT GGAGCATACG AAAATACACC
251 CTTCCGGCAG GACATACGTC CAAAAACTCG ACGACCGCAA ATTGAAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CCGTCGAAAC
351 CGCACAAAAC CTCTACAATC AGGCACCTCA ACACATATCA AACGGCAGGT
401 TTTCTGCCCG AGCCGCCCTG TTGAAGGGGG CGGACGGCGG AGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGGAACTGT GAATCTGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCCAACCGCG CCCGAAGTCA TATTCAAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGCGCACTT GCGCGACGCT
651 GATACAGACC TATCCCGGCA GCCCGCGGCG AAAACGCGCC GCCGCAGCCG
701 TACGCAAAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

```
g774.pep
1  MKTKLPLFII WLSVSASCAS VLPVPEGSRT EMPTQENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVEML NGKVKALEHT KIHPSGRITYV QKLDDRKLKE
101 HYLNTEGGSA SAHTVETAQN LYNQALKHYQ NGRFSAAAAL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEVIFKIGEC
201 QYRLQKQDIA RATWRSLIQT YPGSPAARKA AAARVRR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

```
m774.seq
1  ATGAAGATCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCCGCCTC
51  CTGTGCTTCC GTTTTACCCG TTCCGGCAGG CAGCCAAACC GAAATGTCGA
101 CACGGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC GACCTTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201 GGAACCTTA AACGGCAAAAG TCAAAGCACT GGAACACGCA AAACACATT
251 CTTCCGGCAG GGCATACGTC CAAAAACTCG ACGACCGCAA GTTGAAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CTGTCGAAAC
351 CGCACAAAAC CTCTACAATC AGGCACCTCA ACACATAAAA AGCGGCAAGT
401 TTTCTGCCCG TGCTCCCTG TTGAAAGGCG CGGACGGAGG CGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGCAACTGC GAATCCGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCCAACCGCG CCTGAAGCCA TGTTCAAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGCGCACTT GCGCGACGCT
651 GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701 TGCACAAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

```
m774.pep
1  MKIKLPLFII WLSVSASCAS VSPVPAGSQT EMSTRENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVETL NGKVKALEHA KTHSSGRAYV QKLDDRKLKE
101 HYLNTEGGSA SAHTVETAQN LYNQALKHYK SGKFSAAAAL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEAMFKIGEC
201 QYRLQKQDIA RATWRSLIQT YPGSPAARKA AAARVRR*
```

Computer analysis of this amino acid sequence gave the following results:

1264

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from *N. gonorrhoeae*

m774/g774 92.8% identity in 237 aa overlap

	10	20	30	40	50	60
g774.pep	MKTKLPLFIIWLSVSASCSVLPVPEGSRT	EMPTQENASDGI	PYPVPTLQDRLDYLEGKI			
m774	MKIKLPLFIIWLSVSASCSVSPV	PAGSQTEMSTRENASDGI	PYPVPTLQDRLDYLEGKI			
	10	20	30	40	50	60
	70	80	90	100	110	120
g774.pep	VRLSNEVEMLNGKVKALEHTKIHPSGR	TYVQKLD	DRKLKEHYLNT	EGGSASAHTVETAQN		
m774	VRLSNEVETLNGKVKALEHAKTHSSGR	AYVQKLD	DRKLKEHYLNT	EGGSASAHTVETAQN		
	70	80	90	100	110	120
	130	140	150	160	170	180
g774.pep	LYNQALKHYQNGRFSAAAALLK	GADGGGSIAQ	RSMYLLQSR	ARMGNCS	EVIEIGGRY	
m774	LYNQALKHYKSGKFSAAASLLK	GADGGGSIAQ	RSMYLLQSR	ARMGNCS	EVIEIGGRY	
	130	140	150	160	170	180
	190	200	210	220	230	
g774.pep	ANRFKDSPTAPEVIFKIGECQYRLQ	QKDIARATW	RSLIQTYPG	SPAAKRAAA	AVRKRKX	
m774	ANRFKDSPTAPEAMFKIGECQYRLQ	QKDIARATW	RSLIQTYPG	SPAAKRAAA	AVRKRKX	
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

a774.seq

1	ATGAAGACCA	AATTACCGCT	TTTTATCATT	TGGCTGTCCG	TATCCGCCGC
51	CTGTTCTTCC	CCTGTTTCCC	GCAATATTCA	GGATATGCGG	CTCGAACCGC
101	AGGCAGAGGC	AGGTAGTTCG	GACGCTATTC	CCTATCCCGT	TCCCACCTCTG
151	CAAGACCGTT	TGGATTATCT	GGAAGGCACA	CTCGTCCGCC	TGTCGAACGA
201	AGTGGAAACC	TTAAACGGCA	AAGTCAAAGC	ACTGGAGCAT	GCGAAAACAC
251	ACCCTTCCAG	CAGGGCATA	GTCCAAAAC	TCGACGACCG	CAAGTTGAAA
301	GAGCATTACC	TCAATACCGA	AGGCGGCAGC	GCATCCGCAC	ATACCGTCGA
351	AACCGCACAA	AACCTCTACA	ATCAGGCACT	CAAACACTAT	AAAAGCGGCA
401	GGTTTCTGCG	CGCTGCCTCC	CTGTTGAAAG	GCGCGGACGG	AGGCGACGGC
451	GGCAGCATCG	CGCAACGCAG	TATGTACCTG	TTGCTGCAAA	GCAGGGCGCG
501	TATGGGCAAC	TGCGAATCCG	TCATCGAAAT	CGGAGGGCGT	TACGCCAACCC
551	GTTTCAAGA	CAGCCCAACC	GCGCCTGAAG	CCATGTTCAA	AATCGGCCGA
601	TGCCAATACA	GGCTTCAGCA	AAAAGACATT	GCAAGGGCGA	CTTGGCGCAG
651	CCTGATACAG	ACCTATCCCG	GCAGCCCGGC	GGCAAAACGC	GCCGCCGCAG
701	CCGTGCGCAA	ACGATAG			

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

a774.pep

1	MKTKLPLFII	WLSVSAACSS	PVSRNIQDMR	LEPQAEAGSS	DAIPYPVPTL
51	QDRLDYLEGT	LVRLSNEVET	LNGKVKALEH	AKTHPSSRAY	VQKLDRLK
101	EHYLNTEGGS	ASAHTVETAQ	NLYNQALKHY	KSGRFSAAAS	LLKGADGGDG
151	GSIAQRSMYL	LLQSRARMGN	CESVIEIGGR	YANRFKDSPT	APAMFKIGE
201	CQYRLQKDI	ARATWRS LIQ	TYPGSPA AKR	AAAAVRKR*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

	10	20	30	40	50	60
a774.pep	MKTKLPLFIIWLSVSAACSSPVSRNIQDMR	LEPQAEAGSSDAIPYPVPTLQDRLDYLEGT				
m774	MKIKLPLFIIWLSVSASCSASVSPV	PAGSQTEMSTRENASDGI	PYPVPTLQDRLDYLEGK			
	10	20	30	40	50	

1265

```

      70      80      90      100     110     120
a774.pep  LVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLDLDRKLKEHYLNTTEGGSASAHTVETAQ
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m774      LVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTTEGGSASAHTVETAQ
          60      70      80      90      100     110

      130     140     150     160     170     180
a774.pep  NLYNQALKHYKSGRFSAAASLLKGADGGDGGSSIAQRSMYLLQSRARMGNCEVIEIGGR
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m774      NLYNQALKHYKSGKFSAAASLLKGADGGDGGSSIAQRSMYLLQSRARMGNCEVIEIGGR
          120     130     140     150     160     170

      190     200     210     220     230     239
a774.pep  YANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAAVVRKRX
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m774      YANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAAVVRKRX
          180     190     200     210     220     230

```

g790.seq not found yet

g790.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2671>:

```

m790.seq
1  ATGGCAAGAA GGTCAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCAGCAGCG AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATATGC CTTAACGATG TCCAAGGCGA TACGACCATC AACAAACATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ATGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTCG
551 CCCCCTCGCA GTACACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCTG
601 CCGGTTATCG AAAAGGGGGA CTTGCTGGTG GTCGAGCCGC GTATGTGCCC
651 TCGCGACGAA GACATCGCGC TGATTGAACT GTCCGACAAG CGGCTGGTCG
701 TCGCGACCTT TGTTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
751 TCCGCTTCCA CTGAAGCCTT TGACCTGCCG GAAGGCAGCA CGATTTTAGG
801 TGTGGTGTCT GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGTAT TCGGATTACC GCCCTGATG TGTGGACGGT TGGTATGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2672; ORF 790>:

```

m790.pep
1  MARRSKTFEE AAEEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCRSR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSIV LNDVQGDTTI NNHHTHTNNH SDADGKALSM
151 RLTPRPLLSR RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIKGDLLV VEPRMCPADE DIALIELSDK RLVAHLVID IAGRM LIYQT
251 GRPSEAFDLP EGSTILGVVL ESKNGLCPFH RQEGVLIRIT APDVWTVGMI
301 SASKTSCTRP TAARSAVCF LRFWQATRGI PKTRSWRNP NA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2673>:

```

a790.seq
1  ATGGCAAGAA GGTCAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCAGCAGCG AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATATGC CTTAACGATG TCCAAGGCGA TACGACCATC AACAAACATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ACGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTCG
551 CCGCTTACCA ATATACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCTG
601 CCGGTTATCG AAAAGGGGGA TTTGCTGGTG GTCGAGCCGC GTATGCGCCC
651 TCGCGACGAA GACATCGTAC TGATTGAACT GTCCGACAAG CGGCTGGTCG
701 TCGCGACCTT TGTTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG

```

1266

```

751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCC GAAGGCAGCG TGATTTTAGG
801 TGTGGTGTCTG GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGTGAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AACGTCGTG TACGCGCCCG ACCGCAGCCC GGAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAACCC
1001 GTTCGTGGCG AATCCGAAC AACGCCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
1  MARRSKTFEE AAEEVEERFG HRIKLVFEF GTAKPCVINC PKHGNQTCSR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSII LNDVQGDTTI NNHHTHTNH SDADGKALSM
151 RLTPRPLSD RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVAHLVID IAGRMLIYQT
251 GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

```

a790/m790 98.2% identity in 342 aa overlap

a790.pep      10      20      30      40      50      60
MARRSKTFEEAAAEVEERFGHRIKLVFEFEGTAKPCVINC PKHGNQTCSRYSNMFIGSSW
|||||
m790          10      20      30      40      50      60
MARRSKTFEEAAAEVEERFGHRIKLVFEFEGTAKPCVINC PKHGNQTCSRYSNMFIGSSW
|||||

a790.pep      70      80      90      100     110     120
GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSII
|||||
m790          70      80      90      100     110     120
GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSIV
|||||

a790.pep     130     140     150     160     170     180
LNDVQGDTTINNHHHTHTNHSDADGKALSMRLTPRPLSDRQAAAFARTGKLTGSFDLFA
|||||
m790         130     140     150     160     170     180
LNDVQGDTTINNHHHTHTNHSDADGKALSMRLTPRPLSDRQAAAFARTGKLTGSFDLFA
|||||

a790.pep     190     200     210     220     230     240
SVVAPSQYTF AVAMPDTSMSPVIEKGDLLVVEPRMRPADEDIVLIELSDKRLVAHLVID
|||||
m790         190     200     210     220     230     240
SVVAPSQYTF AVAMPDTSMSPVIEKGDLLVVEPRMCPAEDIALIELSDKRLVAHLVID
|||||

a790.pep     250     260     270     280     290     300
IAGRMLIYQTRPSEALDLP EGSVILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGTI
|||||
m790         250     260     270     280     290     300
IAGRMLIYQTRPSEAFDLPEGSTILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGMI
|||||

a790.pep     310     320     330     340
SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
|||||
m790         310     320     330     340
SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAX
|||||

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

```

g791.seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CTACTTGTTC
51  TGGTTTGTTC TTTGGTTTTT GTGTATTTGG AGTGGGCTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AACTGCCGT CTTTGGATTC TTTGCAGCAT
151 TACCAGCCTA AAATGCCGT GACTATTAT TCGCGGATG GAGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAATC GCGGATTTCC
251 CCGAGGTGTT GCGGAATGCG GTTATTGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTTGG GGGTGGATGT TTGGGGTGT GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

```

1267

```

401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTGAG TTGTATTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGATC TGCCGCGCAA ATCTATTCA ATAAGAATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCGCTCTGC
651 CTATAATCCG ATTGTTAATC CGGAGCGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCATTGA ATGAGGAAC TGCATTATGAG CGGTTTGTTT GGAATAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCGGGAA CTGTATGAGA
851 AATATGGTGA AGATGCCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCACCGATC ATCAGAAGGC GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCAT CGCGGCAGCA GCTACCGCGG TCGGGAATAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTTATACCGG TCGATAAAAT GGTTCGCGCC GTTGTGTTGG ATGTTACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTGCCTTGG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGAG CGGTCGATAA TGAGAAAAATG
1201 GGGGAGGACC GTATCCGCGG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCTGCCG GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCGGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGCCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GCGCGAGGCA TATAGTGAT
1751 TTGCGAACGG CGGATATAGG GTTCTCTGCG ACGTGATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAAATG CAACCTTTGG TGGCAGGGCA
1851 AATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGATAAGA
1901 TTATGACAGG TGTGGTCCGT GTCGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAAACGGGT ACGACCAACG ACAATAAAGA
2001 TCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCCG GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG CCGGTACGGC CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATCCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAAGGG ATGAAAATGC CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAT GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAGAAG ATGATGAAGC
2301 GCGAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCCGGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGGATTCCC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

```

g791.pep
1  MVNYYSAMIK KILTTCTGLF FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAEDKRFY
101 RHWGVVDVWG ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR OKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRRE LYEKYGEDAY TQGFKYVTTV
301 RTDHQKAATE ALRKALRNFD RGSSYRGAEN YIDLKSESDV EETVSQYLSG
351 LYTVDKMVPA VVLDVTKKKN VVIQLPGGRR VALDRRALGF AARAVDNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRPSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRLRAQM OPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRAGYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVSS NGEYMKERM VTDPLMLDN
751 SGIAPOPSRR AKEDDEAAVE NEQQGRSDET RQDVQETPVL PSNTDSKQQQ
801 LDSLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

```

m791.seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51  TGGTTTGGTT TTTGGGTTTT GTGTATTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AACTGCCGT CTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AATGCCGTT GACTATTTAT TCGGCGGATG GGGAAAGTAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAAATC GCGGATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGT GCCCGCGCTG CCGTCGGCAA
351 TCTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGCGGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC

```

1269

	130	140	150	160	170	180
g791.pep	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
g791.pep	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPINPERAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPINPERAKLRQKYILNNMLE					
	190	200	210	220	230	240
	250	260	270	280	290	300
g791.pep	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFKVYTTV					
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFKVYTTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
g791.pep	RTDHQKAATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA					
m791	RADHQQVATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA					
	310	320	330	340	350	360
	370	380	390	400	410	420
g791.pep	VVLDTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIRRGAVIRVKNNGGRW					
m791	VVLDTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW					
	370	380	390	400	410	420
	430	440	450	460	470	480
g791.pep	AVVQEPQLLQALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
m791	AVVQEPQLLQALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
	430	440	450	460	470	480
	490	500	510	520	530	540
g791.pep	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
m791	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
	490	500	510	520	530	540
	550	560	570	580	590	600
g791.pep	GVGYAQQYIRRFGRPSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQQYIRRFGRPSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
	610	620	630	640	650	660
g791.pep	DRDGLRLAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRDIAKGTG					
m791	DRDGLRLAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRDIAKGTG					
	610	620	630	640	650	660
	670	680	690	700	710	720
g791.pep	TTNDNKDAWFVGFNPDVVTAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGKQKKG					
m791	TTNDNKDAWFVGFNPDVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKKG					
	670	680	690	700	710	720
	730	740	750	760	770	780
g791.pep	MKMPEGVSSNGEYYMKERMVTDPLGLDLSNGIAPQPSRRAKEDDEAAVENEQQGRSDET					
m791	MKMPEGVSSNGEYYMKERMVTDPLGLDLSNGIAPQPSRRAKEDDGGAAEGGRQAADDEV					
	730	740	750	760	770	780
	790	800				
g791.pep	RQDMQETPVLPSTGSKQQQLDSLFX					
m791	RQDMQETPVLPSTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:



1270

a791.seq

```
1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51 TGGTTTGGTT TTTGGGTTTT GTGTATTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAAGTCCGTT CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTAT TCGGCGGATG GGGAAATCAT
201 CGGTATGTAT GGGGAGCAGC GGGCGGAATT TACAAAAATC GGCAGATTCC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTGGG GGGTGGATGT TTGGGGTGTG GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTGTT AGCAGTGAAG AAACGTTTAC ACGCAAAATC
451 AATGAGGTGT TGCTTGCCTA TAAAATCGAG CAGTCTTTAA GCAAAAGACAA
501 AATCCTCGAG TTGTATTTC AATCAGATTTA CCTCGGTGAG CCGCGCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC AATAAGATGT CCGAGATTGT
601 ACTTTGGCGG AAGCCGCCAT GCTTCCGCGA CTGCCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCCG CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGCGCTTGA ATGAGGAATC GCATTACGAG CGGTTTGTTC GGAATATCGA
801 TCAGAGTGCT TTATATGTGG CCGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCTTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CCGCGCGGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCAT CCGCGCAGCA GCTACCGCGG TGCGGAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCGC GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCCG CCGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCGCGCG CGGTCAATAA TGAAGAAATG
1201 GGGGAGGACC GTATCCGCGG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CCGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCGAGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCCG CGGTTATGAT
1351 TTTACACGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCCGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTCCCTGCCG GGGGAAAGGG
1501 CCGAACCGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCGGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGTCGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGCGAGGCA TATAGCGTAT
1751 TTGCGAACCG CGGATATAGG GTTCTTCCG CAGTAATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAATG CAACCTTTGG TGGCCGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCATATAT ATGTATAAGA
1901 TTATGCAAGG TGTGTTCCGT GTTGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACCG ATATTGCCGG TAAACCGGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCCG GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGCGGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCCG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTGAGCAGC AATGCGGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CCGCGCAGAA GCGCGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAAGTA
2351 TGCAGGAAC GCCGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTTAA
```

This corresponds to the amino acid sequence &lt;SEQ ID 2680; ORF 791.a&gt;:

a791.pep

```
1 MVNYYSAMIK KILTTCTFGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAAMLG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TOGFKVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLKSESDV EETVSQYLSG
351 LYTVDKMPVA VVLDVTKKKN VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIIRGAV IRVKNNGGRW AVVQEPLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGLRLRAQ QPLVAGONAP QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDPKPS MGRVVGGTI
701 AVPVVVDYMR FALKGKQKKG MKMPEGVVSS NGEYMKERM VTDPLGLDN
751 SGIAFPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPV LPSNTGSKQQQ
801 LDSLF*
```

a791/m791 99.9% identity in 805 aa overlap

10 20 30 40 50 60

1271

```
a791.pep  MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
|||||
m791      MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
          10      20      30      40      50      60

          70      80      90      100     110     120
a791.pep  SADGEVIGMYGEQRREFTKIGDFEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVVS
|||||
m791      SADGEVIGMYGEQRREFTKIGDFEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVVS
          70      80      90      100     110     120

          130     140     150     160     170     180
a791.pep  GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
|||||
m791      GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
          130     140     150     160     170     180

          190     200     210     220     230     240
a791.pep  RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPINPERAKLRQKYILNNMLE
|||||
m791      RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPINPERAKLRQKYILNNMLE
          190     200     210     220     230     240

          250     260     270     280     290     300
a791.pep  EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFKVYTTV
|||||
m791      EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFKVYTTV
          250     260     270     280     290     300

          310     320     330     340     350     360
a791.pep  RADHQKVATEALRKALRNFDRGSSYRGAENYIDLKSKSEDVEETVSQYLSGLYTVDKMVPA
|||||
m791      RADHQKVATEALRKALRNFDRGSSYRGAENYIDLKSKSEDVEETVSQYLSGLYTVDKMVPA
          310     320     330     340     350     360

          370     380     390     400     410     420
a791.pep  VVLDVTTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
|||||
m791      VVLDVTTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
          370     380     390     400     410     420

          430     440     450     460     470     480
a791.pep  AVVQEPLLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
|||||
m791      AVVQEPLLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
          430     440     450     460     470     480

          490     500     510     520     530     540
a791.pep  KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI
|||||
m791      KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI
          490     500     510     520     530     540

          550     560     570     580     590     600
a791.pep  GVGYAQQYIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
|||||
m791      GVGYAQQYIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
          550     560     570     580     590     600

          610     620     630     640     650     660
a791.pep  DRDGRRLAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
|||||
m791      DRDGRRLAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
          610     620     630     640     650     660

          670     680     690     700     710     720
a791.pep  TTNDNKDAWFGFNPDDVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKGQKGK
|||||
m791      TTNDNKDAWFGFNPDDVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKGQKGK
          670     680     690     700     710     720

          730     740     750     760     770     780
a791.pep  MKMPEGVSSNGEYYMKERMVTDPLGLTDNSGIAPQPSRRAKEDDGGAAEGGROAADDEV
|||||
m791      MKMPEGVSSNGEYYMKERMVTDPLGLTDNSGIAPQPSRRAKEDDGGAAEGGROAADDEV
```

1268

```

451 AATGAGGTGT TGCTTGCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTC AATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC AATAGAAATGT CCGAGATTGT
601 ACTTTGGCGG AAGCCGCCAT GCTTGCAGGA CTGCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAACT GCATTACGAG CGGTTTGTTT GGAATATCGA
801 TCAGAGTGGG TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCACCGGAG GCATTGCGCA AGGCTCTACG
951 GAATTTCCGAT CGCGGCAGCA GCTACCGCGG TCGGGAACAT TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCGCC GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTT GCGGCCGCGG CGGTCAATAA TGAAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGGTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTTCG CGGTTATGAT
1351 TTTACAGACA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTT TCTATTCCGG GCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCGGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAA ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTGCGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCCGCT TCAGGTGCTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGTACGCGGC GAGACAACGC CGTTGAAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTTCG ACGTAATCGA TAAGATTTAT
1801 GACAGAGACG GCAGGTGCGC CGCCCAATG CAACCTTTGG TGGCTGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATAT ATGTATAAGA
1901 TTATGACGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACCGGGT ACGACCAATG ACAATAAGGA
2001 TGCCTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAATGC CTGAAGGTGT GGTACGACG AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAGAAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAC GCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2678; ORF 791>:

```

m791.pap
1 MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEORREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LKAPSAYNP IVNPERAKLR QKYLNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLSKSEDV EETVSQYLSG
351 LYTVDKMVPA VVLDVTKKKN VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIIRGAV IRVKNNNGRW AVVQEP LLQG ALGSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVNN DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGLRLAQM QPLVAGQNAQ QAIIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVT A VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKG MKMPEGVVSS NGEYYMKERM VTDPLGLTLDN
751 SGIAPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

g791/m791 97.3% identity in 805 aa overlap

          10      20      30      40      50      60
g791.pap  MVNYYSAMIKKILTTFCGLVFGFCVFGVGLVAIAAILVTYPKLPSLDSLQHYQPKMPLTIY
          |||
m791      MVNYYSAMIKKILTTFCGLVFGFCVFGVGLVAIAAILVTYPKLPSLDSLQHYQPKMPLTIY
          10      20      30      40      50      60

          70      80      90      100     110     120
g791.pap  SADGEVIGMYGEORREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVVS
          |||
m791      SADGEVIGMYGEORREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVVS
          70      80      90      100     110     120

```

1272

	730	740	750	760	770	780
	790	800				
a791.pep	RQDMQETPVLPSNTGSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

g792.seq

```
1 ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51 CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAA
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GTCCGTTTGT
251 CCggacacgg gggcttcGat GGGGACGGCA tTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGATCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAAG
401 GGGAAAGAGG GGCATTACG GCAATGATGG AAGCTGTTAC CGACAAAAAC
451 AGGATTTTCG AACTGTATTT AAACCAATC GAATGGCACT ACGGCgtTTT
501 CGGCGCGGAA GCTGCGTCCC GgtatTttTA TAAAAACCG GCcgcaGACC
551 TGACcAAACA GCAGgcggcG aaactgacgg tactcgtccc cgccccgttt
601 tactactctg accatccaaa aagcaaacgg ctgcgcaaca aaaccaatat
651 cgtgctcaga cgcattgggt cggcaaatTA ccccaagcg aaacgggactg
701 attgttccag atatggaaat gccgcctgaa ctgggggttcg aacggcatat
751 gttttctggg acttataa
```

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

g792.pep

```
1 MFRIVKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51 EGRDVALDYR WVPYNRISTN LKKALIASD VRFAGHGGFD GDGIQNAIRR
101 NRNSGEVKAG GSTISQQLAK NLFLNESRNY LRKGEEAAIT AMMEAVTDKN
151 RIFELYLNSI EWHYGVFGAE AASRYFYKKP AADLTQQAQ KLTVLVPAPF
201 YYSDHKSKR LRNKTNIIVL RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
251 VFWDL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

m792.seq

```
1 ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51 CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
251 CCGGGCACGG CGGCTTCGAT TGGGGCGGCA TTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCAAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401 GCGAAGAAGC GCGGATTACC GCGATGATGG AAGCCGTTAC CGACAAAGAC
451 AGGATTTTGT AACTGTATTT AAACCAATC GAATGGCACT ACGGCgTTTT
501 CGGCGCGGAA GCGCGTCCC GGTATTTTA TCAAAATACCC GCCGCCAAGC
551 TGACCAACA GCAGGCGGCA AAACGACGG CGCGCGTCCC CGCCCCGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CGTGCTCAA CGCATGGGT CGGCAGAGT GCCTGAAAGC GACACGGACT
701 GA
```

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

m792.pep

```
1 MFRIVKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51 EGRDVALDYR WMPYKRISTN LKKALIASD ARFAGHGGFD WGGIQNAIRR
101 NRNSGKVKAG GSTISQQLAK NLFLNESRSY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTQQAQ KLTARVPAPL
201 YYADHFKSKR LRNKTNIIVL RMGSAELPES DTD*
```

g792 / m792 90.4% identity in 230 aa overlap

	10	20	30	40	50	60
g792.pep	MFRIVKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
m792	MFRIVKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
	10	20	30	40	50	60
	70	80	90	100	110	120
g792.pep	WVPYNRISTNLKKALIASDVRFAGHGGFDGDGIQNAIRNRNSGEVKAGGSTISQQLAK					

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	52
--	---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

```
a792.seq
1      ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51     CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCGCTCG
101    CGCCCATCTCG GACTCGCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151    GAAGGTCGCG ATGTCGCATC GGATTACGCC TGGATGCCCT ACAAAACGAT
201    TTCCACCAAC CTGAAAAAAG CCTGTATTGC TTCCGAAGAT CGCGGTTTTCG
251    CGGGGCACGG CGGCTTCGAT TGGGGCGGCA TTCAAAAACG CATCAGGCGC
301    AACCGGAACA CGCGGAAGA GTGGCGGGCG GGCTCGACCA TCAGCAGGCA
351    GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401    CGGAAGAAGC GGGCATTACC CGCATGATGG AAGCGGTTAC CGCAACAGAC
451    AGGATTTTTG AACTGTATTT AAATCAATC GAATGGCAAT ACGGCGTTTC
501    CGGGCGGGAA CGCGCGTCCC GGATTTTTTA TCAAATGCTC GCGGCCAAGC
551    TGACCAACAA CAGGCGGGCA AACTGACGG CTGCGGCTCC CGCCCGCTCC
601    TACTACGCCG ACATATCCGA AAGCAAACGG CTCGCGAACA AACCAATAT
651    CGTGCTCAGA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701    GA
```

a792.pap

1	MFRIIKWLIA	LPVGIFFFN	AYVYGNIIY	RAVAPHRATF	MSMRMKQFEQ
51	EGRDVALDYR	WMPYKRSTN	LKKALIASD	ARFAGHGGFD	WGGINAIRR
101	NRNSGKVGAT	GSTISQQLAK	NLFNLSRSY	IRKGEEAAIT	AMMEAVTDKD
151	RIFELYLNLS	EWTHGVGFGE	AASRYFQIP	AAKLTKQQA	KLTRVVPAPL
201	YYADHPKSKR	LRNKTNVLVR	RMGSALPELS	DTD*	

	10	20	30	40	50	60
a792.pep	MFRIIKWLI	ALPVGIFIF	FNAYVYGNII	TYRAVAPHRT	AFMSMRMKQ	FEQEGRDVALDYR
m792	MFRIIKWLI	ALPVGIFIF	FNAYVYGNII	TYRAVAPHRT	AFMSMRMKQ	FEQEGRDVALDYR
	10	20	30	40	50	60
a792.pep	70	80	90	100	110	120
a792.pep	WMPYKRIST	NLKKALIA	SEDARFAG	HGGFDWGG	IQNAIRNR	NRNSGKVKAGG
a792.pep	STISQQLAK					
m792	WMPYKRIST	NLKKALIA	SEDARFAG	HGGFDWGG	IQNAIRNR	NRNSGKVKAGG
m792	STISQQLAK					
	70	80	90	100	110	120
a792.pep	130	140	150	160	170	180
a792.pep	NLFLNESRS	YIRKGEEA	AITAMAEAV	TDKDRIFEL	YLSNIEWHY	GVFGAEASRYFYQIP
a792.pep						
m792	NLFLNESRS	YIRKGEEA	AITAMAEAV	TDKDRIFEL	YLSNIEWHY	GVFGAEASRYFYQIP
m792						
	130	140	150	160	170	180
a792.pep	190	200	210	220	230	
a792.pep	AAKLTQQA	AKLTARVP	APLYYADHP	PKSKRLRN	KNKTNIVL	RRMGSael
a792.pep	PESD	TD				
m792	AAKLTQQA	AKLTARVP	APLYYADHP	PKSKRLRN	KNKTNIVL	RRMGSael
m792	PESD	TD				
	190	200	210	220	230	

9793.869

1274

```

1  ATGTTGATTA  AAAGCGAATA  TAAGCCCCGG  ATGCTGCCCA  AAGAAGAGCA
51  GGTCAAAAAG  CCGATGACCA  GTAACGGACG  GATTAGCTTC  GTCCTGATGG
101 CAATGGCCGT  CTTGTTTGCC  TGTCTGATTG  CCCGCGGGCT  GTATCTGCAG
151 ACGGTAACGT  ATAACCTTTT  GAAAGAACAG  GGCAGCAACC  GGATTGTGCG
201 GACTCAAACA  TTGCCGGCTA  CACGCGGTAC  GGTTCGGAC  CGGAACGGTG
251 CGGTTTTGGC  GTTGAGCGCG  CCGACGGAGT  CCCTGTTTGC  CGTGCCATAA
301 GATATGAAGG  AAATGCCGTC  TGCCGCCCAA  TTGGAACGCC  TGTCAGAGCT
351 TGTGATGTG  CCGGTCGATG  TTTTGAGGAA  CAACTCGAA  CAGAAAGGCA
401 AGTCGTTTAT  TTGGATCAAG  CGGCAGCTCG  ATCCCAAGGT  TGCCGAAGAG
451 GTCAAAAGCT  TGGGTTTGGA  AAACCTTGTA  TTTGAAAAG  AATTAAACG
501 CCATTACCCG  ATGGGCAACC  TGTTTGACAC  CGTCATCGGA  TTTACCGATA
551 TTGACGGCAA  AGGTCAGGAA  GGTTTGGAAC  TTTGCTTGA  AGACAGCCTG
601 TATGGCGAAG  ACGGCGCGGA  AGTTGTTTGG  CGGACCGGCG  AGGGCAATAT
651 TGTGGACAGC  TTGGAATCCC  CGCGCAATAA  AGCACCGCAA  AACGGCAAG
701 ACATCATCCT  TTCCCTCGAT  CAGAGGATTC  AGACCTTGGC  CTATGAAGAG
751 TTGAACAAGG  CGGTGCGGGA  CCATCAGGCA  AAAGCCGGAA  CGGTGGTGGT
801 TTTGGATGCC  CGCACGGGGG  AAATCCTCGC  CTTGGCCAAT  ACGCCCGCCT
851 ACGATCCCAA  CAGACCCGGC  CGGGCAGACA  GCGAACAGCG  GCGCAACCGT
901 GCCGTAACCG  ATATGATCGA  ACCTGGTTCG  GCAATCAAAC  CGTTCGTGAT
951 TGCGAAGGCA  TTGGATGCGG  GCAAAACCGA  TTTGAACGAA  CGGCTGAATA
1001 CGCAGCCTTA  TAAATCGGA  CCGTCTCCCG  TGCGCGATGA  TACCCATGTT
1051 TACCCCTCTT  TGGATGTGCG  CGGCATTATG  CAGAAATCGT  CCAACGTCGG
1101 CACAAGCAAA  CTGCTGCGC  GTTTCGGCGC  CGAAGAAATG  TATGACTTCT
1151 ATCATGAATT  GGGCATCGGT  GTGCGTATGC  ACTCGGGCTT  TCCGGGGGAA
1201 ACTGCAGGTT  TGTGTAGAAA  TTGGCGCAGG  TGCGCGCCCA  TCGAACAGGC
1251 GACGATGTCT  TTCGGTTACG  GTCTGCAATT  GAGCCTGCTG  CAATTGGCGC
1301 GCGCCTATAC  CGCACTGACG  CACGACGGCG  TTTTGTGTCG  GCTCAGCTTT
1351 GAGAAGCAGG  CGGTGCGGCC  GCAAGGCAAA  CGCATATTCA  AAGAATCGAC
1401 CCGCGCGCAG  GTACGCAATC  TGATGGTTTC  CGTAACCGAG  CCGGGCGGCA
1451 TCGGTACGGC  GGGTGCGGTG  GACGGTTTCG  ATGTCGGCGC  TAAAACCGGC
1501 ACGGCGCGCA  AGTTCGTCAA  CGGCGTTTAT  GCCGACAACA  AACACGTCGC
1551 TACCTTTATC  GGTTTTGCCC  CCGCCAAAAA  CCCCCGTGTG  ATTGTGGCGG
1601 TAACCATCGA  CGAACCGACT  GCCACGGCT  ATTACGGCGG  CGTAGTGGCA
1651 GGGCCGCCCT  TCAAAAAAAT  TATGGGCGGC  AGCCTGAACA  TCTTGGGCAT
1701 TTCCCGGACC  AAGCCACTGA  CCGCCGCGAG  CGTCAAAACA  CCGTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

g793.pep

```

1  MLIKSEYKPR  MLPKEEQVKK  PMTSNGRISF  VLMAMAVLFA  CLIARGLYLQ
51  TVTYNFKLEQ  GDNRIVRTQA  LPATRGTVSD  RRGAVLALSA  PTESLFAVPK
101 DMKEMPSAAQ  LERLSELVDV  PVDVLRNKLE  QKGKSFIIWK  RQLDPKVAEE
151 VKALGLENFV  FEKELKRHPY  MGNLFAHVIG  FTDIDGKGQE  GLELSLEDSL
201 YGEDGAEVVL  RDRQGNIVDS  LDSPRNKAPQ  NGKDIIISLD  QRIQTLAYEE
251 LNKAVEYHQA  KAGTVVVLDA  RTGEILALAN  TPAYDPNRPQ  RADSEQRNR
301 AVTDMTEPGS  AIKPFVIAKA  LDAGKTDLNE  RLNTQPKYK  PSPVRDDTHV
351 YPSLDVRGIM  QKSSNVGTSK  LSARFGAEEM  YDFYHELIG  VRMHSGFPG
401 TAGLLRNWRR  WRPIEQATMS  FGYGLQLSL  QLARAYTALT  HDGVLLPLSF
451 EKQAVAPQGG  RIFKESTARE  VRNLMVSVTE  PGGTGTAGAV  DGFVDVAGKT
501 TARKFVNTRY  ADNKHVATFI  GFAPAKNPRV  IVAVTIDEPT  AHGYYGVVVA
551 GPPFKKIMGG  SLNILGISPT  KPLTAAAVKT  PS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

m793.seq

```

1  ATGTTGATTA  AGAGCGAATA  TAAGCCTCGG  ATGCTGCCCA  AAGAAGAGCA
51  GGTCAAAAAG  CCGATGACCA  GTAACGGACG  GATCAGCTTC  GTCCTGATGG
101 CAATAGCCGT  CTTGTTTGCC  GGTCTGATTG  CTCGCGGACT  GTATCTGCAG
151 ACGGTAACGT  ATAACCTTTT  GAAAGAACAG  GGCAGCAACC  GGATTGTGCG
201 GACTCAAACA  TTGCCGGCTA  CACGCGGTAC  GGTTCGGAC  CGGAACGGTG
251 CGGTTTTGGC  GTTGAGTGC  CCGACGGAGT  CCCTGTTTGC  CGTGCCATAA
301 GAGATGAAGG  AAATGCCGTC  TGCCGCACAA  TTGGAACGCC  TGTCAGAGCT
351 TGTGATGTG  CCGGTTGATG  TTTTGAGGAA  CAACTCGAA  CAGAAAGGCA
401 AGTCGTTTAT  CTGGATTAAG  CGGCAGCTCG  ATCCCAAGGT  TGCCGAAGAG
451 GTCAAAAGCT  TGGGTTTGGA  AAACCTTGTA  TTTGAAAAG  AATTAAACG
501 CCATTACCCG  ATGGGCAACC  TGTTTGACAC  CGTCATCGGA  TTTACCGATA
551 TTGACGGCAA  AGGTCAGGAA  GGTTTGGAAC  TTTGCTTGA  AGACAGCCTG
601 CATGGCGAAG  ACGGCGCGGA  AGTCGTTTGG  CGGACCGGCG  AGGGCAATAT
651 TGTGGACAGC  TTGGAATCCC  CGCGCAATAA  AGCCCGGAAA  AACGGCAAG
701 ACATCATCCT  TTCCCTCGAT  CAGAGGATTC  AGACCTTGGC  CTATGAAGAG
751 TTGAACAAGG  CGGTGCGGGA  CCATCAGGCA  AAAGCCGGAA  CGGTGGTGGT
801 TTTGGATGCC  CGCACGGGGG  AAATCCTCGC  CTTGGCCAAT  ACGCCCGCCT
851 ACGATCCCAA  CAGGCGCGGC  CGGGCAGACA  GCGAACAGCG  GCGCAACCGT
901 GCCGTAACCG  ATATGATCGA  ACCCGGTTTC  GCAATCAAAC  CGTTTGTGAT
951 TGCGAAGGCA  TTGGATGCGG  GCAAAACCGA  TTTGAACGAA  CGGCTGAATA

```

1275

```

1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TCGCGGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACCTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGCTTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGGCGACCG
1451 GTACGGCGGG TCGGGTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTTGCCCCCG CCAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGGCGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCCGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

m793.pep

```

1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMIAVLFA GLIARGLYLQ
51  TVTYNFIKEQ GDNRIVRTQT LPATRGTVSD RNgAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQDPKVAEE
151 VKALGLENFV FEKELKRHPY MGNLFAHVG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEEVVL RDRQGNIVDS LDSPRNKAPK NGKDIIISLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRP RADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPKYIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DfYHELIGIV RMHSGFPGET
401 AGLLRNRRWR RPIEQATMSF GYGLQLSLQ LARAYTALH DGVLLPVSE
451 KQAVAPQGRK IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYYGGVVAG
551 PPFKKINGGS LNILGISPTK PLTAAAVKTP S*

```

g793/m793 98.5% identity in 582 aa overlap

	10	20	30	40	50	60
g793.pep	MLIKSEYKPRMLPKEEQVKKPMTSNGRISFVLMAMAVLFACLIARGLYLQTVTYNFIKEQ					
m793	MLIKSEYKPRMLPKEEQVKKPMTSNGRISFVLMIAVLFAGLIARGLYLQTVTYNFIKEQ					
	10	20	30	40	50	60
g793.pep	GDNRIVRTQALPATRGTVSDRNGAVLALSAPTESLFAVPKMDKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
g793.pep	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHPYMGNLFAHVG					
m793	PVDVLRNKLEQKGKSFIIWKRLDPKVAEEVKALGLENFVFEKELKRHPYMGNLFAHVG					
	130	140	150	160	170	180
g793.pep	FTDIDGKGQEGLELSLEDSLYGEDGAEEVVLDRQGNIVDSLDSPRNKAPQNGKDIIISLD					
m793	FTDIDGKGQEGLELSLEDSLHGEDGAEEVVLDRQGNIVDSLDSPRNKAPKNGKDIIISLD					
	190	200	210	220	230	240
g793.pep	QRIQTLAYEELNKAVEYHQAAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR					
m793	QRIQTLAYEELNKAVEYHQAAGTVVVLDAARTGEILALANTPAYDPNRPGRADSEQRNR					
	250	260	270	280	290	300
g793.pep	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPKYIGPSPVRDTHVYPSLDVRGIM					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPKYIGPSPVRD-THVYPSLDVRGIM					
	310	320	330	340	350	360
g793.pep	QKSSNVGTSKLSARFGAEMYDFYHELIGIVRMHSGFPGETAGLLRNRRWRPIEQATMS					
m793	QKSSNVGTSKLSARFGAEMYDFYHELIGIVRMHSGFPGETAGLLRNRRWRPIEQATMS					
	370	380	390	400	410	420
g793.pep	QKSSNVGTSKLSARFGAEMYDFYHELIGIVRMHSGFPGETAGLLRNRRWRPIEQATMS					
m793	QKSSNVGTSKLSARFGAEMYDFYHELIGIVRMHSGFPGETAGLLRNRRWRPIEQATMS					
	360	370	380	390	400	410

1276

```

          430      440      450      460      470      480
g793.pep  FGYGLQLSLLQLARAYTALHTDGVLLPLSFEKQAVAPQGKRIFKESTAREVRNLMVSVTE
          |||
m793      FGYGLQLSLLQLARAYTALHTDGVLLPVSFEKQAVAPQGKRIFKESTAREVRNLMVSVTE
          420      430      440      450      460      470

          490      500      510      520      530      540
g793.pep  PGGTGTAGAVDGFVDVGAKTGTARKEVNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          |||
m793      PGGTGTAGAVDGFVDVGAKTGTARKEVNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          480      490      500      510      520      530

          550      560      570      580
g793.pep  AHGYGGVVAGPPFFKKIMGGSNLILGISPTKPLTAAAVKTPSX
          |||
m793      AHGYGGVVAGPPFFKKIMGGSNLILGISPTKPLTAAAVKTPSX
          540      550      560      570      580

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

```

a793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAACT TTGCGGGCTA CACGCGGTAC GGTTCGAGAC CGGAACGGTG
251 CGGTTTGGC GTTGAGTGGC CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCAGACT
351 TGTCGATGTG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAAGCT TGGGTTTGA AACTTTGTA TTTGAAAAG AATTAACCG
501 CCATTACCCG ATGGGCAACC TGTTTGACCA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTGG CCGGACCGGC AGGCAATAT
651 TGTGGACAGC TTGGAATCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGCCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCGCTAACCG ATATGATCGA ACCCGGTTCC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACGT TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGCTCTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGGCGCGCA AGGCAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGGCGACCG
1451 GTACGGCGGG TGCGGTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGGCGAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTTGCCCCCG CCAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGGCGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTT
1701 CCCGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

```

a793.pep
1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFLKEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKFSFIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYD MGNLFAHVIG FTDIDKGQGE GLELSLEDSL
201 HGEDGAIEVL RDRQGNIVDS LDSFRNKAPK NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPD RADSEQRNR
301 AVTDMIEPDS AIKPFVIAKA LDAGKTDLNE RLNTQPKYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFIHELIGIV RMHSGFPGET
401 AGLLRNWRW RPIEQATMSF GYGLQLSLLQ LARAYTALTH DGVLLPVSE
451 KQAVAPQKKR IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYYGGVVAG
551 PPFFKKIMGS LNILGISPTK PLTAAAVKTP S*

```

a793/m793 100.0% identity in 581 aa overlap



1277

a793.pep	10	20	30	40	50	60
	MLIKSEYKPRMLPKKEQVKKPMTSNGRISFVLMIAIVLFAGLIARGLYLQTVTYNFLKEQ					
m793	MLIKSEYKPRMLPKKEQVKKPMTSNGRISFVLMIAIVLFAGLIARGLYLQTVTYNFLKEQ					
	10	20	30	40	50	60
a793.pep	70	80	90	100	110	120
	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
a793.pep	130	140	150	160	170	180
	PVDVLRNKLEQKGKFSIWIQRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
m793	PVDVLRNKLEQKGKFSIWIQRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
	130	140	150	160	170	180
a793.pep	190	200	210	220	230	240
	FTDIDGKGQEGLELSLEDHLGEDGAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
m793	FTDIDGKGQEGLELSLEDHLGEDGAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
	190	200	210	220	230	240
a793.pep	250	260	270	280	290	300
	QRIQTLAYEELNKAVEYHQAAGTGVVLDARTGEILALANTPAYDPNRPGRADSEQRNR					
m793	QRIQTLAYEELNKAVEYHQAAGTGVVLDARTGEILALANTPAYDPNRPGRADSEQRNR					
	250	260	270	280	290	300
a793.pep	310	320	330	340	350	360
	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
	310	320	330	340	350	360
a793.pep	370	380	390	400	410	420
	KSSNVGTSKLSARFGAEEMDFYHELIGVGRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
m793	KSSNVGTSKLSARFGAEEMDFYHELIGVGRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
	370	380	390	400	410	420
a793.pep	430	440	450	460	470	480
	GYGLQLSLQLARAYTALHDGVLLPVSFEKQAVAPQKRIKSTAREVRNLMVSVTEP					
m793	GYGLQLSLQLARAYTALHDGVLLPVSFEKQAVAPQKRIKSTAREVRNLMVSVTEP					
	430	440	450	460	470	480
a793.pep	490	500	510	520	530	540
	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
m793	GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
	490	500	510	520	530	540
a793.pep	550	560	570	580		
	HGYYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
m793	HGYYGGVVAGPPFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
	550	560	570	580		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq

```

1  gtgcggtttca ATCATTTCAT AATGGTAACG ATTATTATAT ATGTGATTTC
51  CCTGCAAAC AAGCCGGTCC GCCGCCCGG CGTTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTCACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCTGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGTGCCCG CATACCCGTC
301 AATCCCGCGT CCACGATGAA GCTCGTTACC GCGTTGCCG CCTTCAAAAC
351 CTTCGGCAGC AATTACCGCT GGGCGACCGA GTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTGT ATTGGGCGGG CAGCGCGGAC
451 CCCGTTTTCA ATCAGAAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 CAAAGGCATC CGCAATATCA CGGGGCGCCT GATGCTCGAC CACAGCCTGT

```

1278

```

551 GGGGCGAAGT CGGCAGTCCC GACCATTTTG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCAATCC GACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGGCGCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTGGCC CAAAACAAC TGAATAATAC CGCTCCCAA
751 GCTGCGTCCG CTTGCGTCAA AAAACTGATG CGCGCATCTT TTTCGGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCGG GATGTTCCGG CTTGACGAAC TGATCCGCCA AAGTTTACC
901 AACCGTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGTTCCTGCT TCCTCAAAC CCGCGGCGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGCGC GCGTCTGCCG TCCGGCGAGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CGGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCGAAATG TTGGAAACGG CTTATTTTCA
1251 CCGGTTTGCA CAAGATTTC TCGACACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGTGGGCGA
1401 CAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCCGGCGGC
1501 GACGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

```

g794.pep
1 VRENHFIMVT IIIYVISPAN KPVRRPGVPT YPALPYNCF YVTDSPMNEP
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRAGIPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFES NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLA VQRQLRDKGI RNITGRLMLD HSLWGEVGSF DHFEADSGSP
201 FMTPPNPMTL SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKML RASFSGNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NRWLLGGGRI SDGIGIADTP EGAQTLAVAH SKPMKEILTD MNKRSNLI
351 RSVFLKLGGD GKLPAVSEQA ASAVRRELAV SGIDVADLVL ENSGLSRKE
401 RVTARMMAQM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLLRK
451 TGTLLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVAKNIISGG
501 DGWLDAKLMC KERRA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

```

m794.seq
1 GTGCGTCTCA ATCATTTTCA ATGATAGCG ATTATTATAT ATGTGATTTC
51 CCCTGCAAAAC AAGCCGGCCC GCCGCCACAG CGTTCCTACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCTGATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGCTC
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTGCGCAGC AATTACCGCT GGGCGACCGA GTTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTAT ATTTGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGAT GCTCAAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCC AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCCTATCC AACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATAC CGCTCCCAA
751 GCTGCTGCTC CTTGATCAA AAAACTGATG CGTGCATCTT TTTCGGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGTA TCGGCATAGC
951 CGACACGCGG GAAGGCGCGC AGACACTTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGCTT TCCTCAAAC CCGCGGCGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGCGC GCGTCTGCCG TCCGGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CGGGCTGTGC CAGAAAAGAA
1201 AGGTAACCGG CGAGAATGAT GCGCGAAATG TTGGAAACGG CTTATTTTCA
1251 CCGGTTTGCA CAAGATTTC TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACCTTACG CAACCGCTTC AAACAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGTGGGCGA
1401 CAACCCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

```

m794.pep
1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCF YVTDLPMNEP
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSVDPV

```

1279

```

101 NPASTMKLVT AFAAFKTFGS NYRWATEFES NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLD AQKQLREQGI LNTIGHMLMD HSLWGEVGGP DDFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSNDTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILTD MNKRSDNLIA
351 RSVFLKLGSD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGLLRNRF KQSGGLLRK
451 TGTLLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVANNIISGG
501 DGWLDKLMC KERRA*

```

g794/m794 95.5% identity in 515 aa overlap

```

-- g794 --
      10      20      30      40      50      60
g794.pep VRENHFIMVTIIIVISPAKPVRRPGVPTYPALPYNCFYVTDSPMNFPKTAASLLLLL
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     VRLNHFMIAIIIVISPAKPARRHVSPTYPALPYNCFYVTDLPNFPKTAASLLLLL
      10      20      30      40      50      60

      70      80      90     100     110     120
g794.pep ASLAHAHALDTGRIPQNEIAVYVQELDSGKVIIDHRAGIPVNPASTMKLVTAFAAFKTFGS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     ASLAHAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS
      70      80      90     100     110     120

      130     140     150     160     170     180
g794.pep NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRQLRDKGIRNITGRMLMD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQKQLREQGI LNTIGHMLMD
      130     140     150     160     170     180

      190     200     210     220     230     240
g794.pep HSLWGEVGGSPDFEADSGSPFMTPPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     HSLWGEVGGSPDFEADSGSPFMTPPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
      190     200     210     220     230     240

      250     260     270     280     290     300
g794.pep QNNLKITASQAACPSVKKLMRASFSGNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     QNNLKITASQAACPSIKKLMRASFSNDTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
      250     260     270     280     290     300

      310     320     330     340     350     360
g794.pep NRWLLGGGRISDGIGIADTPGAQTLAVAHAKPMKEILTD MNKRSDNLARSVFLKLGSD
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     NHWLLGGGRISDGIGIADTPGAQTLAVAHAKPMKEILTD MNKRSDNLARSVFLKLGSD
      310     320     330     340     350     360

      370     380     390     400     410     420
g794.pep GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
      370     380     390     400     410     420

      430     440     450     460     470     480
g794.pep QDFIDTLPIAGTDGTLNRNRFKQSGGLLRKLTGTLLNNVRALAGYWLGDKPMVAVVVIINSGR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     QDFIDTLPIAGTDGTLNRNRFKQSGGLLRKLTGTLLNNVRALAGYWLGDKPMVAVVVIINSGR
      430     440     450     460     470     480

      490     500     510
g794.pep AVSLLPDLN FVAKNIIISGGDGWLDKLMCKERRAX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794     AVSLLPDLN FVANNIISGGDGWLDKLMCKERRAX
      490     500     510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

a794.seq

```

1   GTGCGTCTCA ATCATTTTCAT AATGATAGCG ATTATTATAT ATGTGATTTT
51  CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTTCCTTCT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTCCTCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACA GGTCGCATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCCGTC

```

1280

```
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTCCGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAACCTGT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTC ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGCGGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTGCGCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCGGAA CGCAATGCCG CCGACAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCCTGCC CTTGCATCAA AAAACTGATG CGTGCACTTT TTTGCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTGCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CCGACGGATT TCAGACGGCA TCGGCATATC
951 CGACACGCCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCAAAGCCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCGTCT TCCTCAAACT CGGCGGCGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGGCA GCGCTGCGCG TCCGGCGTGA ACTTGCCGTG TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTTG GAAAACGGTT CAGGCTGTGC CAGAAAAGAA
1201 ACGGTAAACG CGAGAAATGAT GCGGCAATG TTGGAACCG CTTATTTCAG
1251 CCCGTTTGCA CAAGATTTCA TCGATACGCT GCCCATCGCC GGCACAGACG
1301 GCACCTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GCGTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCGCGCGCG
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

a794.pep

```
1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFY YVTDLPMNFP
51 KTAASLLLLL ASLAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSDVPV
101 NFASTMKLV TFAAFKTFGS NYRWATEFKS NGTVNDGTLG GNLWAGSGD
151 PVFNQENLLA VQRQLREQGI RNITGHLMLD HSLWGEVGSF DDFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGISDTP EGAQTLAVAH SKPMKEILTD MNKRSDNLIA
351 RSVFLKLGSD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMMQM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLLRK
451 TGTLLNNVRL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVANNIISGG
501 DGWLDKLMC KERRA*
```

a794/m794 98.6% identity in 515 aa overlap

a794.pep	10	20	30	40	50	60
a794.pep	VRLNHFIMIAIIIYVISPAN	KPARRHSVPTYPALPYNCFY	YVTDLPMNFPKTAASLLLLL			
m794	VRLNHFIMIAIIIYVISPAN	KPARRHSVPTYPALPYNCFY	YVTDLPMNFPKTAASLLLLL			
a794.pep	70	80	90	100	110	120
a794.pep	ASLAHALDTGRIPQNEIAV	YVQELDSGKVIIDHRSDVPV	NPASTMKLVTAFAAFKTFGS			
m794	ASLAHALDTGRIPQNEIAV	YVQELDSGKVIIDHRSDVPV	NPASTMKLVTAFAAFKTFGS			
a794.pep	130	140	150	160	170	180
a794.pep	NYRWATEFKSNGTVNDGTL	DGNLYWAGSGDPVFNQENLLA	VQRQLREQGIRNITGHLMLD			
m794	NYRWATEFKSNGTVNDGTL	DGNLYWAGSGDPVFNQENLLA	QKQLREQGILNITGHLMLD			
a794.pep	190	200	210	220	230	240
a794.pep	HSLWGEVGSPPDDFEADSGS	PFMTPPNPTMLSAGMVMVRAE	RNAADSTDILTDPPLPHIFA			
m794	HSLWGEVGSPPDDFEADSGS	PFMTPPNPTMLSAGMVMVRAE	RNAAGSTDILTDPPLPHIFA			
a794.pep	250	260	270	280	290	300
a794.pep	QNNLKITASQAACPSIKKLM	RASFSDNTLKLGRNIPESCL	GKPVGVRMFALDELIRQSFT			
m794	QNNLKITASQAACPSIKKLM	RASFSDNTLKLGRNIPESCL	GKPVGVRMFALDELIRQSFT			
a794.pep	310	320	330	340	350	360
a794.pep	NHWLLGGGRISDGIGISDTP	EGAQTLAVAHSKPMKEILTD	MNKRSDNLIARSVFLKLGSD			

g900.seq

This corresponds to the amino acid sequence <SEQ ID 2700; ORF 900.ng:

g900.pep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2701>:

m900.veg

1 ATGCCGCTGTG AAACGCGGCA GCGGAGGTT CGGACGGCAT CGGGTTCATT  
51 TCAACGGGCG GATGcCGACC GCATCg.TA CTTTGTCcAA TAATTcCGGT  
101 GCTTCcTTTAC GCGCtTTTCG CGCGCCTGCC TGcAAAATCT CTTcGATTtTG

1282

```

151 CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
201 CGGCGTTGAT TTTCCGCCCC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
251 CCGTCGGCAA GCATTTTCGT AAATCCACC GTTTCAGACG GCGTGGAGAA
301 GCGTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TTCGGCTCGC
351 CCGGCTCTTT CATATTGGTG ATGATTTTGT TGACCGATT TGGGTTTTTT
401 tTGTCGTTTT CCCAAAGCGG AATGGTGTG CCGTAGGATT TGGACATTTT
451 GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
501 CGGGCAGGGT GAAGAGTTCC CGGAAGCGGT GGTGAAGCG GCCGCGCATG
551 TCGCGCGCCA TTTCGACGTG TTGGATTGG TCGCGCCCGA CgGGCaCTTC
601 GTTGGCGTTG AACATCAGAA TATCGGCAGT CATCAGAATC GGATAACTGA
651 ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCTGCCCC GTTTTCTGCA
701 TTTGCCTGCA CGGCGGCTTT GTAGGCATGG GCGCGGTTCA TCAAACCCTT
751 GGCAGTGATG CAGGTCAGAA TCCAGTTCAA TTCCATCACT TCgGGAGTGT
801 CGCTTTGGCG GTAGAAGGTG GTGCGCTCGG GGTGAGTCC GCAGGCAAGC
851 CAAGTGGCGG CAACGGCTTG GGTGGATTGG TGAATCATCT CCGGCTCGTG
901 GCATTTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTCCGGTAT
951 CGAGGTTTTG CGCCGCGCGG ACGGCGGGGC GGATGGGCC GACGTAGTTG
1001 CCCAGATGCG GGATGCCGGT GGTGGTTACG CCGGTCAGAA CTCGTTTTTT
1051 GCTCATAAAA ATGTCCTTGC GGCATCAATG CCGTCTGAAA GGGAAAAAGA
1101 TGTGCCGATT ATACCCGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
1151 TTCCATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

m900.pep

```

1 MPSETRQAEV RTASGSFQRA DADRIXVFQ *FACFFTRFR RACLQNLFDL
51 RRVGGQLVVA FARFGEFGVD FRQKFFGFT PRQAVGKHFR KFHRFRRRGE
101 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVFPR NGVAVGFGHF
151 ASVQTDQFDF VFIDFHFGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVEHQNIGS HQNRITEQTH FHTAIRVFLP VFCICLHGGF VGMGAVHQL
251 GSDAGQNPVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNHRLRV
301 AFDDTVVIGE EEEFGFIEVL RRADGGADGA DVVAQMRDAG GGYAGQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QOTFPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

m900/g900

```

              10      20      30      40      50
m900.pep      MPSETRQAEVRTASGSFQRADADRIXVFQXFACFFTRFRRAACLQNLFDLRRVGGQ
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g900          MPSEMPSETWQAEVRTALGLFQRADADRIAYFIQQFARFFARFLRAACLQNLFDLRRIRGQ
              10      20      30      40      50      60

              60      70      80      90      100     110
m900.pep      LVVAFARFGEFGVDFFRQKFFGFTPRQAVGKHFRKFHRFRRRGEFGFVDFKQWAFVGLFRL
              ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g900          CVVAFQAQFCQFGVDFRRRKFFRLAPSQAVGKHLRKFRFRRRRGEFGFIDFKQRAFVGLFRL
              70      80      90      100     110     120

              120     130     140     150     160     170
m900.pep      ARLFHIGDDFVDRFLGFFVVFPRKNGVAVGFGHFASVQTDQFDFVFIDFHFGQGEFPEA
              ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g900          ARLFHVGNDFVDRFLGFFVVFPRKNGIAGVFGHFASVQTDQFDFVDFVDFHFGQGEFLET
              130     140     150     160     170     180

              180     190     200     210     220     230
m900.pep      VVEAAGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTAIRVFLPVFCICL
              ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g900          VGEAAGNVARHFDVLDLVAPDGHFVGVEHQNVGSHQNRITEQTHFHTIGVFLPVFRIGL
              190     200     210     220     230     240

```

```

      240      250      260      270      280      290
m900.pep HGGFVGMGAHVHQTLSGDAQNPVQFHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNH
          :|||:|||||:|||||:|||:|||||
g900      NGGFVGVGAHVHQTLSGDAQNPVQLHFGNVALAVEGGALGVESAGKPSGGNGLGGLVNH
          250      260      270      280      290      300

      300      310      320      330      340      350
m900.pep LRLVAFDDTVVIGEEEEFGFIEVLRRADGGADGADVVAQMRDAGGGYAGQNSFFFAHKNVL
          | |||:|||||
g900      LLLVAFDDAVVIGEEEEFGFIVLRRADGGADGADVVAQMRGAGGGYAGQNSFFFAHKNVL
          310      320      330      340      350      360

      360      370      380
m900.pep AAMPSEEREKDVPIIPDLPTSSRQQTFFPYX
          :|||:|||||
g900      TAAMPSEEREKDAPIIPDLPHRTSSRQQTFFPYX
          370      380      390

```

a900.seq (partial)

```
1 GAGGTTTCGGA CGGCATTGGG TTTATTTCAA CGGGCGGATA CCGACCGCAT
51 CACGTACTTT GCCCAATAAT TCGCGTGCCT CTTTACGGCG TTTTTCGCGC
101 CCTGCTGCA AAATCTCTTC GATTTCGAA GGGTCGGCGG TCAGCTCGTT
151 GTAGCGTTCG CGCGGTTTCG CGAGTTCGCG GTTGATTTTC CGGCCCAAAA
201 GTTTTTTTTC CTCGCCCAA GCCAAGCCGT CGGCAAGCAT TTTCGTAAAT
251 TCTGCCGTTT CAGACGGCGT GGAGAAAGCT TTGTAGATTT CAAACAGAGG
301 GCTTTCGTCG GGCTTCTTCG CTCGCCCGGT CTCTTTTCATA TTGGTGATGA
351 TTTTGTGAC CGATTTTTCG GTTTTTTTGT CGTTTTCCCA AAGCGGAATG
401 GTGTGTGCCG TACGATTGGA CATTTTGCCT CGGTCCAAAC CAACCAAGAG
451 TTCGACGTTT TCCTCGATTT TCACTTCGGG CAGTGTGAAG AGTTCGCCGA
501 AGCGGTGGTT GAAGCGGCCG GCAAATATCG GTGCCATTTC AACGTGTTGG
551 ATTTGGTCGC GACCGACTGG AACTTCATGG GCATTGAACA TGAGAATGTC
601 GGCAGTCATG AGGATAGGTT AGCTGTACAA ACCCATTTC ACGCCGAAAT
651 CGGGGTCCTT CTGCCCGTTT TCCGCATTTC CTGCAACGGC GGCTTTGTAG
701 CGGTGGGCGC GGTTTCATCA ACCCTTGGCG GTGATCAGG TCAGAATCCA
751 GTTCAATTCC ATCACTTCGG GAATGTCGCT TTGACGGTAG AAGGTGGTGC
801 GCTCGGGGTC GAGTCCGCAG GCAGCCAAAG TGGCGGCAAC GGCTTGGGTG
851 GATTGGTGA TCACTCCGG CTCGTGGCAT TTGATGATAC CGTGGTAAATC
901 GGCAGGAAG AGGAAGGATT CCGTATCAGG GTTTTGCGCC CGCGCGACGG
951 CGGGGCGGAT AGCACCGACG TAGTTGCCCA GATGCGGGAT GCCGGTGGTG
1001 GTTATGCCGG TCAGAACTCG TTTTTTGCTC ATAAAAATGT CCTTGGCGCA
1051 TCAATGCCCT CTGAAAGGGA AAAAGATGCG CCGATTATAC CCGATTTGCC
1101 ACCTACATCC AGCCGACAA ACAGCTTTTC ATATTAA
```

a900.pep (partial)

1	EVRTAGLGFQ	RADTDRTITYF	AQ*FACFFTR	FLRACLQNLF	DLRRVGGQLV
51	VAFARFGEFG	VDFRKQKDFD	LAPSQAVGKH	FRKFCRFRRR	GESFVDFKQR
101	AFVGLRLRLR	LFHIGDDFFD	RFLGFVVVF	KRNGVAVGFG	HFASVQTNQE
151	FDFVDFHFHG	QCEEFPEAVV	EAGNIAICHF	NVLDLVATDW	NFMGIEHENV
201	GSHEDRVAVQ	THFHA <u>IGVF</u>	LPVFRICLHG	GFVGVGAVHQ	TILGGDAGNP
251	VQHFHFNGVA	LTVEGGALGV	ESAGKPSGND	GLGGLVNHLR	LVAFDDTVVI
301	GEHEEGFGIR	VLRRADGGAD	SDTVVAQMRD	AGGGYAGQNS	FFAHKNVLAA
351	SMPSEREKDA	PIIPDLPPTS	STQTFPY*		

```
m900.pap      MPSETRQAEVRTASGSFQRADADRIXFYVQXFACFFTRFRRAQLQNLFDLRRVGGLVVVA  
              ||||| :|||||:|||::|||::::|||::|||::|||::|||::|||::|||  
a900          EVRTALGIFQRADTDRIITYFAQXFCFFTRFLRAQLQNLFDLRRVGGLVVVA  
               |         |           |             |            |  
                70        80          90           100          110          120
```

1284

```

m900.pep  FARFGEFGVDFRRQKFFGFTPRQAVGKHFRKFHRRRRGEGFVDFKQWAFVGLFRLARLF
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900      FARFGEFGVDFRRQKFFCLAPSQAVGKHFRKFCRFRRRGESFVDFKQRAFVGLLRLARLF
          60      70      80      90      100     110

          130     140     150     160     170     180
m900.pep  HIGDDFVDRFLGFFVVPKRNGVAVGFGHFASVQTDQEFDFIDFHFQGEFFPEAVVEA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900      HIGDDFVDRFLGFFVVPKRNGVAVGFGHFASVQTNQEFDFVDFHFQGEFFPEAVVEA
          120     130     140     150     160     170

          190     200     210     220     230     240
m900.pep  AGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTAIRVFLPVFCICLHGGF
          ||::| ||:||||| | :||:||||:||||:|:| ||||:| ||||:|||||
a900      AGNIACHFNVDLVATDWNFMGIEHENVGSHEDRVAVQTHFAEIGVFLPVFRICLHGGF
          180     190     200     210     220     230

          250     260     270     280     290     300
m900.pep  VGMGAVHQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNHLRLV
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900      VGVGAVHQTLGGDAGQNPVQFHHFGNVALTVEGGALGVESAGKPSGGNGLGGLVNHLRLV
          240     250     260     270     280     290

          310     320     330     340     350     360
m900.pep  AFDDTVVIGEEEGFGIEVLRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVLAASM
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a900      AFDDTVVIGEEEGFGIRVLRADGGADSTDVVAQMRDAGGGYAGQNSFFAHKNVLAASM
          300     310     320     330     340     350

          370     380
m900.pep  PSEREKDVPIIPDLPTSSRQQTFFPYX
          |||||:|||||:|||||:|||||:|||||
a900      PSEREKDAPIIPDLPTSSRQQTFFPYX
          360     370

```

g901.seq not found yet

g901.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

```

m901.seq
1  ATGCCCCGATT TTTCGATGTC CAATTGGGCC GTTGCCCTTTT CCATCACATT
51  GGCTGCCGGT TTGTTTACCG TATTakGyAG TGGCTTGGTG ATGTTTTCOA
101 AAACGCCCAA TCCGCGTGTG TTGTCGTTTG GTTTGGCGTT TGCCGCGCGT
151 GCGATGGTAT ATGTTTCCCT GACGAGATT TTCAGTAAGT CCAGCGAGGC
201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTCGCGCG GCGACCATGG
251 CATTTTTGGC CGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
301 AACCCGCATG AAACTTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGCGCGTTT GCGATTACTG
401 CGCACAATTT CCCCGAAGGC TTGGCGACGT TTTTGCCAC ATTGGAAT
451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
501 GGAGGGCATT TCCATCGCCG CGCCGTTTA TTTTGCCACC CGCAGCCGTA
551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTGGGG
601 CCGGCTTTGG GCTATTGGT TTTGCAGCCG TTTTGTGCG CTGCCGTGTT
651 TGGTTCGGTA TTCGCGTGA TAGCCGTTG GATGGTGTG TTGGCGTTGG
701 ACGAGCTGnt GCCGCTGCC AAACGCTATT CAGACGGCCA TGAAACGTT
751 TACGGCCTGA CAACGGGTAT GGCGGTGATT GCCGTCAGCC TGGTATTGTT
801 CCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2706; ORF 901>:

```

m901.pep
1  MPDFSMSNLA VAFSITLAAG LFTVLXSLV MFSKTPNPRV LSFGLAFAGG
51  AMVYVSLTEI FSKSSEAFAE IYDKDHAFAA ATMAFLAGMG GIALIDRLVP

```



1285

101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN  
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWVAC LLSGLAEPLG  
 201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELXPAA KRYSDGHETV  
 251 YGLTTGMAVI AVSLVLFHF\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

a901.seq  
 1 ATGCCCGATT TTTCGATGTC CAATTGCGCC GTTGCCTTTT CCATTACGTT  
 51 GGCTGCCGGT TTGTTTACCG TATTAGGCAG CGGCTTGCTG ATGTTTTCCA  
 101 AAACGCCCAA TCCGCGCGTG TTGTCGTTG GTTTGGCATT TGCCGGCGGT  
 151 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC  
 201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG  
 251 CATTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG  
 301 AACCCGCATG AAACCTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA  
 351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGGCGGTTT GCGATTACTG  
 401 CGCACAATTT CCCCAGAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAAAT  
 451 CCAGCAGTCG GGATGCCTTT GGCCTTGCGC ATTGCCATCC ATAATATTCC  
 501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGCCACC CGCAGCCGTA  
 551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGCCGA GCCGTTGGGG  
 601 GCGGCTTTGG GCTATTTGGT TTTGCAGCCG TTTTGTGCG CTGCCGTGTT  
 651 TGGTTCGGTA TTCGGCGTGA TAGCCGCTGT GATGGTGT TTTGGCGTTG  
 701 ACGAGCTGCT GCCGGCTGCC AAACGCTATT CAGACGCCA TGAAACCGTT  
 751 TACGGCCTGA CAATGGGCAT GCGGTGATT GCCGTCAGCC TGGTATTGTT  
 801 CCATTTTAA

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

a901.pep  
 1 MPDFMSNLA VAFSITLAAG LFTVLGSLV MFSKTPNPRV LSFGLAFAGG  
 51 AMVYVSLTEI FSKSSEAFAE IYDKDHAFAA ATMAFLAGMG GIALIDRLVP  
 101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN  
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWVAC LLSGLAEPLG  
 201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV  
 251 YGLTMGMAVI AVSLVLFHF\*

m901/a901 98.9% identity in 269 aa overlap

m901.pep	10	20	30	40	50	60
	MPDFMSNLA VAFSITLAAG LFTVLXSLV MFSKTPNPRV LSFGLAFAGG AMVYVSLTEI					
a901	MPDFMSNLA VAFSITLAAG LFTVLGSLV MFSKTPNPRV LSFGLAFAGG AMVYVSLTEI					
	10	20	30	40	50	60
m901.pep	70	80	90	100	110	120
	FSKSSEAFAEIYDKDHAFAAATMAFLAGMG GIALIDRLV NPHE TLDAQD PSFQESKRRH					
a901	FSKSSEAFAEIYDKDHAFAAATMAFLAGMG GIALIDRLV NPHE TLDAQD PSFQESKRRH					
	70	80	90	100	110	120
m901.pep	130	140	150	160	170	180
	IARVGMMAAF AITAHNFPEGLATFFATLEN PAVGMPLALA IAIHNIPEGISIAAPVYFAT					
a901	IARVGMMAAF AITAHNFPEGLATFFATLEN PAVGMPLALA IAIHNIPEGISIAAPVYFAT					
	130	140	150	160	170	180
m901.pep	190	200	210	220	230	240
	RSRKKTWVAC LLSGLAEPLGAALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELXPAA					
a901	RSRKKTWVAC LLSGLAEPLGAALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA					
	190	200	210	220	230	240
m901.pep	250	260	270			
	KRYSDGHETV YGLTTGMAVI AVSLVLFHFX					
a901	KRYSDGHETV YGLTMGMAVI AVSLVLFHFX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

g902.seq

```

1  ATGCCGTCGG AACCCGAACG GCGGCATGGC AATACTGCCC TACCCTTCCC
51  GATAGCCGCA CGCCCAACGG TCGGTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCGTATTG CGCCGCCGCA TTGTCCAAGC GGTGATTTC
151 ACGCCGCGCC TGTTGCGCGT CCGGCATTTC GCCGATGTAC CAGCCTATGT
201 GTTTGCGTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCATG
251 GCGCGGATGT GGTTCAAAAT GCGCGCTCTG CATTCTGCCA AACTCAAGGC
301 AGGCGGTAAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGGCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GGCGGCGGTT
401 TGTTTGAGGA cggCGGCGGC TTTTgCggc GAagtGATGT CGCCGTTGac
451 cCaggCCGGG ATGTTcAGAc ggCTTTGgT CTCGgcatg agttCGTAAC
501 gcGCCTCGCC TTTGTACATT TCGGTGcgcG CGcgccgtg aacggcaaGg
551 gcggaatgc cgcaatcttc ggcgattttg gcgacggcg gacggttttg
601 atcgtcgtcg tgccaaccCa AacggGTTTT GaggGTAACG GGTAcgcCCG
651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgg CTCGTCTCTGc
701 ATCagcGCGC TACCGGCTTG GACGTTGCAC ACTTCTcttg cgggGCAGCC
751 CATAttgATG TCGATGACCT GCGCCCCGAG TCCGACGTTg taacgcgcgg
801 catCCGCCAT CtggtcggGG TCGCTGCCGG CAATCTGCAC GGCAACGATG
851 CCGccttcat cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTcCT
901 GAGCGTCGGA TCGCTGGCCA GCATTTCGCA CACCGCCCA CTTGCGCCAA
951 ACGCCCGACA GAGGCGCGG AAGGGTTTGT CGGCAATGCC CGCCATCGGC
1001 GCAAGTGCGA TGGGGTTGTC GATAAAATAA CCGCCGATGT GCATAATGGG
1051 CCCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

g902.pep

```

1  MPSEPERRHG NTALFPPIAA RPTVGFSGKP FKITGKCVVL RRRIVQAVDF
51  TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGADVQON GGS AFCQTQG
101 RR*NAVFGIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGGG FLRRSDVAVD
151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGNAAIF GDFG DGGQVL
201 IVVPTQTGF EGNFYARRLD HRLQNGGNQR LVLHQRATGL DVAHFLGGAA
251 HIDVDDLPE SDVVTRRIH LFGVAAGNLH GNDAAFIGKI TAVQGFSGIP
301 ERRIAGQHFA HRPTCAKRPT EAAEGFVGNA RHRRKCDGVV DKITADVHNG
351 PAFQKSAPLY IF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

m902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTG GGGCGGTAGG
51  CGCACGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA
101 AGCATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTGA TTTCACGACG
151 TgTCTgTTCG CCGTcGGGCA TTTCTGCGAT GTACAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTGCGCGT AAAACGCGTG TATGGCGCGG
251 ATGTGGTTCA AAATAGCGGC GCGCATTCT GCCAACTCA AGGCAGGCGG
301 CAAAACACCG TGTTGCGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC
351 TGCTTGC GC CGCGGCCCT ATCATAATGC CGTCGCGGCG GGTGTTGTTG
401 AGGACGGCTT GGGCTTTTTC CGGCGAAGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTC AGACGGCATT TGGTTTCGGC GATGAGTTTC TAACGCGCTT
501 CGCCTTTGTA CATTTGCGTA CGCGTGCCTC CGTGGACGGC AAGGGCGGCG
551 ATGCCGCAAT CTTGCGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCTGCCGCAC
651 GGACGACGGC TTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAAACG CCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATT CGCACACCGC CCAACTGCG CCAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGcGCaAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

1287

m902.pep

```

1  LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
51  CLFAVGHFVD VPAYVFACDA HTGGVAVKRV YGADVQNSG GAFQQTQGRR
101 QNTVFGIMFQ IAEEPRPALR AAPYHNAVGG GLFEDGLGFL RRSNVAVDPD
151 RDVQTAFFG DEFVTRFAFV HLRTRASVDG KGGDAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYACRTDDG FQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNARH RRKCDGVVDK IAADVHNGSA
351 FQKSTPLYIF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 902 shows 80.9% identity over a 345 aa overlap with a predicted ORF (ORF 902.ng) from *N. gonorrhoeae*:

m902/g902

m902.pep	10	20	30	40	50
	LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTTCLFAVGHF				
g902	10	20	30	40	50
	MPSEPERRHGNTALPFPPIAARPTVGFSGKPFKITGKCVLRRRIVQAVDFTPRLFAVGHF				
m902.pep	60	70	80	90	100
	VDVPAYVFACDAHTGGVAVKRVYGADVQNSGGAFQQTQGRRQNTVFGIMFQIAEEPRPA				
g902	60	70	80	90	100
	ADVVPAYVFACDAHTDGLTIKRVHGADVQNGGSFAFQQTQGRRXNAVFGIMLQIAEKPRPA				
m902.pep	120	130	140	150	160
	LRAAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFFGFGDEFVTRFAFVHLRTRASV				
g902	120	130	140	150	160
	LRAAPYHNAVGGGLFEDGGGFLRRSDVAVDPGRDVQTAFFGLGDEFVTRLAFVHLRARAPV				
m902.pep	180	190	200	210	220
	DGKGGDAIFGDFGDDGQVLMVVVPTQTGFEGNGYACRTDDGFQNGGNQRLVHLQRATGL				
g902	180	190	200	210	220
	NGKGGNAIFGDFGDDGQVLIIVVPTQTGFEGNGYARRLDHRLQNGGNQRLVHLQRATGL				
m902.pep	240	250	260	270	280
	DIADFFSGTAHVVDKLRPKADVTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSIS				
g902	240	250	260	270	280
	DVAHFLGGAHIDVDDLRPESDVVTRIRHLFGVAAGNLHGNDAAFIGKITAVQGFSGIP				
m902.pep	300	310	320	330	340
	ERRVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLY				
g902	300	310	320	330	340
	ERRIAGQHFAHRPTCAKRPTAAEGFVGNARHRRKCDGVVDKITADVHNGPAFQKSAPLY				
m902.pep	360				
	IFX				
g902	360				
	IFX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2713>:

a902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
51  CGCAGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA

```

1288

```
101 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TGTCTGTTTCG CCGTCGGGCA TTTCTGTCGAT GTACCAGCCT ATGTGTTTTCG
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG CATGGCTCGG
251 ATGTGGTTCA AAATAGTGGC GGTACATTCT GCCAACTCA AGGCAGGCGG
301 TAAAACACCG TGTTCGGCGT AATGTTTCAA ATCGCGGAAG AACCACGGTC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCTGCGGC GGTTTGTGTTG
401 AGGACGGCTT GGGCTTTTTG CCGCGAGGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
501 CGCCTTTGTA CATTTGCGTG CGCGTGCGTC CGTGGACGGC AAGGGCGGCA
551 ATGCCGCAAT CTTGCGCGAT TTTGGCGATG ACGGGCAGGT TTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTGAGGGT AACGGGTACG CCCGCCGCTT
651 TGACCACCGC CTCCAAATG GCGGCAACCA GCGGCTCGT CTGCATCAGC
701 CCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAAACG CCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGGCAA AATCGCTGCG GTGCAAGTT TTTCTAGTAT TTCTGAGCGT
901 CCGGTCGCTG GTCAGCATT CGCACCCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGCGCAAGT
1001 GCGATGGGGT GTTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

```
a902.pep
1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT
51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV HGSDVVQNSG GTFCQTQGRR
101 *NTVFGVMFQ IAEPRALSAR AAPYHNAVCG GLFEDGLGFL RRGNVAVDPD
151 RDVQTAFGFG NQVVSRAFAV HLRARASVDG KGNAAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYARREDHR LQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNAHR RRCDCGVVDK IAADVHNGSA
351 FQKSTPLYIF *
```

m902/a902 94.7% identity in 360 aa overlap

```
10 20 30 40 50 60
m902.pep LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAVGHFVD
|||||
a902 LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAVGHFVD
10 20 30 40 50 60

70 80 90 100 110 120
m902.pep VPAYVFACDAHTGGVAVKRVYGADVQNSGGAFQCTQGRRQNTVFGIMFQIAEPRPALR
|||||
a902 VPAYVFACDAHTGGVAVKRVHGSDDVQNSGGTFCQTQGRRXNTVFGVMFQIAEPRALSAR
70 80 90 100 110 120

130 140 150 160 170 180
m902.pep AAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFGFGDEFVTRFAFVHLRTRASVDG
|||||
a902 AAPYHNAVCGGLFEDGLGFLRRGNVAVDPDRDVQTAFGFGNQVVSRAFAFVHLRARASVDG
130 140 150 160 170 180

190 200 210 220 230 240
m902.pep KGGDAAIFGDFGDDGQVLMVVVPTQTGFEGNGYACRTDDGFQNGGNQRLVLHQRATGLDI
|||:|||||
a902 KGNAAIFGDFGDDGQVLMVVVPTQTGFEGNGYARREDHRLQNGGNQRLVLHQRATGLDI
190 200 210 220 230 240

250 260 270 280 290 300
m902.pep ADFFSGTAHVDVDKLRPKADVVTGRIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER
|||||
a902 ADFFSGTAHVDVDKLRPKADVVTGRIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER
250 260 270 280 290 300

310 320 330 340 350 360
m902.pep RVAGQHFAHRPTCAKISAKSAERFVGNAHRRCDCGVVDKIAADVHNGSAFQKSTPLYIF
```

1289

```

|||||
a902  RVAGQHF AHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF
      310      320      330      340      350      360

m902.pep  X
          |
a902      X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattcg gatgaggCAA GCCCCTGCTT
51  TCCTATTTCT GAGGTGGaAT TGGTGGGTGA aGaaacggct aAATTCCGgt
101 tTGCgCTcaa ccaTGCCCTTG tgccAAACAC ATTTTGtttc cGgcaagtgt
151 CTGcATGcgg gcgacatTAA TCAAAtcaTG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAaccctga tgccggGCTA TctgcgctcC
301 ATAcgaATCG atcgggtccaa cgatgatcaa ACCCATgcAG GACGTATTGC
351 AGCATTCCAA AACAAATTTT CCACCCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTTGGA ACAAGGACTG GAAAATCTCA AATGTCTCC GACTGCGGAA
451 CCGGATCTCC AAATCgttcc cgtaGAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGGTAAc GTCTGTGCC CTACTGTGTG AGTGTGGGGA
551 TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCCG ACAATCCTTT TggactgAGT GATATGTTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAaAATTTT GACGGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC AGCCCTTTTC
751 GGTAaATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTTCCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA AGTTACAACA
851 CTGATTTCCG CTTCAACCGC CTGTGTATC GTGATGCCAA ACGCAAAACC
901 TATCTCAGTG TAAaACTGTG GACGAGGGAA ACAaAAGTT ACATTGATGA
951 TGCCGAAC TGCTGACAAC GGCGTAAaAC CACAGGTTGG TTGGCAGAAC
1001 TTTCCACAA AGGATATATC GGTGCGAGTA CGGCAGATT TAAGTTGAAA
1051 TATAAACACG GCACCGGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGGCGAA GGCACGTCAC GTATGAAaAT TTGGACGGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACCcCGCTA ACATCGCAAG ACAaACTGGC
1251 TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG GCAATTAAAA
1351 CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG TTTCAGGACA
1401 ATCCGCCAAA TGTTATCGG GCCAAACTCT AGCCGGCACA GCAATTGGGA
1451 TACGCGGGCA GATAAAGCTT GGCGGCAACC TGCATTACGA TATATTACC
1501 GGCCGTGCAT TGAAaAGCC cgaatatttt cAGACGAAGA Aatgggtaac
1551 ggggtTTCAG gtgggttatt cgTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
51  LHAGDINQIM SLAQNALIGR GYTTTRILAA PQDLNSGKLQ LTLMPGYLRS
101 IRIDRSNDDQ THAGRIAAFO NKFPTRSNDL LNLRLDLEQGL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVVQ WRXRLLPYCV SVGMDNSGSE ATGKYQGNIT
201 FSADNPFGLS DMFYVNYGRS IGGTPDEENF DGHKKEGGSN NYAVHYSAPF
251 GKWTWAFNHN GYRYHQAVSG LSEVYDYNK SYNTDFGFNR LLYRDAKRKT
301 YLSVKLWTRT TKSyIDDAEL TVQRRKTGW LAELSHKGYI GRSTADFKLK
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTPFQI GKQLFAYDTS
401 VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE MSLPAERGWE WRNDLSWQFK
451 PGHQLYLQAD VGHVSGQSAK WLSGQTLAGT AIGIRGQIKL GGNLHYDIFT
501 GRALKKPEYF QTKKWVTGFQ VGYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

```

m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTAACTG ATGCAAAATGT
51  CCGTTTCGAG CAACCATGG AGAAGAACAA TTATGTCCTG AGTGAAGATG
101 AAACACCGTG TACTCGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

```

1290

```

151 CGCAAATTTT CTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
201 AACTGGGATG TGTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAAGCCG
251 CGCAACAGAT ACTGATCGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
301 CAaCCACAGA ATATGGATTC GGAATTTCTG AAATTACGGG TATCAGCAGG
351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
401 AGGGCAGTAT TAGTGCATTC AATAACAAAT TTCCCTTATA TAGGAACAAA
451 ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAAAACC TCGTCTGTTT
501 GCCGAGTGTT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
551 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTTCAGT
601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTATG
701 TTTCATATGG ACGCGGTTTG GCGCACAAAA CGGACTTGAC TGATGCCACC
751 GGTACGGAAA CTGAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGACTTCA
951 TAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTACAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCTGCACCGG
1151 AAGAAAACGG CGGCGATATT CTTCCAGGTA CATCTCGTAT GAAAATCATT
1201 ACTGCCAGTT TGGACGCAGC CGCCCCATTT AyTTTAGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCGTTGGTTG
1301 CCCAAGATAA ATTGTCAATC GGCAGCCGCT ACACCGTTCG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTA

```

This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:

```

m903 . pep
1  MQRQQHIDAE LLTDANVRFE QPLEKNYVL SEDETPCTRV NYISLDDKTV
51  RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEKRDG KSAEGSISAF NKNFPLYRKN
151 ILNLRDVEQG LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQNKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL AHKTDLTDAT
251 GTETESGSR S YSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNVDYNGKQ
301 YQSSLAERM LWRNRLHKT S VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHRAYLN RWQLDGKLSY KRGTMQRSM PAPEENGDI LPGTSRMKII
401 TASLDAAAPF XLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 903 shows 48.9% identity over a 519 aa overlap with a predicted ORF (ORF 903.ng) from *N. gonorrhoeae*:

m903/g903

```

          10      20      30      40      50      60
m903 . pep  MQRQQHIDAE LLTDANVRFE QPLEKNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL
g903              MATQVGGANSDEASPCFP ISEVELVGEETAKFRFALNHA
                   10      20      30

          70      80      90      100     110     120
m903 . pep  MKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG
g903          : : | : | | : : : : : : : : : : : : : : : : : : : : : : : : : :
          40      50      60      70      80      90
g903          LCQTHFVSGKCLHAGDINQIMSLAQNALIGRGT TTRILAAPQDLNSGKLQLTLPGYLR

```

[illegible]

a903.seq

1	ATGCAGCGTC	AGCAGCACAT	AGATGCTGAA	TTGTTAATCTG	ATGCAAATGT
51	CCGTTTCGAG	CAACCATTGG	AGAAGAACAA	TTATGTCCTG	ACTGAAGATG
101	AAACACCGTG	TACTCGGGTA	AATTACATTA	GTTTAGATGA	TAAGACGGCG
151	CGCAAAATTTT	CTTTTCTTCC	TTCGTGCTC	ATGAAAGAAA	CAGCTTTTAA
201	ACCTGGGATG	TGTTTAGGTT	CCAATAATT	GAGCAGGCTA	CAAAAAGCCG
251	CGCAACAGAT	ACTGATTGTG	CGTGCTACC	TCACTCCCA	AGCTATTATC
301	CAACCACAGA	ATATGGATTG	GGGAATTCTG	AAATTACGGG	TATCAGCAGG
351	CGAAATAGGG	GATATCCGCT	ATGAAGAAAA	ACGGGATGGG	AAGTCTGCCG
401	AGGGCAGTAT	TAGTGCATTG	AATAACAAAT	TTCCTTATA	TAGGAACAAA
451	ATTCFCAATC	TTCGCGATGT	ATGACAGGGC	TTGGAAAACC	TGCGTCGTTT
501	GCCGAGTGTT	AAAACAGATA	TTAGATATAT	ACCGTCCGAA	GAGGAAGGCA
551	AAAGCGATTT	ACAGATCAAA	TGGCAGCAGA	ATAAACCAT	ACGGTTTCAGT

a903.pwp

1	MQRQQHIDAE	LLTDANVRFE	QPLEKNNYVL	SEDETPCTRV	NYISLDDKTA
51	RKFSFLPSVL	MKETAFKTM	CLGSNNLSRL	QKAAQQILIV	RGYLTSQAII
101	QPQNMRDSEI	KLRVSAEIG	DIRYEKKRD	KSAGSISAF	NNKFPLYRNN
151	ILNLRDVEQG	LENLRALPSV	KTDIIQIPSE	EEGKSDLIQK	WQONKPIRFS
201	IGIDAGGKT	TKGYQGNVAL	SFDNPLGLSD	LFYVSYGRGL	VHKTDLTDAT
251	GTETESGSR	YSVHYSVPVK	KWLFSFNHNG	HRHYEATGEY	SVNYDYNKGQ
301	YQSSLA AERM	LWRNRFHKTS	VGMKLWTRQT	YKYIDDAEIE	VQRRRSAGWE
351	AELRHRA YLN	RWQLDGKLSY	KRGTMGRQSM	PAPEENGGGT	IPGTSRMKII
401	TAGLDA AEP	MLGKQFFYYA	TAIQAQWNKT	PLVAQDKLSI	GSRYTVXGFD
451	GEQSLFGERG	FYWGQNTLTWY	FHPNHQFVYL	ADYVSGSGES	AQYVSGKQLM
501	GAVVGFRGGH	KVGGMFAYDL	FAGKPLHKPK	GFQTTNTVYG	ENLNYSF*

**m903/a903 98.4% identity in 547 aa overlap**

	10	20	30	40	50	60
m903.pep	MQRQQHIDAE	LLTDANVRFE	QPLEKNNYVL	SEDETPCTRV	NYISLDDKTV	RKFSFLPSVL
a903	MQRQQHIDAE	LLTDANVRFE	QPLEKNNYVL	SEDETPCTRV	NYISLDDKTAR	KFSFLPSVL
	10	20	30	40	50	60
m903.pep	70	80	90	100	110	120
	MKETAFKTM	GLSGSNNLS	RLOKAAQQI	LIVRGYLT	SQAI IQPN	MDSGILKLR
a903	MKETAFKTM	GLSGSNNLS	RLOKAAQQI	LIVRGYLT	SQAI IQPN	MDSGILKLR
	70	80	90	100	110	120
m903.pep	130	140	150	160	170	180
	DIRYEEKRD	GKSAEGSIS	AFNNKFP	LYRNKILN	LRDVEQGLE	NLRRLPSV
a903	DIRYEEKRD	GKSAEGSIS	AFNNKFP	LYRNKILN	LRDVEQGLE	NLRRLPSV
	130	140	150	160	170	180
m903.pep	190	200	210	220	230	240
	EEGKSDLQ	IKWQKNK	PIRFSIG	IDDAGGKT	TGKYQGN	VALSFDN
a903	EEGKSDLQ	IKWQKNK	PIRFSIG	IDDAGGKT	TGKYQGN	VALSFDN
	190	200	210	220	230	240
m903.pep	250	260	270	280	290	300
	AHKTDLT	DATGTET	ESGSRSY	SVHYSVP	VKKWLFS	FNHNGHRY
a903	AHKTDLT	DATGTET	ESGSRSY	SVHYSVP	VKKWLFS	FNHNGHRY



1293

	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSLAERMLWRNRLHKTSGVMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
a903	YQSSLAERMLWRNRFHKTSGVMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRGTGMRQSMPEENGDDILPGTSRMKIITASLDAAAPFXLGKQFFYA					
a903	RWQLDGKLSYKRGTGMRQSMPEENGDDIPGTSRMKIITAGLDAAAPFMLGKQFFYA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYQNTLTWYFHPNHQFYLG					
a903	TAIQAQWNKTPLVAQDKLSIGSRYTVXGFDGEQSLFGERGFYQNTLTWYFHPNHQFYLG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
a903	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
	490	500	510	520	530	540
m903.pep	FNLNYSFX					
a903	FNLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

g904.seq

```

1  ATGATGCAGC ACAATCGTTT CTTCCGCGTC GGGGCCGGTg gaGACGATGG
51  CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTCCGCGCA
151 GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTCACACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGC CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGAATGCA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGCGGCGAT
351 CAAACCAGCC GCAGCGGCGC GCGCGGCCGG TTACCGAACC GAATTCGTGT
401 CCGCGCTCCG CCAAACCTGC GCCTACTTCG TCGAACAATT CGGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC CGCGCCGCGC
551 AGACAGTTGG ACGAGGTAAC GAAAGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TCGCGCCTT CAAACAGCAG TTTTCGCCG TTTTGTGTTT
651 TTTGTTTCAA CACGCGgggaC acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGTCCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTCACG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CCGCGTGCCA CTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCGGATTTTG CCTTTGCCGC GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCCGAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAAGAT ACCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACGACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACgacGct
1201 gCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTgc gccGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGatatTA A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

g904.pep

```

1  MMQHNRFfAV GAGGDDGDRR AADFFNPFQI CFGIGRQCVV AFHADSRFAP

```

m904.seq

1	ATGATGTCAGC	ACAATCGTTT	CTTCTCGGTC	GGGGCCGgTG	GAGACGATGG
51	CGACCGGCGC	GCCGCAGACT	TCTTCAATCC	GTTTCAAATA	TGCTTTGGCG
101	TTTTCGGGCA	ATGCGCCGTA	GTCCTTCACG	CCGAAAGTGG	ATTTCGCGCCA
151	GCCGGGCGATG	GATTTCGTAAA	TCCGGCTTGA	GGTTTCCACC	GCATCGGAAG
201	CGCAAGGCAG	GATGTGCGTT	TGCGCCCGT	CGGGCAATTG	ATAGCCGACG
251	CAGATATTGA	TGGTTTCAAC	GCCGTCCATT	ACATCGAGTT	TAGTAATATACA
301	CATACCGGAA	ATGCCGTTGA	TTTGATGGA	GCGTTTCAGG	GCGGCGGCAT
351	CAAACCGACC	GCAGCGGCGT	GCGCGTCCGG	TTACCGAACC	GAATTCGTGT
401	CCGCGTCTCG	CCAAACCTAC	GCCTACTTTC	TCGAACAATT	CGGTTCGGGAA
451	CGGGCCCGAA	CCGACGCGCG	TGGTATAGGC	TTTTCAGATG	CCCCAAACAT
501	AATCCAGCAT	TTGAGGACCT	ACGCCCGCGC	CTGCCGAAGC	TGCGCCCGCC
551	AGACAGTTGG	ACGAGGTAAC	GAAGGGATAA	GTCCCGTAGT	CGATGTCCAA
601	CAACGCACCT	TGCGCGCCTT	CAAACAGCAG	TTTTTCGCCG	TTTTTGTTTT
651	TCTCGTTCAA	CACGCGGGAC	ACGTCCGGTAA	TCATCGGCGC	AATGCGCGGC
701	GCGCACTTTT	CGATAACCGC	CATCACGCTCT	TCCGCTTTAA	CCGGCTCGGC
751	ATTGTGCAGA	TTGTGCAGTT	GGACATTGTA	ATAGGCAAGG	ACGGCATCCA
801	GTTTTTCACG	CAGTTTtTCA	GGATGCAGCA	AATCGCGCGC	GCGAATGGCG
851	CGGCGTGCCA	CTTTGTCTTC	GTAGGCAGGG	CCGATGCCGC	GGCCGGTCGT
901	GCCGATTTTG	CCTTTGCCGC	GCG .ATcTTC	GCGGGCTTGG	TCGAGCGCGA
951	TGTGGTAAGG	CAGGATCAGC	GGGCAAGTGC	GCBCGATTTT	CAGACGGCCT
1001	TCGACGTTTT	TCACGCCTGC	CGCCTTCAAC	TCGTGATTTT	CGCCCCAAGC
1051	GGCTTCGGGG	GAGACGACAA	GCCGCCGAAG	GATGAAGCAG	TCCAAACTTT
1101	CATGCAGGAT	GCCGCTCGGA	ATCAGGCGCA	AAATGGTTTT	TTTGGCGCGC
1151	ACAACCAAGG	TATGGCCCCG	ATTGTGGCCG	CCTTGAAGAC	GCACCAcGCC
1201	GCCGGCTTCT	TCCGCCAGCC	AGTCAACGAT	TTTACCTTTA	CCCTCGTCGC
1251	CCCACTGTGC	GCCGATTAsT	ACAACATTTT	TAGCCATAGC	CATATAACCT
1301	ATCGATATTA	A			

m904 . pep

1	MMQHNRFFSV	GAGGDDGDRR	AADFFNPFOI	CFGVFGQCAV	VLHAESGFAP
51	AGHGFVNRRLA	GFHRJGTARQ	DVGFAAVGQF	IADADIDGFN	AVHYIEFSNT
101	HTGNAVLDLG	AFQGGGKIPA	AACASGYRT	EFVSATCQTY	AYFVEQFGRE
151	RARTDARGID	FDDAQNIIOH	LRTYARACRS	CARQTVGRGN	EGISAVVDVQ
201	QRTLRAFQKQ	FFAVFVFLVQ	HAGHVGNHRR	NARRDFFDNR	HHVFRFNRLG
251	IVQMLQLDIV	IGKDGIOFFT	QFXRMQOIGG	ANGAACHFVF	VGRADAAAAGR
301	ADFAFAAXIF	AGLVERDVDR	QDQQRAGRDF	QTAFAVDFHAC	RVQLVDFAQQ
351	GFGGDDNART	DEAVQTFMDD	AARNQAQNGF	FAADNQGMAR	IVAALAEAHHA
401	AGFFRPQVND	FTFTLVAPLC	ADXYNIFSHS	HITYRY*	

ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng) from *N. gonorrhoeae*:

m904/g904

	10	20	30	40	50	60
m904.pep	MMQHNRRFFSVGAGGDDGDRRAADFFNPFFQICFGVFGQCAVLHAESGFAPAGHGfVNRLA					
	:                                 :			: :     :		:
g904	MMQHNRRFFAVGAGGDDGDRRAADFFNPFFQICFGIGRQCvVAfhADSrFAPAGHGfVNRFa					
	10	20	30	40	50	60
	70	80	90	100	110	120

m904 . pep	GFHRIGTARQDVGFAAVQQFIADADIDGFNAVHYIEFSNTHGTGNAVDLDGAFQGGGIKPA				
	:   :             :				
g904	GFHRIRTARQDVGFAAAWQFVADADIDGFNAVHYIEFGNAHTGNAVDLDGAFQGGGIKPA	70	80	90	100
		110	120		
		130	140	150	160
m904 . pep	AAACASGYRTEFVSAFQCQTYAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS				
	:       :				
g904	AAARAAGYRTEFVSALRQTCAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS	130	140	150	160
		170	180		
		190	200	210	220
m904 . pep	CARQTVGRGNEGISAVVDVQORTLRAFKQQFFAVFVFLVQHAGHVGNHRRNARRDFFDNR				
	:       :				
g904	RAGETVGRGNEGVSAVVDVQORTLRAFKQQFFAVFVFFVQHAGHVGNHRRNARRDFFDNR	190	200	210	220
		230	240		
		250	260	270	280
m904 . pep	HHVFRFNRLGIVQMLQLDIVIGKDGIOFFTQFXRMQQIGGANGAACHFVFGGRADAAAGR				
	:   :   :   :				
g904	HHVFRFNRSQVMQVLELDVVIGKDGIOFFTQFFRMQQIGGANGAACHFVFGGRADAAAGR	250	260	270	280
		290	300		
		310	320	330	340
m904 . pep	ADFAFAARI FAGLVERDVVRQDQGRRRDFQTAFDVFHACRVQLVDFAQQGFGGDDNART				
g904	ADFAFAARCFAGLVERDVVRQDQGRRRDFQTAFDVFHACRVQLVDFAQQGFGGDDNART	310	320	330	340
		350	360		
		370	380	390	400
m904 . pep	DEAVQTFMQDAARNQAQNGFFAADNQGMARIVAALAEAHHAAGFFRQPVNDFTTLVAPLC				
	:   :   :             :				
g904	DEAIQSFVQDTARNQAQNGFFAADNQGMARIVAALAEAHDAAGFFRQPVNDFTTLVAPLC	370	380	390	400
		410	420		
		430			
m904 . pep	ADXNIFSHSHITYRX				
g904	ADYXNIFSHSHITYRX				
	430				

a904.seq

1	ATGATGCAGC	ACAATCGTTT	CTTCGCGGTC	GGGGCCGGTG	GAGACGATGG
51	CGACCGGCGC	ACCGCAGACT	TCTTCAATCC	GTTTCAAATA	TGCTTTGGCA
101	TTGGCAGGTA	ATGCGTCTGA	GCTTTTCAGC	CCGAAAGTGG	ATTCGCTCCA
151	ACCGGGCATG	GTTTCGTAAA	TCGGCTTCGA	GGCTTCTACC	GCATCAGAGC
201	CGCAAGCGAG	GATGTCGGTT	TCCGCGCGGT	CGGGCAATTC	GTAGCCGACG
251	CAGATATTGA	TGGTTTCAAC	GCCGTCCATT	ACATCGAGTT	TGGTAATACA
301	CATACCGGAA	ATGCCGTTGA	TTTGGATGGA	GC GTTTCAGG	GCGGCGGCAT
351	CAAACGACCC	GCAGCGGGCT	GCGCGTCCGG	TTACCGAATC	GAATTCTGTT
401	CCGCGTTCTG	CCAAACCTGC	TCCGACTTCG	TCGCAAAATT	CGGTCGGGAA
451	CGGGCCCCGA	CCGACGCGCG	TGGTATAGGC	TTTGACGATG	CCCAAAACAT
501	AATCCAGATT	TTGAGGGCCT	ACGCCCGCGC	CTGCCGAAGC	CGCGCCGGCG
551	AGCGACGTTG	ACGAAGTAAC	GAAGGGGTA	GTGCCGTAGT	CGATGTCCAA
601	CACACGACCT	TGCGCGCCTT	CAACACGACG	TTTATCGCGG	TTTTTGTGTT
651	TTTCGTTCAA	CACGCGGGAC	ACGTCGGTAA	TCATCGCGCT	AATGCGCGCG
701	GCGCATTTTT	CGATAACCGC	CATCACGTCT	TCCGCTTTCA	CCGACTCGGC
751	ATTGTGCAGA	TGTTGCAGTT	GGAGTCTGTA	ATAAGCAAAG	ACGGCATCCA
801	GTTTTTCACG	CAGTPTTTCA	GGATGCAGCA	AATCGGCGGC	GCGAATTGGCG
851	CGGCGTGCCA	CTTTGTCTTC	GTAGGCAGGG	CCGATGCGGC	GCGCGGTCGT
901	GCCGATTTTG	CCTTTGCCGC	GCGATGCTTC	TCGGGCTTGG	TCGAGCGCGCA

1296

```
951 TGTGATAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGGTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAGACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACAACCAAGG TATGACCCGC ATTGTGGCCG CCTTGAAGC GCACCACGCC
1201 TCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 .TCGATATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2726; ORF 904.a>:

```
a904.pep
1  MMQHNRRFFAV GAGGDDGDRR TADFFNPFQI CFGIGR*CVV AFHAESGFAP
51  TGHGFVNRLA GFYRIRAARQ DVGFAAVGQF VADADIDGFN AVHYIEFGNT
101 HTGNAVDLDG AFQGGGIKPA AAACASGYRT EFVSAFCQTC SDFVEQFGRE
151 RARTDARGIG FDDAQNIIQH LRAYARACRS RAGEAVGRSN EGVSAVVDVQ
201 QRTLRAFQKQ FFAVFVFFVQ HAGHVGNNRR NARRDFFDNR HHVFRFHLRG
251 IVQMLQLDVV ISKDGIOFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADEFAAARCF SGLVERDVIR QDQRAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQMTR IVAALEAHHA
401 SGFFRQPVND FTFTLVAPLC ADYYNIFSHS HITXRY*
```

m904/a904 91.3% identity in 436 aa overlap

```
10      20      30      40      50      60
m904.pep MMQHNRRFFSVGAGGDDGDRRAADFFNPFQICFGVFGQCAVVLHAESGFAPAGHGFVNRLA
          |||||:|||||:|||||:|||||:|:|:|||||:|||||
a904      MMQHNRRFFAVGAGGDDGDRRTADFFNPFQICFGIGRXCVAFAESGFAPTGHGFVNRLA
          10      20      30      40      50      60

70      80      90      100     110     120
m904.pep GFHRIGTARQDVGFAAVGQFIADADIDGFNAVHYIEFSNTHGTGNAVDLDGAFQGGGIKPA
          |||:|||||:|||||:|||||:|||||:|||||
a904      GFYRIRAARQDVGFAAVGQFVADADIDGFNAVHYIEFGNTHGTGNAVDLDGAFQGGGIKPA
          70      80      90      100     110     120

130     140     150     160     170     180
m904.pep AAACASGYRTEFVSAFCQTYAYFVEQFGRERARTDARGIGFDDAQNIIQHLRTYARACRS
          |||||:|||||:|||||:|||||:|||||:|||||
a904      AAACASGYRTEFVSAFCQTCSDVEQFGRERARTDARGIGFDDAQNIIQHLRAYARACRS
          130     140     150     160     170     180

190     200     210     220     230     240
m904.pep CARQTVGRGNEGISAVVDVQORTLRAFQKQFFAVFVFLVQHAGHVGNNRRNARRDFFDNR
          |::|:|||||:|||||:|||||:|||||:|||||
a904      RAGEAVGRSNEGVSAVVDVQORTLRAFQKQFFAVFVFFVQHAGHVGNNRRNARRDFFDNR
          190     200     210     220     230     240

250     260     270     280     290     300
m904.pep HHVFRFNRLGIVQMLQLDIVIGKDGIOFFTQFXRMQQIGGANGAACHFVFVGRADAAAGR
          |||||:|||||:|||||:|||||:|||||:|||||
a904      HHVFRFHLRGIVQMLQLDVVISKDGIOFFTQFFRMQQIGGANGAACHFVFVGRADAAAGR
          250     260     270     280     290     300

310     320     330     340     350     360
m904.pep ADEFAAAXIFAGLVERDVVRQDORAGRRDFQTAFDVFHACRVQLVDFAQQFGGDDNART
          |||||:|||||:|||||:|||||:|||||:|||||
a904      ADEFAAARCFSGLVERDVIRQDQRAGRRDFQTAFDVFHACRVQLVDFAQQFGGDDNART
          310     320     330     340     350     360

370     380     390     400     410     420
m904.pep DEAVQTFMQDAARNQAQNGFFAADNQMTRIVAALAHHAAGFFRQPVNDFTFTLVAPLC
          |||||:|||||:|||||:|||||:|||||:|||||
a904      DEAVQTFMQDAARNQAQNGFFAADNQMTRIVAALAHHASGFFRQPVNDFTFTLVAPLC
          370     380     390     400     410     420
```

430

1297

```

m904.pep      ADXYNIFSHSHITYRYX
               || ||||| ||||| |||
a904          ADYYNIFSHSHITXRYX
               430

```

g906.seq not found yet

g906.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

```

m906.seq
1  ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTT
51  GTTGGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTGGGAAT
101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAAACAA
301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

```

m906.pep
1  MKYIVSISLA MGLAACSFSG FKNPNWDAAS FWELKNYANP YPGSASAALD
51  QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDPPYPENK
101 KYEWPREEGK TK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

```

g907.seq (partial)
1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGcaAC GCCGCCGCCT
51  GCTGTGTGCC GCCGGCGCGC TGTGTATCAG CCCGCTGGCG CACGCCGGCG
101 CGCAACGTGA AGAAACGctt gCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTGACA ATCCGAAAGA
201 GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGCA AGATTCTGTC
251 CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
351 aagcgggtac cgagctcgaa tcatatca..

```

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

```

g907.pep (partial)
1  MKKPTDTLPV NLQRRRLCA AGALLISPLA HAGAOREETL ADDVASVMRS
51  SVGSVNPPRL VFDNPKGER WLSAMSARLA RFVPDEGERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESGY RARIIS...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

```

m907.seq
1  ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT
51  GTTGTGTGCC GCCGGTGGCT TGTGTCTCAG TCCTCTGGCG CACGCCGGCG
101 CGCAACGTGA GGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGCA AGGTTCTGTC
251 CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTTAT GCCGTTktGG AAAAActACA TCGGCAAAAC GGCGCACAAc
451 CTGTTGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCGCTT GCCCGCTTTA
551 ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTT GGgCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

```

m907.pep
1  MRKPTDTLPV NLQRRRLCA AGALLSPLA HAGAOREETL ADDVASVMRS
51  SVGSVNPPRL VFDNPKGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAISGVA RGLMQVMPXW KNYIGKPAHN

```

1298

151 LFDIRTNLRY GCTILRHRYN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW  
201 RNRWQWR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from *N. gonorrhoeae*:

g907/m907

```

      10      20      30      40      50      60
g907.pep  MKKPTDTLPVNLQRRRLCAAGALLISPLAHAGAQREETLADDVASVMRSSVGSVNPRL
          |:|||||||||||||||||:|||||||||||||||||:|||||
m907      MRKPTDTLPVNLQRRRLCAAGALLISPLAHAGAQREETLADDVASVMRSSVGSVNPRL
          10      20      30      40      50      60

      70      80      90     100     110     120
g907.pep  VFDNPKEGERWLSAMSARLARFVPDEGERRLLVNIQYESSRAGLDTQIVLGLIEVESGY
          |||||||||||||||||||:|||||||||||||||||:|
m907      VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF
          70      80      90     100     110     120

g907.pep  RARIIS
          ||||
m907      RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHRYNLEKGNIVRAL
          130     140     150     160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2733>:

a907.seq

```

1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGCAAC GCCGCCGCCT
51  ATGTGTGTGCT GCCGGCGCGC TGTTGCTCAG CCCGCTGGCA CAAGCCGGCG
101 CGCAACGTGA AGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGC
151 TCTGTCGGCA GCATAAATCC GCCGAGGCTG GTGTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGCTGTCCG CGATGTCTGC TCGGTTGGCA AGGTTCGTCC
251 CCGATGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCGG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTTAT GCCGTTTGG AAAAATACTA TCGGCAAAAC GGCGCACAAAC
451 CTGTTGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCACTC GCCCGTTTTA
551 ACGGTAGCCT CGGCAGCAAT AAATATCCGA ACGCCGTTT GGGCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>:

a907.pep

```

1  MKKPTDTLPV NLQRRRLCA AGALLSPLA QAGAQREETL ADDVASVMRS
51  SVGSINPPRL VFDNPKEGER WLSAMSARLA RFVPDEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAISGVA RGLMQVMPFW KNYIGKPAHN
151 LFDIRTNLRY GCTILRHRYN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW
201 RNRWQWR*

```

m907/a907 97.6% identity in 207 aa overlap

```

      10      20      30      40      50      60
m907.pep  MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAQREETLADDVASVMRSSVGSVNPRL
          |:|||||||||||||||||:|||||||||||||||||:|||||
a907      MKKPTDTLPVNLQRRRLCAAGALLSPLAQAGAQREETLADDVASVMRSSVGSINPPRL
          10      20      30      40      50      60

      70      80      90     100     110     120
m907.pep  VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF
          |||||||||||||||||||:|||||||||||||||||:|
a907      VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF
          70      80      90     100     110     120

```

1299

	70	80	90	100	110	120
m907.pep	130	140	150	160	170	180
	RQYAIISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHRYNLEKGNIVRAL					
a907	130	140	150	160	170	180
	RQYAIISGVGARGLMQVMPFWKNYIGKPAHNLFDIRTNLRYGCTILRHRYNLEKGNIVRAL					
m907.pep	190	200				
	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
a907	190	200				
	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

```

g908.seq
1  ATGAG.AAAA GCCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTTGTCGCA GGTGTAAC TG CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTACGATG ACTGATTTAT
151 CAAAACGGTC CGCATTAGA AATGTTTGAT GCGGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 acaagtgaac cctgacagta ttgtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa ttagccatT Ttagcttcgc tgaaacttcg
451 ttttcgtaTC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

```

g908.pep
1  MXKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAA YDFHRLR*LIY
51  QNGPHLEMF DGEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LPPIIREQVK PDSIVYTDCY RSYDVLVDSE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

```

m908.seq
1  ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAACT
51  GTTTGTCACA GGTGTAAC TG CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTGGA AATGTTTGAT GCGGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCGCTACT TTATTCCTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTTTATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

```

m908.pep
1  MRKSRLSRYK QXKLIELFVT GVTARTAAEL VGVNKNTAA YFHLRLLLIY
51  QNSPHLEMF DGEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LPPIIREQVK PDSIFYTDCY RSYDVLVDRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng) from *N. gonorrhoeae*:

```

g908/m908
10 20 30 40 50 60
g908.pep MXKSRLSRYKQNKLIGLFVAGVTARTAAELVGINKNTAAAYDFHRLRLXLIYQNGPHLEMF

```

m908	MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNTAAAYFYHRLRLLIYQNSPHLEMPD
	10 20 30 40 50 60
g908.pep	GEVEADESYFGGQRKGKRGRGAAGKVAVFGLLKRNKGKVIYTVTPNQTATLFPIIREQVK
	70 80 90 100 110 120
m908	GEVEADESYFGGQRKGKRGRGAAGKVAVFGLLKRNKGKVIYTVTPNQTATLFPIIREQVK
	70 80 90 100 110 120
g908.pep	PDSIVYTD CYRSYDVLDVSEF SHFSFAETSF SYQSQHTFCRTTKPYX
	130 140 150 160
m908	PDSIFYTD CYRSYDVLDVREF SHFSFAETSF SYQSQHTFCRTTKPYX
	130 140 150 160

```
a908.seq
1  ATGAGAAAAA  GTCGCTAAG  CCAGTATAAA  CAAAATAAAC  TCATTGAGCT
51  ATTTTGTGCGA  GGTGTAACCT  CAAAGAACGCG  AGCAGAGTTA  GTAGGCGGTTA
101 ATAAAAAATAC  CGCAGCGCTAT  TATTTTCATC  GTTTACGATT  AACTATTATAT
151 CAAACAGCTC  CGCATTTGGA  AATGTTTGAT  GCGGAAGTAG  AAGCAGATGA
201 AAGTTATTTT  GGCGGACAAC  GCAAAGGCAA  ACGCGGTGCG  GGTGCTGCCG
251 GTAAAGTCGC  CGTATTCGGT  CTTTGAAGC  GAAATGGTAA  GGTTTATACG
301 GTTACAGTAC  CGAATACTCA  AACCGCTACT  TTATTTCCTA  TTATCCGTGA
351 ACAAGTGAAA  CCTGACAGCA  TTGTTTATAC  GGATGGTTAT  CGTAGCTATG
401 ATGTATTAGA  TGTGCGCGAA  TTTAGCCATT  TTAGCTTCG  TGAAACTTCG
451 TTTTCGTATC  AATCAGACGA  CACATTTTGC  CGAACGACAA  AACCATTATTA
501 A
```

```
a908.pep
1  MRKSRLSQYK QNKLIELFVA GVTARTAAEL VGVNKNTAAY YFHLRLLIY
51  QNSPHLEMFQ GEVEADESYF GGQRKGKGRG GAAGKVAVFG LLKRNGKVYT
101 VTPVNTQTAT LFPIIREQVK PDSIVYTDY RSYDVLVRE FSHFSFAETS
151 FSYQSQTFC RTTKPY*
```

	10	20	30	40	50	60
m908.pep	MRKSRLSQYKQXKLI	ELFVTGTARTAAELV	GVNKNNTAAYYFHR	LRLLIYQNSPHE	MF	
a908	MRKSRLSQYKQXKLI	ELFVTGTARTAAELV	GVNKNNTAAYYFHR	LRLLIYQNSPHE	MF	
	10	20	30	40	50	60
m908.pep	GEVEADESYEGGQR	KGKRGRGAAGKVAV	FGLLRNGKQVYTV	VPNTQTATLFPI	IREQVK	
a908	GEVEADESYEGGQR	KGKRGRGAAGKVAV	FGLLRNGKQVYTV	VPNTQTATLFPI	IREQVK	
	70	80	90	100	110	120
m908.pep	PDSIFYTDCYRSYD	VLVDVREFSHFSFA	ETSFSYQSQHTFC	RTTKPYX		
a908	PDSIVYTDYRSYD	VLVDVREFSHFSFA	ETSFSYQSQHTFC	RTTKPYX		
	130	140	150	160		

```

1   atgcgtaaaa ccgctacttat cCTgaccatc tccgcgcgcc ttttgtcggg
51  ctgcacatgG gaaacttatc aagacggcag cggcaaaacc gccgtccgtg
101 caaaatgttc caccggcacg ccgctgtgtt ggcaagacgg gcgcggctcg

```



1301

151 aaaaaggtgg actgcgacga gtacggtggc gaacgccggg ccgtgttgcg  
 201 caaccaaag cgggggaagc ccgcgacgag gagagccgca acgctgggga  
 251 aaccgagttt ccgggagagg gacggggggg ggcgggtgaa cagggcagaa  
 301 acgggggagg ggaagcgatc ggcgagg..

This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:

g909.pep (partial)

1 MRKTVLILTI SAALLSGCTW ETYQDGSgKT AVRACSTGT PLCWQDGRGS  
 51 KKVDCDEYGG ERRAVLNRNQK RGKPATRRRA TLGKPSFRAR DGGGRVNRAE  
 101 TGEGRKSAR..

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2743>:

m909.seq

1 ATGCGTAAAA CCTTCCTCTT CCTGACCGCT GCCGCCGCC TTTGTGCGGG  
 51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC  
 101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG  
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC  
 201 CAATCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA  
 251 AACCAGAGTT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:

m909.pep

1 MRKTFLEFLTA AALLSGCAW ETYQDNGGKT AVRQKYPAGT PVYYQDGSYS  
 51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng) from *N. gonorrhoeae*:

m909/g909

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AALLSGCAW	ETYQDNGGKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
		:	:	:	:	:
g909	MRKTVLILTI	SAALLSGCTW	ETYQDGSgKT	AVRAKSTGT	PLCWQDGRGS	KKVDCDEYGG
	10	20	30	40	50	60
	70	80	90			
m909.pep	ERHAVLPNQT	GNNADEEHRQ	HWQKPKFQNR			
			::	::		:
g909	ERRAVLRNQK	RGKPATRRRA	TLGKPSFRAR	DGGGRVNRAE	TGEGRKSAR	
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2745>:

a909.seq

1 ATGCGTAAAA CCTTCCTTAT CCTGATGACT GCCGCCGCC TTTGTGCGGG  
 51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC  
 101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG  
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC  
 201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA  
 251 AGCCCAAATT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:

a909.pep

1 MRKTFILILMT AALLSGCAW ETYQDNGGKT AVRQKYPAGT PVYYQDGSYS  
 51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR \*

m909/a909 96.7% identity in 90 aa overlap

	10	20	30	40	50	60
m909.pep	MRKTFLEFLTA	AALLSGCAW	ETYQDNGGKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
		:	:	:	:	:
a909	MRKTFILILMT	AALLSGCAW	ETYQDNGGKT	AVRQKYPAGT	PVYYQDGSYS	KNMNYNQYRP
	10	20	30	40	50	60

1302

	70	80	90
m909.pep	ERHAVLPNQTGNNADEEHRQHWQKPKFQNRX		
a909	ERHAVLPNQTGNNADEEHRQHWQKPKFQNRX		
	70	80	90

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

```

g910.seq
1  ATGAAAAAAC TGTTATTGGC CGCCGTTGTT TCCCTAAATG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAACAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCAAACCTG TTTTGGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

```

g910.pep
1  MKKLLLAADV SLNAATAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDYW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

```

m910.seq
1  ATGAAAAAAC TGTTATTGGC TGCCGTTGTT TCTCTGAGTG CCGTGCCCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCT GTGAAAATGT TGGAGCAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACCATTGG GGTAAAGCCTG TGCTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

```

m910.pep
1  MKKLLLAADV SLSAAAAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
g910.pep	MKKLLLAADVSLNAATAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDYW					
m910	MKKLLLAADVSLSAAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDHW					
	10	20	30	40	50	60
	70	80	90			
g910.pep	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
m910	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

```

a910.seq
1  ATGAAAAAAC TGTTATTGGT CGCCGTTGTT TCCTTGAGTG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCTATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAACAGCG CGGTTATCAG
151 GTTCACGATG TCGATGCCGA CGACCATTGG GGCAAACCTG TTTTGGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATTGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

```

a910.pep

```

1303

1 MKKLLLVAVV SLSAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ  
51 VHDVDADDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR\*

m910/a910 95.7% identity in 94 aa overlap

	10	20	30	40	50	60
m910.pep	MKKLLLA	AVVSLS	AAAAFAG	DSAE	RQIYGD	PHFEQNRTKAVKMLEQRGYQVYD
a910	MKKLLLV	AVVSLS	AATAFAG	DSAE	RQIYGD	PYFEQNRTKAVKMLEQRGYQVHDVDADDHW
	10	20	30	40	50	60
	70	80	90			
m910.pep	GKPVLE	VEAYKD	GREYDIVL	SYPDLKIIKE	QLDRX	
a910	GKPVLE	VEAYKD	GREYDIVL	SYPDLKIIKE	QLDRX	
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2753>:

g911.seq  
1 ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCTTGATCGG  
51 CGCGGCGGCG GTTGCCTTTC TCGCTTTCCG CGTGGCGGGC GGCGCGGCGT  
101 TCGGCGGTTC GGACAAACT TACGCCGTTT ATGCCGATTT CGGCGACATC  
151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGAGGCG TATTGGTCGG  
201 GCGCGTCGGC GCTATCGGGC TTGACCCGAA ATCCTATCAG GCGAGGGTGC  
251 GCCTTGATT GGACGGCAAG TATCAGTTCA GCAGTGACGT TTCCGCGCAA  
301 ATCCTGACTT CGGGACTTTT GGGCGAACAG TACATCGGGC TGCAGCAGGG  
351 CGGCGATACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAATT  
401 CTGCAATGGT TCTGAAAAAC CTGATCGGTA AATTCATGAC CAGCTTCGCC  
451 GAGAAAAACG CTGAGGGCGG CAATGCGGAA AAAGCCGcag aAtaa

This corresponds to the amino acid sequence <SEQ ID 2754; ORF 911.ng>:

g911.pep  
1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI  
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDDGK YQFSSDVSAQ  
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA  
151 EKNAEGGNAE KAAE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2755>:

m911.seq  
1 ATGAAGAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCCTGATTGG  
51 CGCGGCGGCG GTTGCCTTTC TCGCTTTCCG CGTGGCGGGC GGTGCGGCGT  
101 TCGGCGGTTC GGACAAACT TACGCCGTTT ATGCCGATTT CGGCGACATC  
151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGAGGCG TATTGGTCGG  
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC  
251 GCCTCGATT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA  
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG  
351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAATT  
401 CTGCAATGGT TCTGAAAAAC CTTATCGGCA AATTCATGAC GAGTTTGGCC  
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

This corresponds to the amino acid sequence <SEQ ID 2756; ORF 911>:

m911.pep  
1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI  
51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDDGK YQFSSDVSAQ  
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA  
151 EKNADGGNAE KAAE\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF 911.ng) from *N. gonorrhoeae*:

g911/m911

10 20 30 40 50 60

1304

```

g911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
g911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m911      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          70      80      90      100     110     120

          130     140     150     160
g911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
1  ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTTC TCCTGATTGG
51 CGCGGCGGCG GTTGCCCTTTC TCGCTTTCCT CGTGGCCGCG GGTGCGGCGT
101 TCGGCGGTTTC GGACAAAAC TACGCCGTTT ATGCCGATT TCAGGACATC
151 GCGCGTTTGA AGGTCAATGC CCCCGTCAA TCCGCAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CGCGGACACG GAAAACCTTG CTGCCGCGCA CACCATCTCC GTAACCAAGT
401 CTGCAATGGT TCTGAAAAC CTTATCGGCA AATTCATGAC GAGTTTGGCC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
1  MKKNILEFWV GLFVLIGAAA VAFVAFRVAG GAAFFGGSDKT YAVYADFGDI
51  GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

m911/a911 100.0% identity in 164 aa overlap

```

          10      20      30      40      50      60
m911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
m911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a911      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          70      80      90      100     110     120

          130     140     150     160
m911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAEX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
1  gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTTGAGCAT
51  CGGCATGGCA TTTGCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101 ACGCCACACA GGTTTTGACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```

q912.pep

```

1  VKKSSFISAL GIGILSIGMA FASPADAVGQ IRQATQVLT ILKSGDAASA
51  RPKAEAYAVP YDFQRM TAL AVGNPWR TAS DAQKQALAKE FQTL LIR TYS
101 GTMLKFKNAT VNVKDNPIVN KGGKEIVVRA EVGIPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGTSLVTVYR NQFGEIIKAK GIDGLIAELK AKNGGK*

```

m912.seq

1	ATGAAAAAAT	CCTCCCTCAT	CAGCGCATTG	GGCATCGGTA	TTTGTAGCAT
51	CGGCATGGCA	TTTGCCGCCC	CTGCCGACGC	GGTAAGCCAA	ATCCGTCAAA
101	ACGCCACTCA	AGTATTGAGC	ATCTTAAAAA	ACGGCGATGC	CAACACCGCT
151	CGCCAAAAAG	CCGAAGCCTA	TGCAGTCTCC	TATTTGCAAT	TCCAACGTAT
201	GACCGCATTG	CGCGTGGCCA	ACCTTGGCGC	CACCGCGTCC	GACGCGCAAA
251	AACAAGCGTT	GGCCAAAGAA	TTTCAAACCC	TGCTGATCCG	CACCTATTCC
301	GGCACGATGC	TGAAATTAAT	AAACGCCAAC	GTCACGCTA	AAGACATTC
351	CATCGTCAAT	AAAGGCGGCA	AAGAAATCAT	CGTCCGCGCC	GAAGTCGGCG
401	TATCCGGGCA	AAAACCCGTC	AACATGGACT	TCACCACCTA	CCAAGCGGCG
451	GGTAAATACC	GTACCTACAA	CGTCGCCATT	GAAGGCGCGA	GCCTGTTTAC
501	CGTGATTCCG	AACCAATTCC	CGCAAAATTAT	CAAAGCGAAA	GGCGTGGACG
551	GACTGATTGC	CGAGTTGAAA	GCCAAAAACG	CGGGCAATAA	A

m912.pgp

1 MKKSSLISAL GIGILSIGMA FAAPADAVSQ IRQATQVLS ILKNGDANTA  
51 RQKAEAYAIP YFDFQRM TAL AVGNPWR TAS DAQKQALAKE FQTL LIR TYS  
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVP GQKPV NMDFTTYQSG  
151 GKYRTYNVAI EGASLVTVYR NQFGEI IKAK GVDGLIAELK AKNGGK\*

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng) from *N. gonorrhoeae*:

g912/m912

[illegible]

1306

m912  
 |||||  
 GVDGLIAELKAKNGGKX  
 190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

a912.seq  
 1 ATGAAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT  
 51 CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAACCAA ATCCGTCAAA  
 101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC  
 151 CGCCAAAAAG CCGAAGCCTA TGCATTCCCT TATTTCGATT TCCAACGTAT  
 201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAAA  
 251 AACAAAGCGT GGCCAAAGAA TTTCAAACCC TGCTGATCCT CACCTATTCC  
 301 GGCACGATGC TGAAATTAAA AAACGCCAAC GTCAACGTCA AAGACAATCC  
 351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG  
 401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC  
 451 GGTAAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC  
 501 CGTGTAACGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GCGGTGGACG  
 551 GACTGATTGC CGAGTTGAAG GCTAAAAACG GCAGCAAGTA A

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

a912.pep  
 1 MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQNATQVLS ILKSGDANTA  
 51 RQKAEAYAIP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTL LIR TYS  
 101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPQKPV NMDFTTYQSG  
 151 GKYRTYNVAI EGASLTVYR NQFGEI I KAK GVDGLIAELK AKNGSK\*

m912/a912 98.0% identity in 196 aa overlap

	10	20	30	40	50	60
m912.pep	MKKSSLISALGIGILSIGMAFAAPADAVSQIRQNATQVLSILKNGDANTARQKAEAYAIP					
a912	MKKSSFISALGIGILSIGMAFAAPADAVNQIRQNATQVLSILKSGDANTARQKAEAYAIP					
	10	20	30	40	50	60
m912.pep	YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTL LIR TYS GTMLKLKNANVNVKDNPIVN					
a912	YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTL LIR TYS GTMLKLKNANVNVKDNPIVN					
	70	80	90	100	110	120
m912.pep	YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTL LIR TYS GTMLKLKNANVNVKDNPIVN					
a912	YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTL LIR TYS GTMLKLKNANVNVKDNPIVN					
	70	80	90	100	110	120
m912.pep	KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLTVYRNQFGEI I KAK					
a912	KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLTVYRNQFGEI I KAK					
	130	140	150	160	170	180
m912.pep	KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLTVYRNQFGEI I KAK					
a912	KGGKEIIVRAEVGVPQKPVNMDFTTYQSGGKYRTYNVAIEGASLTVYRNQFGEI I KAK					
	130	140	150	160	170	180
m912.pep	GVDGLIAELKAKNGGKX					
a912	GVDGLIAELKAKNGSKX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

g913.seq  
 1 atGAAAAAAA CCGCCTACGC CATCCTCCTG CTGATCGGGT TCGCTTCCGC  
 51 CCCTGCATTT GCAGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC  
 101 GCGCGTTTC CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCTT  
 151 GCGCGCGCG GCTACCGCAA AGTTACGCG AAACCCGTCC GCGCCGGCGT  
 201 GTCCAATTTT TTAAACAACC TGCGCGACGT GGTCAGTTT GGCAGCAATA  
 251 TCTTGCGTTT GGAcATCAAA cgcgcaAGcg aAGACctcgT CCGcgteggc  
 301 atCAATACCA CCTTCGGTTT GGcgGGCTC ATTGATATTG CCGGcgGgGg  
 351 cggcgttccc gacaataaaa AcacTttgGg cgacacgtt gctcgtGGG  
 401 GctgGAAAaa cagcaATTAT TTCGTgttgc CCGtcttagg cccgtccacc

1307

```

451 gtccgcgacg cgctcggcac gggcattacc tCTGTTTATC CGCccaagaa
501 tatcgttttc catacccttg ccggacgctg GGgcacgact gCCGCTGCCG
551 CCGTcagtac gcgcgaaggc ctctcgatt tgaccgacag Tctggacgaa
601 gccgccatCG ACAAATACAG CTACACGCGc gacctctata tgAAAGTCCG
651 CGcacgGCag AccgGTGCAA CACCTGCCGA AGgtacggaa gataacatcg
701 acatcgacat cgACGAATTG GTCGAAAGTG CCGAAACCGG CGCGGCAGAG
751 CCCGCCGTTT ACGAAGATTG CGTATCCGAA ACACAGGCAG AAGCAGCAGG
801 GGAAGCCGAA ACGCAACCTG GAACACAACC CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2766; ORF 913.ng>:

g913.pep

```

1 MKKTAYAILL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
51 AARGYRKVTP KPVVRAGVSNF FNNLRDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGVP DNKNTLGDTF ASWGWKNSNY FVLPVLGPST
151 VRDALGTGIT SVYPPKNIVF HTPAGRWTG AAAAVSTREG LLDLTDLSDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDIDEL VESAETGAEE
251 PAVHEDSVSE TQAEAGEAE TQPGTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2767>:

m913.seq

```

1 ATGAAAAAAA CCGCCTATGC CTTCTCCTG CTGATCGGGT TCGCTTCCGC
51 CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCGGTTTT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTGCCCCCT
151 GCCGCGCGCG GCTACCGCAA AGTTCGCGCG AAACCCGTCC GCGCCGCGGT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTCAGCTTC GGCAAGCAATA
251 TCTTTCGCTT GGACATCAAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGC
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CCGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCCTCGTGGG
401 GATGGAAAAA CAGCAATTAT TTCGTGTGTC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCACGACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTgCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGCGCGGCAG ACCGGTGCAA CACCTGCCGA AGgtACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2768; ORF 913>:

m913.pep

```

1 MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
51 AARGYRKVAP KPVVRAGVSNF FNNLRDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWKNSNY FVLPVLGPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWTG AVSAVSTREG LLDLTDLSDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 913 shows 94.9% identity over a 277 aa overlap with a predicted ORF (ORF 913.ng) from *N. gonorrhoeae*:

g913/m913

	10	20	30	40	50	60
g913.pep	MKKTAYAILLLIGFASAPAF AETRPADPYE GYNRAVSKFNDQADRYIFAPAARGYRKVTP					
	:					
m913	MKKTAYAFLLLIGFASAPAF AETRPADPYE GYNRAVSKFNDQADRYIFAPAARGYRKVAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g913.pep	KPVVRAGVSNFFNNLRDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGVP					
m913	KPVVRAGVSNFFNNLRDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP					
	70	80	90	100	110	120

```

130      140      150      160      170      180
g913.pep DNKNTLGDTFASWGWNKSNYFVLPVLGPSTVRDALGTGITSVYPPKNIVFHTPAGRWGTT
          |||||
m913      DNKNTLGDTFASWGWNKSNYFVLPVLGPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT
          |||||

130      140      150      160      170      180

190      200      210      220      230      240
g913.pep AAAAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDIDEL
          |::|
m913      AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDI--DEL
          |||||

190      200      210      220      230

250      260      270
g913.pep VESAETGAAEPAVHEDSVSETQAEAAAGEAETQPGTQPX
          |||||
m913      VESAETGAAETAQEDSVSETQAEAAAGEAETQPGTQPX
          |||||
240      250      260      270

```

```

a913.seq
1  ATGAAAAAAA CCGCCTATGC CTTCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTG GCCGAAACCC GCCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCGGTTTT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCTT
151 GCCGCGCGCG GCTACCGCAA AGTTCGCGCG AAACCCGTCC GCGCCGCGGT
201 GTCCATTTTT TTTAACAAAC TGTGCGACGT GGTCAGCTTC GGCAGCAATA
251 TCTTGCCTTT AGACATCAAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGT
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGCGCGCGG
351 CGGCATTCCC GACATAAAAA ACACCTTGGG GCACACGTGT GCTTCGTGGG
401 GATGAAAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCGCGGACG CGCTCGGCAC GGTATTACC TCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCAGCACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTGCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAATAACAG CTACACGCGC GACCTCTATA TGAAGTCCG
651 TGCGCGGCAG ACCGGTGCAA CACCTGCCGA AGGTACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGCGCGCGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC GAAACACAG CAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTGGAAC ACAACCTTAA

```

```
a913.pap
1 MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKEN DQADRYIFAP
51 AARGYRKVP KPVRAVSNF FNNKLDVVSF GSNILRLDIK RASFLDVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNLTGDTF ASWGKNSNY FVELPVLGSP
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGT AVSAVSTREG LLDLTDLSLE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAETA
251 VQEDSVSETQ AEAAGEAETO PGTOPGTOP*
```

	10	20	30	40	50	60
m913.pep	MKKTAYAFLLLLIGFASAPAF	ETRPADPYEGYNRAVFKFNDQ	ADRYIFAPAARGYRKVAP			
a913	MKKTAYAFLLLLIGFASAPAF	ETRPADPYEGYNRAVFKFNDQ	ADRYIFAPAARGYRKVAP			
	10	20	30	40	50	60
m913.pep	70	80	90	100	110	120
	KPVRAGVSNFFNNLCDVVSFG	SNILRLDIKRASEDLVRVGINT	TTFGLGGLIDIAGAGGIP			
a913	KPVRAGVSNFFNNLCDVVSFG	SNILRLDIKRASEDLVRVGINT	TTFGLGGLIDIAGAGGIP			
	70	80	90	100	110	120
m913.pep	130	140	150	160	170	180
	DNKNTLGDTFASWGWKNSNYF	VLPLVLPSTVRDALGTGITSV	SPKNIVFRTPVGRWGTT			
a913	DNKNTLGDTFASWGWKNSNYF	VLPLVLPSTVRDALGTGITSV	SPKNIVFRTPVGRWGTT			



1309

	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pep	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDELVE					
a913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDELVE					
	190	200	210	220	230	240
	250	260	270			
m913.pep	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
a913	SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPGTQPX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacgtttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGGCG AGATGAGGCA
301 ATCCGATGCA GAAAATTCTGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTGGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTT TGCCGATTCG
451 taggctTCGA CGATTTTGTG CACCAGAGGA TGCCGGACAA CGTCTTCGCC
501 GGTGAAGGTA TGGAAATACA GTCCTGCCAC GCCGTGCAGT TTCTCAGGTG
551 CGTCTTTCAA TCCCGATTG ATGTTTTTGG GCAGGTcgaT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCgccgaag ccGATGCGGG TCAGGAACAT
651 TTTCATTGTG TCGGGCGTGg tgTtttGcgC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGag cgTCCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```

1  MKKCILGILT ACAAMPAFAD RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCGDEA
101 IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTTSSPVKV WKYSPATPCS FSRASFNPDL MFLGRSIWLV
201 SPVMTAFAPK PMRVRNIFIC SGVVCASSR MMYAPLSVLP RI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGGCA AGATGAGGCA
301 ATCCGATGCA GAAAATTCTGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCCGTAT CTGTTTTTCT CTGCTGATT
401 TTCCATGCAT CGGGTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC
451 GATTCTAGG CTTCGACGAT TTTTGCACC AAAGGATGCC GGACAACGTC
501 TTCGCCGTA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
551 CACGCGCATC TTTTAATCCC GATTGATGT TTTTGGGCAG GTCGATTTGG
601 CTGGTGTGCG CGGTAATGAC GGCTTTCGCG CCGAAGCCGA TCGGGTCAG
651 GAACATTTTC ATTTGTTCGG GCGTGGTGTT TTGCGCTTCG TCGAGGATGA
701 TGTATGCGCC GTTGAAGCTC CTGCCGCGCA TATAG

```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```

1  MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEEA
101 IRCRKFDXCI GWTDKETDTE TELGFRICFS LPDFPCIGFQ TALECQSCSA

```

1310

151 DSXASTIFCT KGCRTTSSPV KVKYSPSTL CSFSRASFPN DLMFLGRSIW  
 201 LVSPVMTAFA PKPMVRNIF ICSGVVFCAS SRMMYAPLSV LPRI\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng)  
 from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914.pep	MKKCILGILTACAAMPAFADRIDLEARLAQLEHRVAVLESGGNTVKIDLFSGNSTMYVC					
m914	MKKCILGILTACAAMPAFADRIDLEARLAQLEHRVAVLESGGNTVKIDLFSGNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	119
g914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCGDEAIRCRCFDXCIGWTDKETDT-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEAIRCRCFDXCIGWTDKETDTD					
	70	80	90	100	110	120
	120	130	140	150	160	170
g914.pep	-ELGFRICFSLPDFPCIGFQTALEQCSCSADSXASTIFCTRGCRRTSSSPVKVKYSPATP					
m914	TELGFRICFSLPDFPCIGFQTALEQCSCSADSXASTIFCTKGCRRTSSSPVKVKYSPSTL					
	130	140	150	160	170	180
	180	190	200	210	220	230
g914.pep	CSFSRASFPN DLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
m914	CSFSRASFPN DLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	190	200	210	220	230	240
	240					
g914.pep	LPRIX					
m914	LPRIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCAGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTATCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAATGTC AGTCGTGTTT TGCCGATTCTG
451 TAGGCTTCGA CGATTTTGTG CACCAAAGGA TGCCGGACAA CGTCTTCGCC
501 GGTAAAGGTG TGGAAATACA GCCCTTCCAC GCCGTGCAGT TTCTCAGCG
551 CATCTTTTAA TCCCGATTG ATGTTTTTGG GCAGGTCGAT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCGCCGAAG CCGATGCGGG TCAGGAACAT
651 TTTCAATTTGT TCGGGCGTGG TGTTTTGCGC TTCGTGAGG ATGATGTATG
701 CGCGTTGAG CGTCTGCCG CGCATATAG
```

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914.pep

```

1  MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGSNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEDA
101 IRCRKFD*CI GWTDKETDTE LGFRICFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTKG CRTTSSPVKV WKYSPSTPCS FSRASFPN DLMFLGRSIWLV
201 SPVMTAFAPK PMVRNIFIC SGVVFCASSR MMYAPLSVLP RI*
```

m914/a914 98.4% identity in 244 aa overlap

```

      10      20      30      40      50      60
m914.pep  MKKCILGILTACAAMPADFADRIDGLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC
          |||||
a914      MKKCILGILTACAAMPADFADRIDGLEARLAQLEHRVAVLESGSNTVKIDLFGSNSTMYVC
      10      20      30      40      50      60

      70      80      90     100     110     120
m914.pep  SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD
          |||||
a914      SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD--
      70      80      90     100     110

      130     140     150     160     170     180
m914.pep  TELGFRICFSLPDFPCIGFQTALECSQSCSADSXASTIFCTKGCRTTSSPVKVKYSPSTL
          |||||
a914      TELGFRICFSLPDFPCIGFQTALECSQSCSADSXASTIFCTKGCRTTSSPVKVKYSPSTP
      120     130     140     150     160     170

      190     200     210     220     230     240
m914.pep  CSFSRASFPDLMFLGRSIWLVSFVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV
          |||||
a914      CSFSRASFPDLMFLGRSIWLVSFVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV
      180     190     200     210     220     230

m914.pep  LPRIX
          ||||
a914      LPRIX
          240

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

```

g915.seq
1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gtTTTCGCCT TAAGTGCCTG
51  CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2778; ORF 915.ng>:

```

g915.pep
1  MKKTLAIVA VFALSACRQA EEAPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KQIFLNGKP DQPWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMGAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

```

m915.seq
1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTTCGCCT TAAGTGC.tG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCcCGGCAG ATTAGCGACC
101 GTTCGGTCCG ACACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TtTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG

```

1312

451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence &lt;SEQ ID 2780; ORF 915&gt;:

m915.pep

1 MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP  
 51 KQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT  
 101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK  
 151 VVGFDMPDT YIFK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng)

from *N. gonorrhoeae*:

m915/g915

	10	20	30	40	50	60
m915.pep	MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g915	MKKTLLAIVAVFALSACRQAEEAPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDGMNVTDWTPNADTEWMDAKKAFYVIDS					
g915	DQPVWFSTVQMFYTKLPEEPKGIRVIYVTDGMNVTDWTPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDTYIFKX					
g915	GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2781>:

a915.seq

1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTTCGCCT TAAGTGCCTG  
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCCCTT ACCCCGGCAG ATTAGCGACC  
 101 GTTCGGTCGG AACTATTGCG AGTATGAACC TGACCGAACA CAACGGCCCC  
 151 AAAGCCCAGA TTTTCTTGAA CGGCAAAACC GATCAGCCCG TTTGGTTCTC  
 201 CACCATCAAG CAGATGTTCC GCTATACCAA GCTGCCCGAA GAGCCTAAAG  
 251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG  
 301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT  
 351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT  
 401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG  
 451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence &lt;SEQ ID 2782; ORF 915.a&gt;:

a915.pep

1 MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP  
 51 KQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT  
 101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK  
 151 VVGFDMPDT YIFK\*

m915/a915 99.4% identity in 164 aa overlap

	10	20	30	40	50	60
m915.pep	MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
a915	MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDGMNVTDWTPNADTEWMDAKKAFYVIDS					
a915	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDGMNVTDWTPNADTEWMDAKKAFYVIDS					

1313

	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX					
a915	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDITYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

```

g917.seq
1  ATGGTCAAac atctgccacT cgcCGTCctg actgctTtgc tgcttgacgc
51  gtgcGGCGGT Tcggacaaac cgcctgccga Aaaaccgca ccggcgGaAA
101 accaaAacgt atTgaAAATT TataACTGGT CGGAATACGT CGATCCGGAA
151 ACCGTGCGG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAATCCG
251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
351 TCTCAACCTT GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGACCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAGTG
501 GGATTTGGTG TTCAACCCCG AATACACGTT CAAACTCAAA CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACAT
601 TTGGGCAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTGCTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTTGGCG CGCGGCGATA CTGCGTAAC AATCGGTTTC
751 GCGGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAATC CGCGTGATGA TGCCGAAAGA GGGCGTGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCTCGA TCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 cgttacCTAC GCGCCTTCGA GCAAGCCGGC GCGCGATTG ATGGAGGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCGA GCGGGGAAGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCGGCCGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

```

g917.pep
1  MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKQNG IKVTYDVYDS DETLESKVLV GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS MIPNYKHLNP EMMRLMDGVD PDHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FNPEYTFKLK QCGISYLD SA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGD LNI AKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPARDL MEDEFKNDNT IFPSGEDLKN
351 SFIMVPIRPA ALKFMVRQWQ DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

```

m917.seq
1  ATGACCAAAC ATCTGCCCTT GGCCGTCCTG ACTGCTTTGC TGCTTGCAGC
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGCGGAAAA
101 ACCAAAACGT ATTGAAAATT TACAACTGGT CGGAATATGT CGATCCGGAA
151 ACCGTGCGG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAGTG
501 GGATTTGGTG TTGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTTGGCG CGCGGCGATA CTGCGTAAC AATCGGTTTC

```

1314

751 GCGCGCGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA  
 801 GGAATAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGG ATTTGGGTGG  
 851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA  
 901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT  
 951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG  
 1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC  
 1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG  
 1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

This corresponds to the amino acid sequence <SEQ ID 2786; ORF 917>:

m917.pep

1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE  
 51 TVADFEKNG IKVTYDVYDS DETLESKVLT GKSGYDIVAP SNAFVGRQIK  
 101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT  
 151 ERVKKALGTD KLPDNQWDLV FDPEYTSKLK QCGISYLD SA AEIYPMVLNY  
 201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF  
 251 GGDNLIAKRR AEEAGGKEKI RVMPKKEGVI IWVDSFVIPK DAKNVANAHK  
 301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN  
 351 SFIMVPIQPA ALKFMVRQWQ DVKAGK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae*:

m917/g917

m917.pep	10	20	30	40	50	60
	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKNG					
g917	MVKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKNG					
	10	20	30	40	50	60
m917.pep	70	80	90	100	110	120
	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
g917	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSMIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	130	140	150	160	170	180
	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLK					
g917	EMMRLMDGVDPDHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFNPEYTFKLK					
	130	140	150	160	170	180
m917.pep	190	200	210	220	230	240
	QCGISYLD SAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
g917	QCGISYLD SAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
	190	200	210	220	230	240
m917.pep	250	260	270	280	290	300
	RGDTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKKEGVIWVDSFVIPKDAKNVANAHK					
g917	RGDTCVTIGFGGDLNIAKRRAEEAGGKEKIRVMPKKEGVIWVDSFVIPKDAKNVANAHK					
	250	260	270	280	290	300
m917.pep	310	320	330	340	350	360
	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKN SFIMVPIQPA					
g917	YINDFLDPEVSAKNGNFVTYAPSSKPARDLMEDEFKNDNTIFPSGEDLKN SFIMVPIQPA					
	310	320	330	340	350	360

370

1315

m917.pep      ALKFMVRQWQDVKAGKX  
                 |||||  
g917            ALKFMVRQWQDVKAGKX  
                 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

a917.seq  
1    ATGACCAAAC ATCTGCCCCT GGCCGTCCTG ACTGCTTTGC TGCTTGCAGC  
51   GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCG CCGGCGGAAA  
101   ACCGAAACGT ATTGAAAAT TACAACTGGT CGGAATACGT CGATCCGGAA  
151   ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT  
201   GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAATCTG  
251   GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAG  
301   GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA  
351   CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG  
401   AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC  
451   GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCACTG  
501   GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA  
551   TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT  
601   TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC  
651   CGCCTTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG  
701   GCTTTATCGA TGATTTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC  
751   GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA  
801   GGAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG  
851   ATTCTTTCGT GATTCGAAA GATGCGAAA ACCTCGCCAA CGCGCACAAA  
901   TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT  
951   CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG  
1001   AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTGAAAAAC  
1051   AGCTTTATCA TGGTGCTTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG  
1101   CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

a917.pep  
1    MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE  
51   TVADFEKNG IKVTYDVYDS DETLESKVLTKSGYDIVAP SNAFVGRQIK  
101   AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT  
151   ERVKKALGTD KLPDNQWDLV FDPEYTSKLG QCGISYLD SA AEIYPMVLNY  
201   LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF  
251   GGDNLIAKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK  
301   YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN  
351   SFIMVPIQPA ALKFMVRQWQ DVKAGK\*

m917/a917      99.7% identity in 376 aa overlap

	10	20	30	40	50	60
m917.pep	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKNG					
a917	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENRNVLKIYNWSEYVDPETVADFEKNG					
	10	20	30	40	50	60
m917.pep	IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
a917	IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
a917	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
	130	140	150	160	170	180
m917.pep	QCGISYLD SA AEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					
a917	QCGISYLD SA AEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA					

1316

```

a917      QCGISYLDAAEIYPMVLNLYGKNPNSSNTEDIREATALLKKNRPNIKRTSSGFIDDLA
           190      200      210      220      230      240
m917.pep  250      260      270      280      290      300
           RGDTCVTIGFGGDLNIAKRRAEAEAGGKEKIRVMPKKEGVGIWVDSFVLPKDAKNVANAHK
           |||||
a917      RGDTCVTIGFGGDLNIAKRRAEAEAGGKEKIRVMPKKEGVGIWVDSFVLPKDAKNVANAHK
           250      260      270      280      290      300
m917.pep  310      320      330      340      350      360
           YINDFLDPEVSAKNGNFVTYAPSSKPAELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           |||||
a917      YINDFLDPEVSAKNGNFVTYAPSSKPAELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           310      320      330      340      350      360
m917.pep  370
           ALKFMVRQWQDVKAGKX
           |||||
a917      ALKFMVRQWQDVKAGKX
           370

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

```

g919.seq
1  ATGAAAAAAC ACCTGCTCCG CTCGCCCTG TACGGcatCG CCGCCgccAT
51  CctegCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCCG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATTT TGCCAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCGTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGC cgtGGCagg tgcaggcaAC GGAAGcCTTG
401 CaggtaaggT TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCTGCCG CTGCCTGCCG GTTTCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGAc ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACGCCCG ACCTCTCCCG ATTCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCgcgcTT GACGGCAAg cccCCATCCT CggttacgcC
751 GAagaccCG tcgaacttTT TTTCATGCAC AtccaaggCT CGGGCCGCTT
801 GAAACCCCG tcgggcaaat acatCCGCAt cggaTaccgc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctATA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcac aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCCGTCG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GCGGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

```

g919.pep
1  MKKHLRLSAL YGIAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
51  GTTVAGGGAV YTVVPHLSMP HWAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTERARFPIY GIPDDFISVP LPAGLRGGKN LVRIRQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGSRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAGS GNEGVPVGLG
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```



1	ATGAAAAAAT	ACCTATTCCG	CGCCGCCCTG	TACGGCATCG	CGCGCCGCAT
51	CCTCGCCGCC	TGCCAAAGCA	AGAGCATCCA	AACCTTTCCG	CAACCCGCAC
101	CATCCGTCAT	CAACGGCCCC	GACCGGCCGG	TCGGCATCCC	CGACCCCGCC
151	GGAAACGACG	TCGGCGGGCG	CGGGGCCGCT	TATACCGTTG	TACCGCACCT
201	CTCCCTGCCC	CACCTGGCGG	CGCAGGATTT	CGCCAAAAGC	CTGCAATCCT
251	TCCGCTCGG	CTGCGCCAAT	TTGAAAAAAC	GCCAAGGCTG	CGAGGATGTG
301	TGCGCCCAAG	CCTTTCAAAC	CCCCGTCCAT	TCCTTTCAGG	CAAAACAGTT
351	TTTTGAACGC	TATTTACAGC	CGTGGCAGGT	TGCAGGCAAC	GGAAGCCTTG
401	CCGGTACGGT	TACCGGCTAT	TACGAACCGG	TGCTGAAGGG	CGACGACAGG
451	CGGACGGCAC	AAGCCCGCTT	CCCGATTTAC	GGTATTCCCG	ACGATTTTAT
501	CTCCGTCCCC	CTGCCTGCCG	GTTTCCGGAG	CGGAAAAGCC	CTTGTCGGCA
551	TCAGGCAGAC	GGGAAAAAAC	AGCGGCACAA	TCGACAATAC	CGGCGGCACA
601	CATACGCGCG	ACCTCTCCcG	ATTCCCCATC	ACCGCGCGCA	CAACAGCAAT
651	CAAAGCGCAG	TTTGAAGGAA	GCCGCTTCTT	CCCTACCAC	ACGCGCAACC
701	AAATCAACGG	CGGCGCGCTT	GACGGCAAAG	CCCCGATACT	CGGTTACGCC
751	GAAAGCCCTG	TCGAACTTTT	TTTTATGCAC	ATCCAAGGCT	CGGGCCGTCT
801	GAAAACCCCG	TCCGGCAAAT	ACATCGCGAT	CGGCTATGCG	GACAAAAACG
851	AACATCCyTA	CGTTTCCATC	GGACGCTATA	TGGCGGATAA	GGGCTTACCT
901	AAACTCGGAC	AAACTCCCAT	GCAGGGCATT	AAGTCTTATA	TGCGGCAAAA
951	TCCGCAACGC	CTCGCCGAAG	TTTTGGGTCA	AAACCCGAGC	TATATCTTTT
1001	TCCCGGAGCT	TGCCGGAAGC	AGCAATGACG	GCCCTGTCCG	CGCATCTGGG
1051	ACGCCCGTGA	TGGGGGAATA	TGCGGGCGAT	GCATCCGGCT	ACTACATTAC
1101	CTTGGGTGCG	CCCTTATTTG	TCGCCACCGC	CCATCCGGTT	ACCCGCAAAG
1151	CCCTCAACCG	CCTGATTATG	GCGCAGGATA	CCGGCAGCGC	GATTAAAGGC
1201	GGGTTGCGCG	TGGATTATTT	TTGGGGATAC	GGCGACGAAG	CCGGCGAACT
1251	TCCGCGGCAA	CAGAAAACCA	CGGGATATGT	CTGGCAGCTC	CTACCCAACG
GTATGAAGCC CGAATACCGc CAGTAA					

This corresponds to the amino acid sequence <SEQ ID 2792; ORF 919>:

1	<u>MKKYLFR</u> AAAL	<u>YGIAAA</u> ILAA	CQSKSIQTFF	QPDTSVINGP	DRPVGIPDPA
51	GTTVGGGGAV	YTVVPHLSLP	HWAAQDFAKS	LQSFRLGCAN	LKNRQGWQDV
101	CAQAQFTPVH	SFQAQKFFER	YFTPWQVAGN	GSLAGTVTGY	YEPVLKGDDR
151	RTAARAFPIY	GIPDDFISVP	YFAGLRSGAK	LVRIRQTGKN	SGTIDNTGGT
201	HTADLSRFPI	TARTTAIKGR	FEGSRFLPHY	TRNRQINGAL	DGKAPILGYA
251	EDPVLEFFMH	IQQSGRLKTP	SGKYIRIGYA	DKNEHPYVSI	GRYMADKGYL
301	KLQGTSYMQI	KSYMRQNQPR	LAELVGQNPV	YTFPRELAGS	SNDGPPVGAIG
351	PTPLMGSEYAGA	VDRHVYITLGA	PLFVATAHPV	TRKALNRLIM	AQDTGSAIKG
401	AVRVDYFWGY	GDEAGELAGK	QKTTGYVVQL	LRNGMKPEYR	P*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF 919.ng) from *N. gonorrhoeae*:

m919/g919

	10	20	30	40	50	60
m919.pep	MKKYLFRAALYGIAAAAILAACQSKSIQTFFPQDTSVINGPDRPVGIPDPAGTTVGGGGAV					
	:   :   :					
g919	MKKHLLRSALYGIAAAAILAACQSRSIQTFPPQDTSVINGPDRPAGIDPDAGTTVAGGGAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWDVCAQAFQTPVHSFQAKQFFER					
	:					
g919	YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWDVCAQAFQTPVHSFQAKRFFER					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2793>:

```

a919.seq
1 ATGAAAAAAT ACCTATTCCG CGCGGCCCTG TCGGCATCG CCGCGCCAT
51 CCTCGCCGCG TGCCAAAGCA AGACGATCCA AACCTTTCGG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGCCCG TCGGCATCCC CGACCCGCGC
151 GGAACGACGG TCGGCGGCGG CGGGGCCGTT TATACCGTTG TCGCGCACTT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATT CGCCAAAAGC CTGCAATCCT
251 TCCGCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGGCGCCAA GCTTTCAAAC CCCGTCAT TCGTTCCAG CAAAACAGTT
351 TTTTGAACGC TATTTCACGC CGTGGCAGGT TGCAGGCAAG CCAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCGGATTAC GGTATTCGG ACGATTTTAT
501 CTCGCTCCCC CTGCTGCGG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCGC ACCTCTCCCA ATTCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA CCGCTTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGGTT GACGGCAAAG CCCGATACT CTTGTACGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGCTC
801 GAAAACCCCG TCCGGCAAT ACATCCGAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAAGCG CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGT AGCAATTGAC GCCCTGTCCG CGCATCTGGG
1051 ACGCGCGTGA TGGGCGAGTA GCGCGGCGCA CTGCACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAA

```

1319

1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC  
 1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GCGGACGAAG CCGGCGAACT  
 1251 TGCCGCGCAA CAGAAAACCA CCGGATATGT CTGGCAGCTT CTGCCCAACG  
 1301 GTATGAAGCC CGAATACCGC CCGTAA

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:

a919.pep

```

      1  MKKYLFRAL CGIAAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
    51  GTTVGGGGAV YTVVPHLSLP HWAQAQDFAKS LQSFRLGCAN LKNRQGWQDV
   101  CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
   151  RTAQAARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
   201  HTADLSQFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
   251  EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
   301  KLGQTSMQGI KAYMQQNPR LAEVLGQNPS YIFFRELTGS SNDGPVGALG
   351  TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
   401  AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

m919/a919  98.6% identity in 441 aa overlap
      10      20      30      40      50      60
m919.pep  MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
          |||
a919      MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
      10      20      30      40      50      60

      70      80      90     100     110     120
m919.pep  YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSQAKQFFER
          |||
a919      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSQAKQFFER
      70      80      90     100     110     120

      130     140     150     160     170     180
m919.pep  YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQAARFPIYGIPDDFISVPLPAGLRSGKA
          |||
a919      YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQAARFPIYGIPDDFISVPLPAGLRSGKA
      130     140     150     160     170     180

      190     200     210     220     230     240
m919.pep  LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGRFLPYHTRNQINGGAL
          |||
a919      LVRIRQTGKNSGTIDNTGGTHTADLSQFPI TARTTAIKGRFEGRFLPYHTRNQINGGAL
      190     200     210     220     230     240

      250     260     270     280     290     300
m919.pep  DGKAPILGYAEDPVELFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
          |||
a919      DGKAPILGYAEDPVELFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
      250     260     270     280     290     300

      310     320     330     340     350     360
m919.pep  KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
          |||
a919      KLGQTSMQGIKAYMQQNPRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
      310     320     330     340     350     360

      370     380     390     400     410     420
m919.pep  VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
          |||
a919      VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
      370     380     390     400     410     420

      430     440
m919.pep  QKTTGYVWQLLPNGMKPEYRPX
          |||
a919      QKTTGYVWQLLPNGMKPEYRPX
      430     440

```

Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al, 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
51  CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
101 ACCTCGTTAC CGCCGAATAT CAGCCTACTT TCCGGTCAAA AAACAAAGCA
151 GGCTGGAAAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
201 ACAAACCCGT ATGTTTCGGTA AAAACATTGT CAACGTGGGA CACGAAAGCG
251 CGGACACCGC CATCATCACC AAACCGGTCG GACAAAACCTT GGAAATCGTC
301 CCGCTGGACA ATCccgcgca caTTCACgtg ggctaacgCt tcaaaGTccg
351 cgttCtggtt cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtacAT
401 TTGacggctt cGAcaccagc gaccgcagca aaacgcacaa Aaccgaagcc
451 caagcctTCT ccgacaccac cgacggcgaa ggcgaagtgg acatcatCCC
501 CTTGcgccaa GGCTTttgga aAgcGAGTGT CGAATAcaaa gccgAttctc
551 CCGATcaaaG CCTGTGccga AAACAggcgA ACTACAcaac TTtaaccttc
601 caaatcgccc attctCacca tTaa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEKGK ENMIQRGTYN YQYRSNRPVK DGSYLVTAEY OPTFRSKNKA
51  GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAIIT KPVGQNLEIV
101 PLDNPAIHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
151 QAFSDTTDGE GEVDIPLRQ GFWKASVEYK ADFPDQSLCR KQANYTTTLTF
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCACGCCC CACCGmGTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAwACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCT
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAArCCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCCTGCC CAATGCCACC GTTACGCCA CCTTTGACGG CTTGACACC
601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CmCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCAAATCG GTCATTGCGA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLLSV SALFATSAAH HRVWVETAHT HGGEYLKADL GYGEPPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YOPTFFSKXK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPAIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
```

1321

201 SDRSKTHXXE AQAFSDSTDD KGEVDIIXLR QGFWKANVEH KTDFFDQSVK  
 251 QKQANYSTLT FQIGHSHH\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 920 shows 91.3% identity over a 207 aa overlap with a predicted ORF (ORF 920.ng)  
 from *N. gonorrhoeae*:

g920/m920

				10	20	30
g920 . pep				PMQLVTEKGKENMIQRGT	YNYQYRSNR	PVK
m920	GGEYLKADLGYGEFF	LEPIAKDRLHIFSK	PMQLVTEKGKENMIQRGT	YNYQYRSNR	PVK	
	40	50	60	70	80	90
g920 . pep	DGSYLVTA	EYQPTFRSK	NKAGWKQAGIK	EMPDASYCEQ	TRMFGKNIVNV	GHE
	40	50	60	70	80	90
m920	DGSYLVIAEYQPTF	WSKXKAGWKQAGIK	EMPDASYCEQTRMFGKNIVNV	GHE	SADTAII	T
	100	110	120	130	140	150
g920 . pep	KPVGQNLEIVPLDNP	ADIVHVGXRFKVRVL	FRGEPLPNATVTAT	FDGFDTS	SDRSKTHKTEA	
	100	110	120	130	140	150
m920	KPVGQNLEIVPLDNP	ADIVHVGXRFKVRVL	FRGEPLPNATVTAT	FDGFDTS	SDRSKTHXXEA	
	160	170	180	190	200	210
g920 . pep	QAFSDTTDGE	GEVDIIP	LQQGFWKASVEYKAD	FPDQSLCRKQANY	TTLTFQIAHSHHX	
	160	170	180	190	200	
m920	QAFSDSTDDKGEVDI	IIXLRQGFWKANVEH	KTDFFDQSVCKQKQAN	YSTLT	FQIGHSHHX	
	220	230	240	250	260	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2799>:

a920 . seq

```

1  TGAAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
51  CGCCACGCC CACCGCGTCT GGTTCGAAAC CGCCACACG CACGGCGCGC
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAACAAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGACAAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGCCAA TGTCGAACAC AAAGCCGACT TCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GCCATTGCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2800; ORF 920.a>:

a920 . pep

```

1  *KKTLLTLLAV SALFAASAHV HRVWVETAHT HGGEYLKADL GYGEFFLEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFFDQSVK
251 QKQANYSTLT FQIGHSHH*

```

m920/a920 97.0% identity in 267 aa overlap

1322

	10	20	30	40	50	60
m920.pep	MKKTLLLSVSALFATS	SAHAHRVWVETAHT	HGGEYLKADL	GYGEFPELEPI	AKDRLHIFS	
a920	XKKTLLTLLAVSALFA	ASAHHRVWVETAHT	HGGEYLKADL	GYGEFPELEPI	AKDRLHIFS	
	10	20	30	40	50	60
	70	80	90	100	110	120
m920.pep	KPMQLVTEKGKENMI	QRGTNYQYRSNR	PVKDGSYLVIAEY	QPTFWSKXKAGW	KQAGIKE	
a920	KPMQLVTEKGKENMI	QRGTNYQYRSNR	PVKDGSYLVIAEY	QPTFWSKNKAGW	KQAGIKQ	
	70	80	90	100	110	120
	130	140	150	160	170	180
m920.pep	MPDASYCEQTRMFGK	NIVNVGHESADTA	ITKPVGQNLEIV	PLDNPANIHVGER	FKVRVL	
a920	MPDASYCEQTRMFGK	NIVNVGHESADTA	ITKPVGQNLEIV	PLDNPANIHVGER	FKVRVL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m920.pep	FRGEPLPNATVTATF	DGFDTSDRSKTHX	EAQAFSDSTDDK	GEVDIIXLRQGF	WKANVEH	
a920	FRGEPLPNATVTATF	DGFDTSDRSKTHK	TEAQAFSDSTDDK	GEVDIIPLRQGF	WKANVEH	
	190	200	210	220	230	240
	250	260	269			
m920.pep	KTDFPDQSVQCQKQ	ANYSTLTFQIGH	SHHX			
a920	KADFPDQSVQCQKQ	ANYSTLTFQIGH	SHHX			
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2801>:

g920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCcggtt TcCGCACTAT TTGCCACATc
51  cgCaCACCCC CACCgCGTCT GGGTCGAAAC CgcccCACACg cAcgGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCTCCGA ACTCGAACCC
151 ATCGccAAAG ACCgctTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGT AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGCAGCAA CCGTCCCGTC AAAGACGGCA GCTACCTCGT TACCGCCGAA
301 TATCAGCCTA CTTCCCGGTC AAAAAACAAA GCAGGCTGGA AACAGGCTGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGTATGTTCC
401 GTAAAAACAT TGTCACCGTG GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAA CTTGGAAATC GTCCCCTGCG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCTA CATTGACGCG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCCCAAGCCT TCTCCGACAC
651 CACCGACGGC AAAGGCGAAG TGGACATCAT CCCCTTGGCG CAAGGCTTTT
701 GGAAAGCGAG TGTCGAATAC AAAGCCGATT TCCCCGATCA AAGCCTGTGC
751 CAAAAACAGG CGAACTACAC AACTTTAACC TTCCAAATCG GCCATTCTCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2802; ORF 920-1.ng>:

g920-1.pep

```

1  MKKTLLTLLAV SALFATSAP HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVTAE
101 YQPTFRSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAFSDTTDG KGEVDIIPLR QGFWKASVEY KADFPDQSLC
251 QKQANYTTLT FQIGHSHH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2803>:

m920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCACGCCC CACCgCGTCT GGGTCGAAAC CGCCACACG CACGCGGCGG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCTCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA

```

1323

```

301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCAAATCG GTCATTCGCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

```

m920-1.pep
1 MKKTLTLLAV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51 IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KTDFFDQSV
251 QKQANYSTLT FQIGHSHH*

m920-1/g920-1 96.3% identity in 268 aa overlap

          10      20      30      40      50      60
m920-1.pep MKKTLTLLAVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
          |||
g920-1      MKKTLTLLAVSALFATSAHPRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
          10      20      30      40      50      60

          70      80      90      100     110     120
m920-1.pep KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE
          |||
g920-1      KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFRSKNKAGWKQAGIKE
          70      80      90      100     110     120

          130     140     150     160     170     180
m920-1.pep MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL
          |||
g920-1      MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL
          130     140     150     160     170     180

          190     200     210     220     230     240
m920-1.pep FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
          |||
g920-1      FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDTTDGKGEVDIIPLRQGFWKASVEY
          190     200     210     220     230     240

          250     260     269
m920-1.pep KTDFFDQSVCKQKQANYSTLTFQIGHSHHX
          |::|
g920-1      KADFFDQSLCQKQANYTTLTFQIGHSHHX
          250     260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

```

a920.seq
1 TGAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
51 CGCCCACGCC CACCGCGTCT GGGTCGAAAC CGCCACACAG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAGGCG AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAACAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGGCCAA TGTCGAACAC AAAGCCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCAAATCG GCCATTCGCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

```

a920.pep
1  *KKTLTLLAV SALFAASAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLIVIAE
101 YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNL EI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFPDQSV
251 QKQANYSTLT FQIGHSHH*

m920-1/a920 98.9% identity in 267 aa overlap

      10      20      30      40      50      60
m920-1.pep MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
a920      XXXKTLTLLAVSALFAASAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
      10      20      30      40      50      60

      70      80      90      100     110     120
m920-1.pep KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLIVIAEYQPTFWSKNKAGWKQAGIKE
a920      KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLIVIAEYQPTFWSKNKAGWKQAGIKQ
      70      80      90      100     110     120

      130     140     150     160     170     180
m920-1.pep MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANIHVGERFKVRVL
a920      MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANIHVGERFKVRVL
      130     140     150     160     170     180

      190     200     210     220     230     240
m920-1.pep FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
a920      FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
      190     200     210     220     230     240

      250     260     269
m920-1.pep KTDFFPDQSVCKQKQANYSTLTTFQIGHSHHX
a920      KADFPDQSVCKQKQANYSTLTTFQIGHSHHX
      250     260

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

```

g921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG
51  Ccagtctatt tatGtgccca cattgacgga aatccccgTg aatcccatca
101 ataCCgtcaa aacggaagCA CCTGCAAAAG GTTTTCGCCT CGCCCCCTTCG
151 CATTGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA
251 ACAACTTCAG AAAACGCCTG GTCGACGCA ATGCCGTCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GGCGGTAGAC AGCCAGCGCG GCGAAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTtggAA AAATATGGAT GCCAAACCCG ATAATCCCGC ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

```

g921.pep
1  MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLAPS
51  HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101 YEIYLRSAVD SQRGEINTEQ SKLYIENALR GWQQRWKNMD AKPDNPAFTN
151 FLMEVMMQMP LK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

```

m921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG
51  CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCCGCCT TGCCTCTTCG
151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA

```



m921.pep

1 MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLESS  
51 HWTDAKISD EATRLGYQVG IGMKTKVQAA QYLNNFRKRL VGRNAVDDSM  
101 YEIYLRSAMD SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN  
151 FLMEVMMQMP LK\*

### Homology with a predicted ORF from *N. gonorrhoeae*

m921/g921

	10	20	30	40	50	60
m921.pep	MKKYL	IPLSIA	AAVL	SGCQ	SIYV	PTLTEIPVNPINTVKTEAPAKGFR
g921	MKKYL	IPLSIA	AAVL	SGCQ	SIYV	PTLTEIPVNPINTVKTEAPAKGFR
	10	20	30	40	50	60
	70	80	90	100	110	120
m921.pep	EATRL	GYQVG	IGKMT	KTQV	AAQYL	NNFRKRLVGRNAVDDSMYEIYLRSAID
g921	EATRL	GYQVG	IGKMT	KTQV	AAQYL	NNFRKRLVGRNAVDDSMYEIYLRSAV
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYI	QNALR	GWQQR	WKNN	MDVKP	NNPAFTNFLMEVMMKMQLPKX
g921	SKLYI	ENALR	GWQQR	WKNN	MDAKP	DNPAFTNFLMEVMMKMQLPKX
	130	140	150	160		

a921.seq

1	ATGAAAAAAT	ACCTTATCCC	TCTTTCATT	GTGGCAGTTC	TTTCCGGCTG
51	CCAGTCTATT	TATGTGCCCA	CATTGACGGA	AATCCCCGTG	AATCCTATCA
101	ATACCCGTCAA	AACGGGAAGCA	CCTGCAAAAG	GTTTCCGCCT	TGCTCTTCG
151	CATTGGACGG	ATGTGTCCAA	ATGACGCAT	GAAGCGACGC	GCTTGGGCTA
201	TCAGTGGGGT	ATCGGTAAAA	TGACCAAGT	TCAGGCGCGC	CAATATCTGA
251	ACAACTTCAG	AAAACGCTG	GTCGGACGCA	ATGCCGTGCA	TGACAGTATG
301	TATGAAATCT	ACCTGCGTTC	GGCGATAGAC	AGCCAGCGGG	GCGCAATCAA
351	TACGGAACAG	TCCAAGCTGT	ATATCCAGAA	TGCCTTCGCG	GGCTGGGCAG
401	AGCGTTGGAA	AAATATGGAT	GTCAAACCCA	ACAACCCCGC	ATTTACCAAC
451	TTTTTGATGG	AAGTGATGAA	GATGCAGCCC	TGAAATGA	

a921.pap

```

1  MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRCLASS
51 HWTDVAKISD EATRLGYQVG IGMKTKVQAA QYLNNFRKRL VGRNAVDDSM
101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
151 FLMEVMKMOP LK*

```

m921/a921 99.4% identity in 162 aa overlap

```

      10      20      30      40      50      60
m921.pép  MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLLASSHWTDVAKISD
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a921      MKKYLIPLSIVAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLLASSHWTDVAKISD
          10      20      30      40      50      60

```

1326

	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
a921	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922.seq

```

1  ATGGAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCGTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAC CGGTATCCGA CAGCGGTTT GCCGCCAATG CAAATGTCCG
201 CCGTTTGTG GACGATGAAG TCGGGAAGG GGATTTTCC CAGGCGAAT
251 GGCAGGATT TTTGACAAA GCGGCTTACA AGGCGGACAT CGTCAAGATt
301 ATGCACCGAC CCTCCACATC GCGtCCGTGG TATGtgttcc gCacggGAAa
351 ttcGGgcagg gcgaaAtttc ACggcgCGCG Caggttttat GcggaaAacc
401 gcgcggttat cgatgatgtg gcgCAAAa acggcgtGCC TGCCGAGCTT
451 ATCGTGGCGA TTATCGGGAT TGAAACGAAT TACGGCAAAA ATACGGGCAG
501 TTTCCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
551 GCGCCGGGTT TTTCCAAAA GAATTGTCG AGCTTTTAAA GCTGGCAAAA
601 GAAGAAGGCG GTGATGTTTT CGCCTTTAAG GGCagcTATG CGGGTGCAAT
651 GGGTATGCCG CAATTTATGC CTTCGAGCTA CCGGAAATGG GCGGTGGATT
701 ATGAcgggga cggacatCGG GATATAtggg GCAACGTcgg tgatgtcgcg
751 gcatcggTTG CCAATTat at gaagCAGCAC GGTTGGCGCA Cgggcggtaa
801 AATGTTGGTG TCGGCGAcgt tggcgccggg tgcggATGTT CaggcaATCA
851 TTGGCGAAAA AACCGCCCTG ACGCGACGG TGGCGGATT GAaggCGTAc
901 ggcacatcc ccgggaaac GCTCGCAGAT GATGAAAag cgGTTTTGTT
951 CAACTGGAA ACCGCACCCG GCGTGTGGA ATATTATTG GGCTTGAACA
1001 ATTTTATAC GGTATGGCAG TACAACCACA GCCGATGTA TGTAAcGgcg
1051 gtcaggGACA TTGCAATTC GTCGCGCGC CCGGATTGT Aa

```

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922.pep

```

1  MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KESRPAFDA
51  AAVPVSDSGF AANANVRRFV DDEVKGDFS QAEWQDFDK AAYKADIVKI
101 MHRPSTSRPW YVFRGTNSGR AKFHGARRFY AENRAVIDDV AQKYGVPAEL
151 IVAIIGIETN YGKNTGSFRV ADALATLGFY YPRRAGFFQK ELVELLKLAK
201 EEGDVFAFK GSYAGAMGMP QFMPSSYRKY AVDYDGDGHR DIWGNVGDVA
251 ASVANYMKQH GWRGTGKMLV SATLAPGADV QAIIGETAL TRTVADLKAY
301 GIIPGETLAD DEKAVLFKLE TAPGVFEYIL GLNNFYTVWQ YNHSRMYVTA
351 VRDIANSLGG PGL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922.seq

```

1  ATGAAAAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCGTGTACG GCGATGGAGG CACGCCACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGTTGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTCCCG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACCGCCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGGAATTT CCGGCAAGGC GAAATTTCGC GCGCGCGCC
401 GGTTTTATGC GGAAAACCGC GCGTTATCG ATGATGTGGC GCAAAATAC
451 GCGGTGCTG CCGAACTTAT CGTGGCGTT ATCGGATTG AAACGAATTA
501 CCGCAAAAT ACGGGCAGTT TCCGTGTGGC GGACGATTG GCGACCTTAG
551 GCTTTGATTA CCCCCCGCGC GCCGGTTTT TCAAAAAGA ATTGGTCGAG

```

```

601 CTTTAAAGC TGGCAAAAGA AGAAGGCGGC GATGTTTTTCG CCTTTAAAGG
651 CAGCTATGCG GCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AACGTCGGCG ATGTCGCGGC ATCGTTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGGAAAA TGCTGGTGTC TGCAACATTG GCGCCGGGTG
851 CGGATGTTCA GGCAATCATT GGCGAAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTGTA AGGCGTACGG CATCATCCCC GGCGAAGAGC TTGCAGATGA
951 TGAAAAGGCG GTTTTGTTC AACTGGAAAC CGCACCGGGC GTGTTTGAAT
1001 ATTATTTGGG CTGAACAAT TTTTATACGG TATGGCAGTA CAACCACAGC
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCCC
1101 GGGATTGTAA

```

-- This corresponds to the amino acid sequence <SEQ ID 2816; ORF 922>:

m922.pep

```

1 MKKRKILPLA ICLAALSACT AMEARPPRAN EAQAPRAVEM KESRPAFDA
51 AAVFDAAAVP VSDSGFAANA NVRRFVDEV GKGDfsraew QDFFDKAAyK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPaelivav IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKKEEG DVFAFKGSYA GAMGMPQFMP SsyRKWAVDY DGDGHRDIWG
251 NVGDVAASVA NYMKQHGWR TGGKMLVSATL APGADVQAI IGEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYYLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 922 shows 95.9% identity over a 369 aa overlap with a predicted ORF (ORF 922.ng) from *N. gonorrhoeae*:

m922/g922

m922.pep	10	20	30	40	50	60
	MKKRKILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKESRPAFDAAAVFDAAAVP					
g922	MEKRKILPLAICLAALSACTAMEARTPRANEQAQAPRADEMKESRPAFDAA-----AVP					
	10	20	30	40	50	
m922.pep	70	80	90	100	110	120
	VSDSGFAANANVRRFVDEVGKGDfsraewQDFFDKAAyKADIVKIMHRPSTSRPWYVFR					
g922	VSDSGFAANANVRRFVDEVGKGDfsQAEWQDFFDKAAyKADIVKIMHRPSTSRPWYVFR					
	60	70	80	90	100	110
m922.pep	130	140	150	160	170	180
	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
g922	TGNSGRAKFGHARRFYAENRAVIDDVAQKYGVPaelivaiIGIETNYGKNTGSFRVADAL					
	120	130	140	150	160	170
m922.pep	190	200	210	220	230	240
	ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSyRKWAVDY					
g922	ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSyRKWAVDY					
	180	190	200	210	220	230
m922.pep	250	260	270	280	290	300
	DGDGHRDIWGNVGDVAASVANyMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV					
g922	DGDGHRDIWGNVGDVAASVANyMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV					
	240	250	260	270	280	290
m922.pep	310	320	330	340	350	360
	ADLKAYGIIPGEELADDEKAVLfkLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI					
g922	ADLKAYGIIPGETLADDEKAVLfkLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI					

1328

	300	310	320	330	340	350
		370				
m922.pep	ANSLGGPGLX					
g922	ANSLGGPGLX					
	360					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2817>:

```

a922.seq
1  ATGAAAAACA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCCGCC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCCGC GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTCCCG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACGCCCCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGGAATTT CCGGCAAGGC GAAATTTTCG GCGCGCGGCC
401 GGTTTTATGC GGAAACCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GGCCTGCCTG CCGAATTAT CGTGGCGGTT ATCGGGATG AAACGAATTA
501 CGGCAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCGCCG CCGGGTTT TCCAAAAGA ATTGGTCGAG
601 CTTTAAAGC TGCAAAAGA AGAAGCGGC GATGTTTTCG CCTTTAAGG
651 CAGCTATGCG GCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AATGTTGGCG ATGTCGCGGC ATCGATTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGGAAA TACTGGTGTC TGCAACATTG GCGCCGGGTG
851 CGGATGTTCG GGCAATCATT GCGGAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTGTA AGCGTACGG CATCATCCCC GGCGAAGAGC TTGCCGATGA
951 TGAAAAGGCG GTTTGTTC AACTGGAAC CGCACCCGGC GTGTTTGAAT
1001 ATTATTTGGG CTGAAACAAT TTTATACGG TATGGCAGTA CAATCACAGT
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2818; ORF 922.a>:

```

a922.pep
1  MKNRKILPLA ICLAALSACT AMEARPPRAN EAQAPRADEM KESRPAFDA
51  AAVFDAAAVP VSDSGFAANA NVRRFVDDEV GKGDfsraew QDFFDKAAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPaelivav IGIETNYGKN TGSFRVADAL ATLGFDPYPR AGFFQKELVE
201 LLKLAKKEGG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASIA NYMKQHGWRT GKKILVSATL APGADVQAI GEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYLLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

m922/a922 98.9% identity in 369 aa overlap

	10	20	30	40	50	60
m922.pep	MKKRKILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKESRPAFDAAAVFDAAAVP					
a922	MKNRKILPLAICLAALSACTAMEARPPRANEQAQAPRADEMKKESRPAFDAAAVFDAAAVP					
	10	20	30	40	50	60
m922.pep	VSDSGFAANANVRRFVDDEVGKGDfsraewQDFFDKAAAYKADIVKIMHRPSTSRPWYVFR					
a922	VSDSGFAANANVRRFVDDEVGKGDfsraewQDFFDKAAAYKADIVKIMHRPSTSRPWYVFR					
	70	80	90	100	110	120
m922.pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
a922	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
	130	140	150	160	170	180
m922.pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
a922	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
	190	200	210	220	230	240

1329

```

m922.pep  ATLGFDYPRRAGFFQKELVELLLKAKEEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
a922      ATLGFDYPRRAGFFQKELVELLLKAKEEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          190      200      210      220      230      240

          250      260      270      280      290      300
m922.pep  DGDGHRDIWGNVGDVAASVANYMKQHGWRTGGKMLVSATLAPGADVQAIIGEXTALTRTV
a922      DGDGHRDIWGNVGDVAASIANYMKQHGWRTGGKILVSATLAPGADVQAIIGEXTALTRTV
          250      260      270      280      290      300

          310      320      330      340      350      360
m922.pep  ADLKAYGIIPGEELADDEKAVLEKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
a922      ADLKAYGIIPGEELADDEKAVLEKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          310      320      330      340      350      360

          370
m922.pep  ANSLGGPGLX
a922      ANSLGGPGLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTTCTGTC
51  CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAAACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTTGTTCCG
201 CGGTGGACG GCGCATACT TGGGTAGTAG GATGTTTCCG CATAAAACCG
251 CGAAAAAGCG TTTTGTGTG CTGTTCCGTC TGAAGTTTC GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTTT GTTCCGCCG AACTTTTTGT
351 AAAACTCGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1  MKRQAFFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRRAVR
51  GKRRIPRHRL LLPALFGGWT GAYLGSRMFR HKTAKKRFV LFRLLTVSGNV
101 LATCILIDYF VPPELFVKLG QHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCTGTC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GCGCGGTATT TCGGCAGCAT GACATTCAAA CATAAGACAG
251 CGAAAAAGCG TTTTGTGTG CTGTTCCGTC TGAAGTTTC AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCCTG CCTTGCCGTA CTATTGTGAC TGTCTGCGG TTCGTCGCCT
401 TGTCTGATT TTGTTAATC CACTATAT.T ATTTGTGCC GCCTGAATTT
451 TTCGTAAAAC TCGGCAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRCRIR
51  GORRIPEHRL LLPALLGGWV GAYFGSMTFK HKTAKKRFV LFRLLTVSGNV
101 LATLILYSG LNLNQYGVAS PCRTICTVCG FVALS*FLLI HYXYFVPPF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

1330

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng)  
from *N. gonorrhoeae*:

g923/m923

	10	20	30	40	50	60
g923.pep	MKRQAFFKPMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL					
m923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCAIRGQRRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100		
g923.pep	LLPALFGGWTGAYLGSRMFRHKTAKKRFVVLFRLLTVSGNVLATCILID-----					
m923	LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
			110	120		
g923.pep	-----YFVPPPELFFVKLGQHLX					
m923	PCRTICTVCGFVALSXFLLIHYIYFVPPPEFFVKLGQNTX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

a923.seq

1	ATGAAGCGGC	AGGCTTTCTT	CAAACATGATG	GCGTGTGCGG	CATTTCTGTC
51	TGCCGTTTCG	CTGCGCCTCC	CCGTATTGGG	CGCGTGTAC	GCAATATTGT
101	CCCTCTATGC	GTTTGCACTT	TACGGCATCG	ACAAACGGCG	TGCCGTGCGG
151	GGAAAACGCC	GCATTCCCGA	ACACCGCCTG	CTGCTGCCTG	CCTTGTTCCG
201	CGGTTGGGCG	GGCGCATACT	TGGGCAGCAG	GATATTCAGG	CATAAAACGG
251	CGAAAAGCG	TTTTGTTGTG	CTGTTCCGTC	TGACTGTTTC	GGGCAATGTC
301	CTGGCGACCC	TCATCCTGAT	TTATAGTGGA	TTAAATTTAA	ACCAGTACGG
351	CGTTGCCTCG	CCTTA.GCTC	AAAGAGAACG	ATTCTCTAAG	GTGCTGAAGC
401	ACCAAGTGAA	TCGGTCCCGT	ACTATTTGTA	CTGCTGCGG	CTTCGTCGCC
451	TTGTCCTGAT	TTTTGTAAAT	CCACTAT.AT	TATTTTGTC	CGCCTGAATT
501	TTTCGTAAAA	CTCGGCAG	ATACCTGA		

This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>:

a923.pep

1	MKRQAFFKLM	ACAAFLSAVS	LRLPVLGACY	AILSLEYAFAL	YGIDKRRRAVR
51	GKRRIPEHRL	LLPALFGGWA	GAYLGSRIFR	HKTAKKRFV	LFRLTVSGNV
101	LATLILIIYS	LNLNQYGVAS	PXAQRERFSK	VLKHQVNRFR	TICTVCGFVA
151	LS*FLLIHYX	YFVPPPEFFVK	LGQNT*		

m923/a923 84.6% identity in 175 aa overlap

	10	20	30	40	50	60
m923.pep	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCAIRGQRRRIPEHRL					
a923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m923.pep	LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS					
a923	LLPALFGGAGAYLGSRIFRHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
			130	140	150	159
m923.pep	PC-----RTICTVCGFVALSXFLLIHYXYFVPPPEFFVKLGQNTX					
a923	PXAQRERFSKVLKHQVNRFRRTICTVCGFVALSXFLLIHYXYFVPPPEFFVKLGQNTX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

g925.seq

```

1  ATGAAACAAA TGCTTTTGGC cgtcggcgtg ggcgcggtgt TGGCGGGCTG
51  CGGCAaggat gcCGGCGGtt acgaggggtTA TTGGCGCGAA AAGTCGGACA
101 AAAAagaggG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTCCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCCTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

g925.pep

```

1  MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
51  KINVFTGKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKCKGQTA QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNKGPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

m925.seq (partial)

```

1  ATGAAACAAA TGCTTTTAGC CGTCGCGGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAG AAAAAGGCAA TTACTTCCTT
.....

```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

m925.pep (partial)

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFL				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKNINVFTGKE				
	10	20	30	40	50
g925	ESLLLSEKDGA LSINTGIGEIPIKLSDDGKELYVERRRYVKTDAAAMKDKIIAHQKCKGQT				
	60	70	80	90	100 110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

g925-1.seq

```

1  ATGAAACAAA TGCTTTTGGC CGTCGCGGTG GCGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTCCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

1332

```

1  MKQMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
51  KINVFTGKEE SLLLSEKDG LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQT QAYLDARNAL PSNQTYYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

```

m925-1.seq
1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAAGAGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT
151 AATAAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTTGTCTGA
201 AAAAGACGGC GCGCTTTTCA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTGCCGTCAG
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAG
501 AAGCCCGGCA TTGTTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

```

m925-1.pep..
1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL
51  NKIHVVTKGE ESLLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
101 KTDAAAMDKI IAHQKKCGQT AQAYRDARNA LPSNQTYYQH LAAIEQLKRR
151 FEAEFDELEK EIKCNRSPPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKHVVTKGE					
	10	20	30	40	50	
g925-1	MKQMLLAVGVAAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKHVVTKGE					
	70	80	90	100	110	120
m925-1.pep	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQT					
	60	70	80	90	100	110
g925-1	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKKCGQT					
	130	140	150	160	170	
m925-1.pep	AQAYRDARNALPSNQTYYQHLAAIEQLKRRFEAEFDELEKEIKCNRSPPALLX					
	120	130	140	150	160	170
g925-1	AQAYLDARNALPSNQTYYQQRQAIEQLKRRFEAEFDELEKEIKCNK-PTLLFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

```

a925-1.seq
1  AATAAAATCA ACGTGTTCAC AGGTAAGGAA GAATCTATGC TTTTGTCTGA
51  AAAAGACGGC GCGCTTTTCA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCCGTCAG
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAG
351 ACCGACATTG TTGTTTTCAG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

```

a925-1.pep
1  NKINVFTGKE ESLLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
51  KTDAAAMDKI IAHQKKCGQT AQAYLDARNA LPSNQTYYQH QAAIEQLKRR
101 FEAEFDELEK EIKCNKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

	10	20	30
a925-1.pep	NKINVFTGKEESMLLSEKDGALSINTGIGE		
	30	40	50
m925-1	AGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKHVVTKGEESMLLSEKDGALSINTGIGE		
	40	50	60
	60	70	80
	80	90	



1333

```

a925-1.pep  IPIKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQTAQAYLDARNALPSNQTYQQH
|||||
m925-1      IPIKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQTAQAYRDARNALPSNQTYQQH
          90      100      110      120      130      140

          100      110      120
a925-1.pep  QAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX
|||||
m925-1      LAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX
          150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2835>:

```

g926.seq (partial)
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCGGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAGGT
151 TCGTATGCAA ATTTGATTG GACATACCAA CCGCCGTGG AAACCATCAA
201 TATCAACACC CTTTGGGCA GTACGCTCGG ACAGTTGTGT CAAGacAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGCTCTATCA GGCAGAGGGT
301 ACGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAAGTGC CAATCCAATA
351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GCGGGGCGCG CCTtaccGCA
401 TCCGTTTACA CGGCATATTG GAACAATAcg GttggACAAT cgggCagaac
451 tgccGACAGT GGGGGGCaag tccgaacgtt gcaactGAa...

```

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

```

g926.pep (partial)
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGTWIGQN
151 CRQWGASPNV ATE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

```

m926.seq
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCAGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAGGT
151 TCGTATGCAA ATTTGATTG GACATACCAA CCGCCGTGG AAACCATCAA
201 TATCAATACC CTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGCTCTATCA GGCAGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAAGTGC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCGTGT GCGGGGCGCG CCTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CCGCAGAAAC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTC ACGAAATCGG TATGCCGTCT GAAACCGAAA
551 CCGCGGAACG CTGTGCGGCG CGCAGGAGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

```

m926.pep
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 AEELSRQLVG FKLPIQYLHI WADGRRVAGA PYRILPDGIL EQYGTWVGRT
151 ADSGQVRTL QLNNGNLNR LVFTEIGMPS ETETPERCAA RTR*

```

g926/m926 91.6% identity in 155 aa overlap

```

          10      20      30      40      50      60
g926.pep  MKHTVSASVILLTACAQLPQNNENLWQPSSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
|||||
m926      MKHTVSASVILLTACAQLPQNNENLWQPSSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
          10      20      30      40      50      60

          70      80      90      100     110     120
g926.pep  PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEGETEDLSRQLVGFKLPIQYLHI
|||||
m926      PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAELSRQLVGFKLPIQYLHI
          70      80      90      100     110     120

          130     140     150     160
g926.pep  WAEGRRVAGAPYRIRSDGILEQYGTWIGQNCRQWGASPNVATE

```

1334

|||||  
m926 WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS  
130 140 150 160 170 180

## a926.seq

```

1 ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51 GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACACCC
101 GCAGTTTCAC GGCGGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAGGT
151 TCGTATGCAA ATTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCGGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAAGTGC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCCTGT GGCGGGCGCG CTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAACC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTCA CCGAGATTGG TATGCCGTCT GAAACCGAAA
551 CCCAAGAACA ATGCGCGGCA CGCATACAGT AA

```

## a926.pep

```

1 MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTAEG RLAVKAEGKG
51 SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES
101 AEELSRQLVG FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT
151 ADSGGQVRTL QLNNGNLNIR LVFTEIGMPS ETETQECAA RIQ*

```

m926/a926 96.9% identity in 191 aa overlap

m926.pep	10	20	30	40	50	60
	MKHTVSASVILLTACAQLPQNNENLWQPS	EHSSFAEGR	RLAVKAEGKGS	SYANFDWTYQ		
a926	10	20	30	40	50	60
	MKHTVSASVILLTACAQLPQNNENLWQPS	EHTRSFTAEG	RLAVKAEGKGS	SYANFDWTYQ		
m926.pep	70	80	90	100	110	120
	PPVETININTPLGSTLGQLCQDRDGALAVD	GKGNVYQAES	AEELSRQLVG	FKLPIQYLHI		
a926	70	80	90	100	110	120
	PPVETININTPLGSTLGQLCQDRDGALAVD	GKGNVYQAES	AEELSRQLVG	FKLPIQYLHI		
m926.pep	130	140	150	160	170	180
	WADGRRVAGAPYRILPDGILEQYGWTVGRT	ADSGGQVRTLQLNNGNLNIR	LVFTEIGMPS			
a926	130	140	150	160	170	180
	WADGRPVAGAPYRILPDGILEQYGWTVGRT	ADSGGQVRTLQLNNGNLNIR	LVFTEIGMPS			
m926.pep	190					
	ETETPERCAARTRX					
a926	190					
	ETETQEQAARIQX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>:

```

g927.seq
1 atgaaaacct acGCACAggC ACTCTATacc GCAGCCCTGC TCACCGCCTG
51 CAGCCCcgca GCcgatTcaa accaTCCGTC CGGAcAaAAT GCCCCGGCCA
101 ATACCGAATC cgacGgaaAA AACATtaccC TGctcaatgc cTcgtacgat
151 gtGACACGGT ATTTttacaa agaatacgac cacTtgtttg tcggaacATA
201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAA TCCCACGGCG
251 GCTTCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCTTC CGACATCGAC CTGCTCGAAA AAAA.GGACT
351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGATCACGCC GCACCCTACA

```

1335

```

401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCcaa ACAGAtccgC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAAGAC
501 CTCGGGCAAC GGACGCTACG CCTTCCTCGG CGCATAACGGT TACGGTCTGA
551 AAGCCAACAA CGGcaaCGAG CAGGAAGCCC AAAAACTCGT CGCATCCATC
601 CTCAAAAACA CACCCGTTTT TGAAAACGGC GGACGCGc.C CGCCGCCACC
651 ACCTTCACAC AACGCAACAT CGGCGACGTA CTCATCACTT TTGAAAACga
701 agCcaactac gtCAGCAAAA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2840; ORF 927.ng>:

g927.pep

```

1 MKTYAQALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51 VTRYFYKEYD HLFVGTQSE HPGTSVSIQQ SHGGFSKQAL SVANGLQADV
101 VTMNQSSDID LLEKXGLVEK GWQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIAKTSN GRYAFLGAY YGLKANNGNE QEAQKLVASI
201 LKNTPVFENG GRXPPPPSH NATSATYSSL LKTKPTTSAK N*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2841>:

m927.seq

```

1 ATGAAACCT ACGCACCGGC ACTCTATACC GCAGCCCTGC TCACCGCCTG
51 CAGCCCCGCA GCCGATTCAA ACCATCCGTC CGGACAAAAT GCCCCGGCCA
101 ATACCGAATC CGACGAAAA AACATTACCC TGCTCAACGC CTCATACGAT
151 GTGGCAGGGG ATTTTACAA AGAATAACA CCCTTATTTA TCAAAACATA
201 CCAATCCGAA CACCCGGCA CATCCGTCAG CATCCAACAG TCCCACGGCG
251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
301 GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT
351 GGTAAGAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA
401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCCAA ACAGATCCGC
451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAATCC
501 CAAACCTCG GGCAACGGAC GCTACGCCTT CCTCGGCGCA TACGTTACG
551 TCTGAAAC CACCAACGGC AACGAACAGG AAGCCCAAAA ACTCGTCGCA
601 TCATCCTCA AAAACACCCC CGTTTTGAA AACGGCGGAC GCKcGCCACC
651 ACCACCTTCA CACAACGCAA CATCGGCGAC GTACTCATCA CTTTGAAAA
701 CGAAGCCAAC TACGTCAGCt AAAAActGA

```

This corresponds to the amino acid sequence <SEQ ID 2842; ORF 927>:

m927.pep

```

1 MKTYAPALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51 VARDFYKEYN PLFIKTYQSE HPGTSVSIQQ SHGGSSKQAL SVANGLQADV
101 VTMNQSSDID LLEKKGLVEK GWQALPDHA APYTSTMVFL VRKNNPKQIR
151 DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYGLKTNG NEQEAQKLVA
201 SILKNTPVFE NGGRXPPPPS HNATSATYSS LLKTKPTTSA KN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng) from *N. gonorrhoeae*:

g927/m927

	10	20	30	40	50	60
g927.pep	MKTYAQALYTAALLTACSPAADSNDHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYD					
m927	MKTYAPALYTAALLTACSPAADSNDHPSGQNAPANTESDGKNITLLNASYDVVARDFYKEYN					
	10	20	30	40	50	60
g927.pep	HLFVGTQSEHPGTSVSIQQSHGGFSKQALSVANGLQADVVTMNQSSDIDLEKXGLVEK					
m927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLEKKGLVEK					
	70	80	90	100	110	120
g927.pep	GWQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSNGRYAFLGA					
m927	GWQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSNGRYAFLGA					
	130	140	150	160	170	180

1336

```

      180      190      200      210      220      230
g927.pep  YGYGLKANNGNEQEAQKLVASILKNTPVFENGGRXPPPPSHNATSATYSSLLKTKPTTS
          |||||:|||||||
m927      YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPP-SHNATSATYSSLLKTKPTTS
          190      200      210      220      230

      240
g927.pep  AKNX
          ||||
m927      AKNX
          240

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2843>:

```

a927.seq
1  ATGAAAACCT  ACGCACCAGG  ACTCTATACC  GCAGCCCTGC  TCAGCGCCTG
51  CAGCCCCGCA  GCCGATTCAA  ACCATCCGTC  CGGACAAAAT  GCCCCGGCCA
101 ATACCGAATC  CGACGGAAAA  AACATTACCC  TGCTCAACGC  CTCATACGAT
151 GTGGCACGGG  ATTTTACAA  AGAATACAAC  CCCTTATTTA  TCAAAACATA
201 CCAATCCGAA  CACCCCGGCA  CATCCGTGAG  CATCCAACAG  TCCCACGGCG
251 GCTCCAGCAA  ACAGGCATTA  TCCGTAGCCA  ACGGCCTTCA  AGCCGATGTC
301 GTAACCATGA  ACCAATCCTC  CGACATCGAC  CTGCTCGAAA  AAAAAGGACT
351 GGTAGAAAAA  GGCTGGCAAC  AAGCCCTCCC  CGACCACGCC  GCGCCCTACA
401 CCAGCACTAT  GGTTCCTT  GTCCGAAAAA  ACAACCCCAA  ACAGATCCGC
451 GATTGGAACG  ACCTTGCCAA  AGACGGCGTT  AACATCGTCA  TCGCCAATCC
501 CAAAACCTCG  GGCAACGGAC  GCTACGCCTT  CCTCGGCGCA  TACGGTTACG
551 GTCTGAAAC  CACCAACGGC  AACGAACAGG  AAGCCCAAAA  ACTCGTCGCA
601 TCCATCCTCA  AAAACACCCC  CGTTTTTGAA  AACGGCGGAC  GCGCGCCACC
651 ACCACCTTCA  CACAACGCAA  CATCGGCGAC  GTACTCATCA  CTTTTGAAAA
701 CGAAGCCAAC  TACGTCAGCA  AAAAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2844; ORF 927.a>:

```

a927.pep
1  MKTYAPALYT  AALLSACSPA  ADSNHPSGQN  APANTESDGK  NITLLNASYD
51  VARDFYKEYN  PLFIKTYQSE  HPGTSVSIQQ  SHGGSSKQAL  SVANGLQADV
101 VTMNQSSDID  LLEKKGLVEK  GWQQALPDHA  APYTSTMVFL  VRKNNPKQIR
151 DWNDLAKDGV  NIVIANPKTS  GNGRYAFLGA  YGYGLKTTNG  NEQEAQKLVA
201 SILKNTPVFE  NGGRAPPPPS  HNATSATYSS  LLKTKPTTSA  KN*

```

m927/a927 99.2% identity in 242 aa overlap

```

      10      20      30      40      50      60
m927.pep  MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          |||||:|||||||
a927      MKTYAPALYTAALLSACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          10      20      30      40      50      60

      70      80      90      100     110     120
m927.pep  PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLEKKGLVEK
          |||||:|||||||
a927      PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLEKKGLVEK
          70      80      90      100     110     120

      130     140     150     160     170     180
m927.pep  GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          |||||:|||||||
a927      GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          130     140     150     160     170     180

      190     200     210     220     230     240
m927.pep  YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPPSHNATSATYSSLLKTKPTTSA
          |||||:|||||||
a927      YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA
          190     200     210     220     230     240

```

m927.pep      KNX  
                  |||  
 a927            KNX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq  
 1 ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG  
 51 CGCCCTGGTT TTGGCACTGC CCGTACCcga CGGGGTCAAG CCTCAGGCTT  
 101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCCCAT TATCGGCAAG  
 151 GTTATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT  
 201 AACC GGCGTA ACCGCCGACA AACC GGCGC GGCATGAGC GATGCGTTGA  
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT  
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT  
 351 TATCGCCGTT TTTGGAAGAA AAAcgctggg CATCGTTAC AGTCTCGCTC  
 401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC  
 451 GCGGCGATTA TACATCcgat TATGCagtcg attgCcgCA GttacggctC  
 501 caatCCCGCA AAAGGCACag aaggcaagat gggtaAATAT TtggcTTtgg  
 551 tcaattaTCA TTCcaatCCC atttcgtcgg ctAtggctat taCTGcaact  
 601 gCCCCcaacc CTTTAATcgt caacttgatt gccGaaaaTt taggcagtag  
 651 tttccgtCTT Tcttgggggg cgTGGGcgtg ggcaaTGGCT Gttcccggcg  
 701 ttatcgccctt TttcgTTATG CTTTGATT TATATTTTT GTATCCGCCT  
 751 GAAATTAAAG AAACGCCCAA TGCTGttcAA TTTGCCAAAG ACCGCTGAG  
 801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG  
 851 GTATCTTGCT GCTGTGTGG GCAGATGTT CCGCCCTTAT TACCGCAAT  
 901 CACGCTTTTA GTATCAacgc caccGCCACC GCATTTATCG GATTAAGCCT  
 951 GCTTTTGCTT TCCGCTGTAT TGACTTGGGA CGATGTTTT AAAGAAAAA  
 1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA  
 1051 TTTTAAATA Aactcggact gattaaatGG TTCTCCGGAG TGTGGCGGA  
 1101 Aagtgtcggc GGTGTGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG  
 1151 TGCTTGctta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT  
 1201 ATTACCGCTA TGTTCCGGCG ATTTCTCGCT GCTGCCGTTT CACTGAATGC  
 1251 CCCGGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA  
 1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCGGCTCG  
 1351 GGCTACACCA CAATGGGAGA ATGGTGAAG GCGGGTTTA TCATGAGCGT  
 1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCATTGG TGGAAAGTTC  
 1451 TGGGATATTG GTAA

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

m929.pep  
 1 MKLGFKPIPL AIAAVLCAV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK  
 51 VMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI  
 101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTSPNTARG  
 151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHSNP ISSAMAITAT  
 201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP  
 251 EIKETPNAVQ FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN  
 301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA  
 351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH  
 401 ITAMFGAFLA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS  
 451 GYTTMGEWVK AGFIMSVVNF LIFSVIGSIW WKVLGYW\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq  
 1 ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG  
 51 CGCCCTGGTT TTGGCACTGC CCGTACCcga CGGGGTCAAG CCTCAGGCTT  
 101 GGACGCTGCT GGCCATGTTT GTCGGTGTGA TTGCCCCAT TATCGGCAAG  
 151 GCCATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT  
 201 AACC GGCGTA ACCGCCGACA AACC GGCGC GGCATGAGC GATGCGTTGA  
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT  
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT  
 351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC  
 401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC

1338

```

451 GGCGGCATTA TACATCCGAT TATGCACTCG ATTGCCGCGA GTTACGGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTTCGTCTG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTCTGTATG CCTTTGATTT TATATTWYT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTATATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTGG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTTGGCGGA
1101 AAGTGTCCGC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGCGC ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GgCCGCATCC AACATTATGA
1301 TGACCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCGGTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

m929.pep

```

1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51 AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTSPNTARG
151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMASTTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng) from *N. gonorrhoeae*:

g929/m929

	10	20	30	40	50	60
g929.pep	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGVIAAIIGKVMPLGALSII					
m929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
g929.pep	AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
m929	AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
	70	80	90	100	110	120
g929.pep	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
m929	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
g929.pep	LALVNYHNSPISSAMAITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
m929	LALVNYHNSPISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240

1339

	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKETPNAVQFAKDRLEMGKMSADEIIMAVIFGILLLLWADV PALITGN					
m929	PLILYXLYPPEIKETPNAVQFAKDRLEMGKMSADEIIMAVIFGILLLLWADV PALITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
g929.pep	FSGVLAESVGG LGVSGTAAGVILVLAYMYAHYMFASSTTAHITAMFGAFLAAVSLNAPAM					
m929	FSGVLAESVGG LGVSGTAAGVILVLAYMYAHYMFASSTTAHITAMFGAFAAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

```

a929.seq
1  ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT ATCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGTGCGCT GTCGATTATT GCCGTGGGT TGGTCGCAGT
201 AACCGGCGTA ACCGCCGACA AACCGGTGC GCGATGAGC GATGCGTTGA
251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAC AGGGCTGGGG ATGCGTATCG GATATTGTGTT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTGTCGCG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGCGC
701 TTATCGCCTT TTTGTTATG CCTTTGATTT TATATTTTTT GTATCCGCCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTCAA TTTGCCAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGTT GCTGTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGAG TGTGGCGGGA
1101 AAGTGTGCGC GGTGTGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTGCGCGC ATTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGCGCATG CCGACCGCGC TGATGATGGC GGCCGCATCT AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGTAATT CGCCTGTGAT TTTGCGTTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTGTT TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

1340

This corresponds to the amino acid sequence <SEQ ID 2850; ORF 929.a>:

```

a929.pep
1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF IGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251 EIKETPNVAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLA MYA HYMFASTTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

m929/a929 99.6% identity in 487 aa overlap

	10	20	30	40	50	60
m929.pep	MKLGFKPIPLAIAAVLCALV LALPVPDGVK PQAWTLLAMFVGVIAAIIIGKAMPLGALSII					
a929	MKLGFKPIPLAIAAVLCALV LALPVPDGVK PQAWTLLAMFVGVIAAIIIGKAMPLGALSII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m929.pep	AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMISRGLLKTGLMRIGYLFIAV					
a929	AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMISRGLLKTGLMRIGYLFIAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m929.pep	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIHPIMQSIAGSYGSNPAKGTEGKMGKY					
a929	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m929.pep	LALVNYHNSP ISSAMFITATAPNPLIVNLI AENLGSSFRL SWGAWAWAMAVPGVIAFFVM					
a929	LALVNYHNSP ISSAMFITATAPNPLIVNLI AENLGSSFRL SWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m929.pep	PLILYXLYPPEIKETPNVAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADVPALITGN					
a929	PLILYFLYPPPEIKETPNVAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADVPALITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
a929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
m929.pep	FSGVLAESVGGGLGVSGTAAGVILVLA MYA HYMFASTTAHITAMFGAFFAAVSLNAPAM					
a929	FSGVLAESVGGGLGVSGTAAGVILVLA MYA HYMFASTTAHITAMFGAFFAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
m929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
a929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
m929.pep	WKVLGYWX					



1341

a929 WKVLGYWX

g930.seq not found yet

g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

m930.seq

```

1  ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCCTGTTT TGCCATTAAC GAATGGGTGT TGGAAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAgTGG aAGCTTCAAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

m930.pep

```

1  MKLPLSYLPN IRFLSWCCLL AGIIAPATLL ASPNPAEIRM QQDIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EWLVEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGSFN *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

g930-1.seq (partial)

```

1  GGCAAGTGTC TGCATGCGGG CGACATTAAT CAAATCATGT CCTTAGCACA
51  AAATGCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101 CACAGGATTT GAATAGTGGC AAGCTTCAAT TAACCTGAT GCCGGGCTAT
151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCGAG
201 ACGTATTGCA GCATTCCAAA ACAAAATTTCC CACCCGCTCG AACGATCTGT
251 TGAATCTGCG TGATTGGGAA CAAGGACTGG AAAATCTCAA ATGCTCTCCG
301 ACTGCGGAAG CCGATCTCCA AATCGTTCCC GTAGAGAGAG AACCAAACCA
351 AAGTGATGTC GTGGTGCAAT GCGCGTAACG TCTGCTGCCC TACTGTGTGA
401 GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGAAGTGTG ATATGTTCTA
501 TGTAATATTG GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAAATTTTG
551 ACGGCCATCG CAAAGAAGGC GGATCAAAAC ATTACGCCGT ACATTATTCA
601 GCCCCTTTTC GTAAATGGAC ATGGGCATTG AATCACAATG GCTACCGTTA
651 CCATCAGGCG GTTTCGGGAT TATCGGAAGT CTATGACTAT AATGGAAGAA
701 GTTACAACAC TGATTTCGGC TTCAACCGCC TGTGTGATCG TGATGCCAAA
751 CGCAAAACCT ATCTCAGTGT AAAACTGTGG ACGAGGGAAA CAAAAAGTTA
801 CATTGATGAT GCCGAAGTGA CTGTACAACG GCGTAAACC ACAGGTGTTG
851 TGGCAGAACT TCCCAACAAA GGATATATCG GTCGCAGTAC GGCAGATTTT
901 AAGTTGAAT ATAAACACGG CACCGGCATG AAAGATGCTC TGCGCGCGCC
951 TGAAGAAGCC TTTGGCGAAG GCACGTCACG TATGAAATT TGGACGGCAT
1001 CGGCTGATGT AAATACTCCT TTCAAATCG GTAAACAGCT ATTTGCCTAT
1051 GACACATCCG TTCATGCACA ATGGAACAAA ACCCCGCTAA CATCGCAAGA
1101 CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GGCGCAACGA TTGAGCTGG
1201 CAATTTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTATTCGGG CCAAACTCTA GCCGCGACAG
1301 CAATTGGGAT ACGCGGGCAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTTACCG GCCGTGCATT GAAAAAGCCC GAATATTTTC AGACGAAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGGTATTCT GTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

g930-1.pep (partial)

```

1  GKCLHAGDIN QIMSLAQNAL IGRGYTTTRI LAAPQDLNSG KLQLTLMPGY
51  LRSIRIDRSN DDQTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKCLP
101 TAEDLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMDNS GSEATGKYQG
151 NITFSADNPF GLSDMFYVNY GRSIGGTPDE ENFDGHRKEG GSNNYAVHYS
201 APFGKWTWAF NHNGYRYHQA VSGLSEVYDY NGKSYNTDFG FNRLLYRDAK
251 RKTYLSVKLW TRETKSYIDD AELTVQRRKT TGWLAELSHK GYIGRSTADF
301 KLKYKHGTGM KDALRAPEEA FEGGTSRMKI WTASADVNTF FOIGKQLFAY
351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGEMSLPAER GWYWRNDLSW
401 QFKPGHQLYL GADVGHVSGQ SAKWLSGQTL AGTAIGIRGQ IKLGGNLHYD

```

451 IFTGRALKKP EYFQTKKWT GFQVGSF\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2855>:

m930-1.seq

```

1 ATGAACTTC CTTATCCTA TTGCTTAAT ATTCGCTTTT TGTCTTGGT
51 CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAACCGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTC TGCCATTAAAC GAAGTGGTGT TGGGAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGGAAACCGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTGGCTGCG
451 CCACAGGATT TGAATAGTGG CAAGCTTCAA TTAACCTGA TACCGAGCTA
501 TCTGCGCTCC ATACGAATCG ATCGGTCTAA CGATGATCAA ACCCATGCAG
551 GACGTATTGC AGCATTCCAG AACAAATTC CCACCCGCTC GAACGATCTG
601 TTGAATCTGC GTGATTGGA ACAAGGACTG GAAATCTCA AACGTCTCCC
651 GACTGCGGAA GCCGATCTCC AAATCGTTCC CGTAGAGGGA GAACCAAAACC
701 AAAGTGATGT CGTGGTGCAA TGGCGGCAAC GTCTGCTGCC CTACCGTGTG
751 AGTGTGGGGA TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG
801 AAATATCACT TTCTCTGCCG ACAATCCTTT GGGACTGAGT GATATGTTCT
851 ATGTAATAA TGGACGTTTCG ATTGGCGGTA CGCCCGATGA GGAAAGTTT
901 GACGCCCATC GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC
951 AGCCCTTTTC GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT
1001 ACCATCAGGC AGTTTCCGGA TTATCGGAAG TCTATGACTA TAATGAAAAA
1051 AGTTACAATA CTGATTTCCG CTTCAACCGC CTGTTGTATC GTGATGCCAA
1101 ACGCAAAACC TATCTCGGTG TAAACTGTG GATGAGGGAA ACAAAGTTT
1151 ACATTGATGA TGCCGAACATG ACTGTACAAC GCGCTAAAAC TGCGGGTTGG
1201 TTGGCAGAAC TTTCCACAA AGAATATATC GGTGCGAGTA CGGCAGATTT
1251 TAAGTTGAAA TATAAACGCG GCACCGGCAT GAAAGATGCT CTGCGCGCGC
1301 CTGAAGAAGC CTTTGGCGAA GGCACGTACG GTATGAAAT TTGGACGGCA
1351 TCGGCTGATG TAAATACTCC TTTTCAAATC GGTAAACAGC TATTGCTTA
1401 TGACACATCC GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG
1451 ACAAACTGGC TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA
1501 ATGAGTTTGT CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG
1551 GCAATTTAAA CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG
1601 TTTCAAGACA ATCCGCCAAA TGGTTATCGG GCCAACTCT AGTCGGCACA
1651 GCAATTGGGA TACGCGGCGA GATAAAGCTT GCGCGCAACG TGCATTACGA
1701 TATATTTACC GGCCGCGCAT TGAAAAAGCC CGAATTTTTC CAATCAAGGA
1751 AATGGCAAG CGGTTTTCAG GTAGGCTATA CGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2856; ORF 930-1>:

m930-1.pep

```

1 MKLPLSYLPN IRFLSWCCLL AGIIPATLL ASPNPAEIRM QODIQQRQRE
51 EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EVVLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGKLQ LTLIPSYLRS IRIDRSNDDQ THAGRIAAFO NKFPTRSNDL
201 LNLRLDLEQGL ENLKRLEPTAE ADLQIVPVEG EPNQSDVVVQ WRQRLPYRV
251 SVGMDSNGSE ATGKYQGNIT FSADNPLGLS DMFYVNYGRS IGGTPDEESF
301 DGRHKEGGSN NYAVHYSAPF GKWTWAFNHN GYRYHQAVSG LSEVYDYNKG
351 SYNTDFGFNR LLYRDAKRKT YLGVKLWMRE TKSVIDDAEL TVQRRKTAGW
401 LAELSHKEYI GRSTADFLK YKRGTGMKDA LRAPEEAFGE GTSRMKIWA
451 SADVNTPFQI GKQLFAYDTS VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE
501 MSLSAERGWI WRNDLSWQFK PGHQLYLGAD VGHVSGQSAK WLSGQTLVGT
551 AIGIRGQIKL GGNLHYDIFT GRALKKPEFF QSRKWASGFQ VGYTF*

```

m930-1/g930-1 95.4% identity in 478 aa overlap

	90	100	110	120	130	140
m930-1.pep	AINEVVLEGEHHA RFQFALKRAL RETGFQAGKCLHAGNINQIMSLAQNALIGR GYTTTRILAA					
g930-1.pep	:					
					10	20
						30
	150	160	170	180	190	200
m930-1.pep	LAAPQDLNSGKLQ LTLIPSYLRSIRIDRSNDDQTHAGRIAAFO NKFPTRSNDLNLRLDLE					
g930-1.pep	:					
	40	50	60	70	80	90
	210	220	230	240	250	260
m930-1.pep	QGLLENLKRLEPTAEADLQIVPVEGEPNQSDVVVQWRQRLPYRVSVGMDSNGSEATGKYQG					

1343

```

g930-1.pep  QGLENLKLPLTAEADLQIVPVEREPNQSDVVVQWRXLLPYCVSVGMDNSGSEATGKYQG
              100      110      120      130      140      150
m930-1.pep  270      280      290      300      310      320
NITFSADNPGLSDMFYVNYGRSIGGTPDEESFDGHRKEGGSNNYAVHYSAPFGKWTWAF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  NITFSADNPGLSDMFYVNYGRSIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAF
              160      170      180      190      200      210
m930-1.pep  330      340      350      360      370      380
NHNGYRYHQAVSGLSEVYDNGKSYNTDFGNRLLYRDAKRKTYLGVKLMWRETKSYIDD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  NHNGYRYHQAVSGLSEVYDNGKSYNTDFGNRLLYRDAKRKTYLSVKLWTRTKSYIDD
              220      230      240      250      260      270
m930-1.pep  390      400      410      420      430      440
AELTVQRRKTAGWLAELSHKEYIGRSTADFKLKYKRGTMKDALARPEEAFGEGTSRMKI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  AELTVQRRKTAGWLAELSHKEYIGRSTADFKLKYKRGTMKDALARPEEAFGEGTSRMKI
              280      290      300      310      320      330
m930-1.pep  450      460      470      480      490      500
WTASADVNTFPQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLSAER
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  WTASADVNTFPQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLPAER
              340      350      360      370      380      390
m930-1.pep  510      520      530      540      550      560
GWYWRNDLSWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLVGTAGIRGQIKLGGNLHYD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  GWYWRNDLSWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLVGTAGIRGQIKLGGNLHYD
              400      410      420      430      440      450
m930-1.pep  570      580      590
IFTGRALKKPEFFQSRKWASGFQVGYTF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  IFTGRALKKPEYFQTKKWTGFGVGYGSFX
              460      470

```

a930-1.seq not yet found

a930-1.pep not yet found

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2857>:

```

g931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCGCGTCCT GATGGAACCC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCTCCAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCGAAA AGGCTTTTAC GACAACACGA TTTCCACCG
201 CGTcatCGGC GGCTTCGTCA TCCAAGGCGA CGGATTGACC GAGGACTTGG
251 TGCAAAAGGC AACCGATAAG GCCGTTGCCA ACGAATCCGG caacgGCTTG
301 AAAAACACCG TCGGCACCAT CGCAATGGCG CGGACGGCAG CCCCCGATTC
351 CGCCGCCGCC CAATTCTTTA TCAATCTGCG GGACAACGGT TCGCTCGACT
401 ACAAAAACCG ACAATACGGC TACACCGTTT TCGGCAGGGT AGAAAAGCGGA
451 ATGGACACCG TTTCCAAAT CGCCGCGTC AAAACGCCA CGCGCGGCTT
501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
551 GGCAGTAACA CGCAGACAGA CGTTCAGACG GCGTCGCCCG TTTCCAAAAA
601 AACGCCGTTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2858; ORF 931.ng>:

```

g931.pep
1  MKPKFKTVLT ALLLAVSLPS MAATRVLMT DMGNIRLVLD ESKASKTVAN
51  FVRYARKGFY DNTIFHRVIG GFVIQGDGLT EDLVQKATDK AVANESGNGL
101 KNTVGTIAMA RTAAPDSAAA QFFINLADNG SLDYKNGQYG YTVFGRVESG
151 MDTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2859>:

```
m931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCCCCAAAAC CGTTGCTAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACGACACCG TTTTTCACCG
201 CGTTATCGAC GGTTTTGTTA TCCAGGCGCG TGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAAACACG CCGGCACCAT CGCCATGGCG CGGACGACAG CCCCCGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGC GGACCA.kct TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
451 ATGAACACCG TTTCCAAAAT CGCCGCGGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTCTG
551 GGCAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2860; ORF 931>:

```
m931.pep..
1  MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
51  FVRYARKGFY DDTVFHRVID GFVIQGGGLT EDLAQKASDK AVANESGNGL
101 KNTAGTIAMA RTTAPDSATS QFFINLADXX SLDYKNGQYG YTVFGRVESG
151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 931 shows 91.9% identity over a 185 aa overlap with a predicted ORF (ORF 931.ng) from *N. gonorrhoeae*:

g931/m931

	10	20	30	40	50	60
g931.pep	MKPKFKTVLTALLLAVSLPSMAATRVLMDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
m931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
	70	80	90	100	110	120
g931.pep	DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
	: :					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
g931.pep	QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNVPVQPVKIRR					
m931	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVPVQPVKIRR					
	130	140	150	160	170	180
g931.pep	VVVGQX					
m931	VVVGQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

```
a931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CACCCAAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACAATACGA TTTTTCACCG
201 CGTCATCGGC GGCTTCGTTA TCCAAGGCGG CGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAAACACTG TCGGCACCAT CGCCATGGCG CGGACGGCCG ATCCGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGT GGACAATGAT TCGCTCAACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
```

1345

451 ATGAACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT  
 501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGTCG  
 551 GGCAGTAA

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

a931.pep  
 1 MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN  
 51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL  
 101 KNTVGTIAMA RTADPDSATS QFFINLVDND SLNYKNGQYG YTVFGRVESG  
 151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ\*

-- m931/a931 94.6% identity in 185 aa overlap

m931.pep	10	20	30	40	50	60
	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
a931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
m931.pep	70	80	90	100	110	120
	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
a931	DNTIFHRVIGGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTVGTIAMARTADPDSATS					
	70	80	90	100	110	120
m931.pep	130	140	150	160	170	180
	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
a931	QFFINLVDNDSLNYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
	130	140	150	160	170	180
m931.pep	VVVGQX					
a931	VVVGQX					

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

m932.seq  
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC  
 51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCCGCTCA TTTTGGGAAT  
 101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC  
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG  
 201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA  
 251 GGAAAAAAGG CTGGTGTCGT AAGGGTTTCG ACCCTTATCC CGAAAAACAA  
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAAATGA

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

m932.pep  
 1 MKYIVSISLA MGLAACSFGG FKPWPDAAS FWELKNYANP YPGSASAALD  
 51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDPPYPENK  
 101 KYEWPREEGK TK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows \_\_\_% identity over a \_\_\_ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

g934.seq  
 1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCG CACTCACCGC

1346

```

51 CTGCCAAGAC GACACGCAGG CGCGGCTCGA ACGGCAGCAG AAACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCCAGG CGCAGGCAAA
201 CGGCAACAAC GGTCAGCCCG TTACCGGCAA .AGAcggGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGA TTGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCGG
351 GCAACCAAGA CAGCCCCGTC GCCCGTCGCG CGCGTGCTGC CTACCATCAG
401 TCCGCACGCC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCGCGCCCGT CAAttaccgc catcgcgcta tgcGCGGTTT CGgcagAagg
551 cggtaaaCCC GCGCGCTCAA TGCCGTCTGA AGGGCTTTCA GACGGCATT
601 TTGTATTGTG TAGGGGCATT GTTATGTTGC CGTTTGATT TCAGACGGCA
651 TTTTGTTC AAGCGTTTGA TGTcggGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2866; ORF 934.ng>:

g934.pep

```

1 MKKIIASALI ATFALTACQD DTQARLERQQ KQIEALQQQL AQQADDTVYQ
51 LTPEAVKDTI PAQAQANGNN GQFVTGKRRR AVYLRPIDRK LAAAKPDWRG
101 GRRVYRQAG KQIHTGGQPR QPRRPSRACC LPSVRTPOCA HQQGFHAQP
151 PKCTTGAGAG ALPPDNAPAR QLPPSRYARF RQKAVNPARQ CRLKGFQTAF
201 LYLGLALLCC RLIFRRHFVS KRLMSGWQF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2867>:

m934.seq (partial)

```

1 ..CGGCTCGAAC AGCAGCAGAA ACAGATTGAA GCCCTGCAAC AGCAGCTCGC
51 ACAGCAGGCA GACGATACGG TTTACCAACT GACTCCCGAA GCAGTCAAAG
101 ACACCATTCG TGCCGAAGCA CAGGCAAAACG GCAACAACG GCAACCCGTT
151 ACCGGTAA.A GACGGGCAGC AGTATATTTA CGACCAATCG ACAGGAAGCT
201 GGCTGCTGCA AAGCTGGTC GCGCGGCGCG CAGGCGCGTT TATCGGCAAC
251 GCGCTGGCAA ACAAAATTCAC ACGGGCAGGC AACCAGACA GTCCCGTCGC
301 CCGGCGCGCG CGTGCAGCCT ACCATCAGTC CGCAGCCTCC AATGCGCGCA
351 yCAGCAGGGA TTTGAACACG CGCAGCCTCC GTGCAAAACA ACAGGCGGCG
401 CAkGCGCAGC GTTACCGCCC GACAACGCGC CCGsCCGsCA ATTACCGCG
451 CCGGCTATG CGCGGTTTCG GCAGGAGGCG GTAAACCCGG CGCGCCAATG
501 CCGTCTGAAG AGCTTTCAGA CGGCATTThT GCATTTGTTA GGGACATTGT
551 TATGTTGCCG TTTGATTTTC AGACGGCATT TTGTTTCCAA GCCTTTGATG
601 TCGGGATGGC AATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2868; ORF 934>:

m934.pep (partial)

```

1 ..RLEQQQKQIE ALQQQLAQQA DDTVYQLTPE AVKDTIPAEA QANGNNGQPV
51 TGXRRRAVYL RPIDRKLAAA KPGRRGRRV YRQAGKQIH TGRQPROSRR
101 PARACSLPSV RTPQCAHQGG FEHAQPPCKT TGGAXAALPP DNAPXRQLPP
151 PRYARFQEA VNPARGCRLK SFQTAFXHLL GTLLCCRLIF RRHFVSKRLM
201 SGWQF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 934 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 934.ng) from *N. gonorrhoeae*:

m934/g934

```

m934.pep
10 20 30
RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
|||:|||||||||||||||||||||||||||||
g934      MKKIIASALIATFALTACQDDTQARLERQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
10 20 30 40 50 60
40 50 60 70 80 90
PAEAQANGNNGQPVGTGXRRRAVYLRPIDRKLAAAKPGRRGRRVYRQAGKQIHTGRQPR
||:|||||||||||||||||||||||||||||
g934      PAQAQANGNNGQPVGTGXRRRAVYLRPIDRKLAAAKPDWRGRRVYRQAGKQIHTGGQPR
70 80 90 100 110 120
100 110 120 130 140 150

```

```

m934 . pep      QSRRPARACSLPSVRTPQCAHQQGF EHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
| |||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g934            QPRRPSPRACCLPSVRTPQCAHQQGF EHAQPPCKTTGGAGAAALPPDNAPARQLPPSRYARF
                130      140      150      160      170      180

                160      170      180      190      200
m934 . pep      RQBAVNPARQCRLKSFQTAFXHL L GTLLCCRLIFRRHFVSKRLMSGWQFX
||:||||| |||:||||| :|||:||||| ||||| ||||| ||||| ||||| |||||
g934            RQKAVNPARQCRLKGFQTAFLYLLGALLCCRLIFRRHFVSKRLMSGWQFX
                190      200      210      220      230

```

```

a934.seq
1  ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCTG CACTCGCCGC
51  CTGCCAAGAC GACGCGCAGG CGCGGCTCGA ACAGCAGCAGG AAACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG GACAGCATATC GTTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCGAAG CACAGGCAAA
201 CGGCAACAAC GGGCAACCGG TTACCGG.TA AAGACGGGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAGCCTGGT TCGGCGCGCG
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAATTCT ACACGGCGAG
351 GCAACCAAGA CAGTCCCGTC GCCCGCGCGC CGCGTGCCGC CTACCATCAG
401 TCCGCACATC CCAATTGCGC CACGAGCAGG GATTTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGCGCG CGCAGGCGCA CGGTTACCGC CCGACAACGC
501 GCCCGCCCGC CAATTACCGC CGCCCCGCCA TCGCGCGTTT CGGCAAGAAG
551 CGGTAATACC GGCCTGCCAA TGCCGTCTGA AGGGCTTTCA GACGGCATT
601 TTGTATTGTG TAGGGACATT GTTATGTATG CGTTTGATT TTAGACGGCA
651 TTTTGTTC AAGAGTTTGA TGTCGGGATG CCAATTCTGA

```

a934.pep

1	<u>MTKKIIASALI</u>	<u>ATFFALAA</u>	<u>ACQD</u>	<u>DAQARLEQQ</u>	<u>RKQIEAL</u>	<u>QQQL</u>	<u>AQQADD</u>	<u>TVYQ</u>
51	<u>LTPEAVKDTI</u>	<u>PAEAAQANGN</u>	<u>N</u>	<u>GQPVTX</u>	<u>RRRA</u>	<u>AVYLRLPDRK</u>	<u>LAAAKPGRG</u>	<u>R</u>
101	<u>GRVRVQRAR</u>	<u>KQIHTRGRQR</u>	<u>P</u>	<u>QSRPRPARACR</u>	<u>LPSVRTSQCA</u>	<u>HQQGFHAQP</u>	<u></u>	<u></u>
151	<u>PKCTTGGAGA</u>	<u>ALPDPNAPAR</u>	<u></u>	<u>QLPPPHARF</u>	<u>RQKAVNPACQ</u>	<u>CRLKGFQTAF</u>	<u></u>	<u></u>
201	<u>LYLLGTLLCC</u>	<u>RLIFRRHFAS</u>	<u></u>	<u>KSLMSGWOF</u>	<u>*</u>	<u></u>	<u></u>	<u></u>

```

m934.pep      10      20      30
                RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
a934          10      20      30      40      50      60
MKKIIASALIAFALAACQDDAQARLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI

m934.pep      40      50      60      70      80      90
PAAEQANGNNGQPVTGXRRAAVYLRPIDRKLAAAKPGRRGGRRVYRQRAGKQIHTGRQPR
a934          70      80      90      100     110     120
PAAEQANGNNGQPVTXXRRAAVYLRPIDRKLAAAKPGRRGGRRVYRQRAGKQIHTGRQPR

m934.pep      100     110     120     130     140     150
QSRRLPARACSLPSVRTPQCAHQQGFEHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
a934          130     140     150     160     170     180
QSRRLPARACRLPSVRTSQCAHQQGFEHAQPPCKTTGGAGAAALPPDNAPARQLPPPRHARF

m934.pep      160     170     180     190     200
RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
a934          190     200     210     220     230
RQKAVNPACQCRLKGFQTAFYLLGTLCCRLIFRRHFVSKSLMSGWQFX

```

g935.seq not found yet

g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1  ATGTTGTATT TCAGATACGG CTTTTTGGTT GTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTGCAGGT GCAGCGGTCT GTGTCGGATA AGTGGGCGGA ATCAGATTGG
151 AAAGTTGAAA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGCGCTC AACGGCAATC
251 AGGCGGATTT AATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAC TG CACGGGGAAA
401 ATCGGCGAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGCAAAATT
501 GGATTTGCCG GCACCGGTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAA
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC
601 AATAGAAATG CCAATAATGC CCGCCCGCAA TATTGCCCGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTC GCGGGCGGGA GCGGGCGGCA GGTTGAATT
701 ATGAAATCGA GCGGAAAAG CTGACGCCGT TGGCAGATAA TCATTATTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTC GAAAAAATC
801 AGCTTATGAT GACGGGTTCG GCAGGGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAAACAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGCTG TCCCATACTT
1001 ACCGCCCAAA CCGGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GCAGGCAGGA
1101 CGGGTTTTAT GTTTCGTCTG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GGCGCGGTCA ATAATGCCGC CTACCGGCGC AACGGTGT TT ATGCCGTTG
1251 GGCGCAGGAG TGGCGGCA GTGGCGGTTT GAACAGTCGG GTTCCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCATTG CGGCTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CGGCGTTGAA TTATCGTTT GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCGGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2872; ORF 935>:

m935.pep

```

1  MLYFRYGLFV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVENDAPRVV DGDFLLAHPK MLEHSLRDAL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRLKSAERH FAEAAKLDLP APVLENVGRF RKKTEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNVEIEAEK LTPLADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGGRAYLGW QYKNARQTAG ILPFYQVQLS
301 LSGDFDAKTK RVNNRRLPPY MLAGVGVQOL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAQE WRQLGGLNSR VSASYARRNY KGIAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNPVYA KRRNSEVFVS
501 ADWRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1  ATGTTGTATT TCAGATACGG TTTTTTGGTT GTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTGCAGGT GCAGCGGTCT GTGTCGGATA AGTGGGCGGA ATCGGATTGG
151 AAAGTTGACA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGTGCTC AACGGCAATC
251 AGGCGGATTT GATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAC TG CACGGGGAAA
401 ATCGGCGAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTCCCGAGG CGGAAAAAAT
501 GGATTTGCCG GCGCCGTTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAG
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC

```



1349

```

601 AATAGAAATG CCAATAATGC CGCGCCGCAG TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGCTTGAATT
701 ATGAAATCGA GCGGAAAAA CTGACGGCGT TGGCAGATAA TCATTATTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTC AATAAAAAATC
801 AGCTTATGAC GACGGGTTTC GCAGAGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAACAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCACTTG TCCCATACTT
1001 ACCGCCCAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GTCGGCAGGA
1101 CGGGTTTTAT GTTTCGTCTG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGTCT GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GCGCGGTGCA ATAATGCCGC CTACCGGCGC AACGGTGTTC ATGCCGGCTG
1251 GCGCGAGGAG TGGCGGCAGT TGGCGGTTT GAACAGTCGG GTTTCGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCGTTG CGGCTTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CCGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

```

a935.pep
1  MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVDNDAPRVV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRLKSAERH FAEAEKLDLP APVLENVGRF RKKAEGITGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAEAA GLNYEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNNRRLPPY MLAGHGVQVL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFEGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAQE WRQLGGLNSR VSASYARRNY KGVAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPIA KRNSEVFVS
501 ADWRF*

```

m935/a935 98.8% identity in 505 aa overlap

	10	20	30	40	50	60
m935.pep	MLYFRYGLVWVWCAAGVSAAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVENDAPRVV					
a935	MLYFRYGLVWVWCAAGVSAAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVNDAPRVV					
	10	20	30	40	50	60
m935.pep	DGDFLLAHPKMLEHSLRDALNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
a935	DGDFLLAHPKMLEHSLRDVLNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
	70	80	90	100	110	120
m935.pep	AEAVARYRELHGENAADERILLDLAAAEFDDFRLKSAERHFAEAAKLDLPAPVLENVGRF					
a935	AEAVARYRELHGENAADERILLDLAAAEFDDFRLKSAERHFAEAEKLDLPAPVLENVGRF					
	130	140	150	160	170	180
m935.pep	RKKTEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
a935	RKKAEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
	190	200	210	220	230	240
m935.pep	LTPLADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
a935	LTALADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
	250	260	270	280	290	300

1350

	310	320	330	340	350	360
m935.pep	GSDGFD AKTKRVNRRLLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
a935	GSDGFD AKTKRVNRRLLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
	310	320	330	340	350	360
	370	380	390	400	410	420
m935.pep	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
a935	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVSASYARRNYKGIAAFSTEQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935	WRQLGGLNSRVSASYARRNYKGIAAFSTEQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	430	440	450	460	470	480
	490	500				
m935.pep	GRTESNVPYAKRRNSEVFVSADWREF					
a935	GRTESNVPYAKRRNSEVFVSADWREF					
	490	500				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

g936.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGcgaACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACCTGGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAccgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

g936.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHL LLL QVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

m936.seq (partial)

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCATTTCAG
51  CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCC...

```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

m936.pep (partial)

```

1  MKPKPHTVRT LIAAIFSLAL SGCVS AVIGS AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHL LLL QVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTA...

```

### Homology with a predicted ORF from *N.gonorrhoeae*

ORF 936 shows 93.8% identity over a 128 aa overlap with a predicted ORF (ORF 936.ng) from *N. gonorrhoeae*:

m936/g936

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2879>:

a936.seq

1	ATGAAACCCA	AACCGCACAC	CGTCCGCACC	CTGACTGCCG	CGTCTCTCAG
51	CCTTGCCCTC	GGCGGTGTCG	TCAGCGCAGT	CGTCGGCGGC	GCGGCGGTTCG
101	GCGCGAAATC	CGCGCTCGAC	CGCGGAACCA	CCGGCGCGCA	AACCGACGAC
151	AACGTAATGG	TGCTCGGTAT	CGAAACACC	CGCCGCTCCT	ATCTCGGCCA
201	AAACAACCAA	ACCAAGGCT	ACAGCGCCCA	AATCTCGGTT	TCGGGTACA
251	ACCGCCACCT	GCTGCTGCTC	GGACAAGTCG	CCACCGAAGG	CGAGAAACAG
301	TTCGTGCGTG	AGATTGCACG	TTCCGAACAG	GCCGCCGAAG	GCGTGTACAA
351	CTACATTACC	GTGCGCTCCC	TGCCCGCGAC	TGCCCGCGAC	ATCGCCGGCG
401	ACACTTGGAA	CACATCCAAA	GTCGCGGCCA	CGCTGTTGGG	CATCACGCCC
451	GCCACACAGG	CGCGCGTCAA	AATCGTTACC	TACGGCAACG	TACCTACGTC
501	TATGGGCATC	CTCACCCCGG	AAGAACAGGC	GCAGATTACC	CAAAAAGTCA
551	GACCCACCGT	CGGCGTACAA	AAAGTCATCA	CCCTCTACCA	AAACTACGTC
601	CAACGCTGA				

This corresponds to the amino acid sequence <SEQ ID 2880; ORF 936.a>:

a936.pep

```

1      MKPKPHTVRT LTAAVLSLAL GGCVSAVVGG AAVGAKSAVD RRTTGAQTDD
51     NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL QGVATEGEKQ
101    FVGQTARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151    AQQARVKIVT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201    QR*

```

m936/a936 95.3% identity in 128 aa overlap

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAksAVDRRTTGAQTDDNVMALRIETT					
a936	::   :   :   :   :   :   :   :   :   :					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQRNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVNYIT					
a936	::   :   :   :   :   :   :   :   :					
	70	80	90	100	110	120

m936.pep VASLPRTA

```

          |||||
a936      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
          130      140      150      160      170      180

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:

```

g936-1.seq
1  ATGAAACCCA  AACCACACAC  CGTCCGCACC  CTGATTGCCG  CCGTCCTCAG
51  CCTTGCCCTC  GCGCGCTGCT  TCAGCGCAGT  CGTCGGCGGG  GCCGCCGTCG
101 GCGCAAAATC  CGTCATCGAC  CGccgAACCA  CCGgcgcgca  AACCGATGac
151 aACGTTATGG  CGTTGCGTAT  CGAAACCACC  GCCCGTTCCT  ACCTGCGCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAAGTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCCGTC  AGATTGCACG  TTCCGAACAG  GCCGCCGAAG  GCGTATACAA
351 CTACATTACC  GTCGCCTCCC  TGCCGCGCAC  TGCGGGCGAC  ATCGCCGGCG
401 ACACTTGGAA  CACGTCCAAA  GTCCGCGCca  cgCTGCTGGG  CATCAGCCCC
451 GCTACACAGG  CGCGCGTCAA  AATCATTACC  TACGGCAATG  TAACCTACGT
501 TATGGGCATC  CTCACCCCG  AAGAACAGGC  GCAGATTACC  CAAAAAGTCA
551 GCACCaccgt  CGGCGTACAA  AAAGTCATTA  CCCTTACCA  AAATACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:

```

g936-1.pep
1  MKPKPHTVRT  LIAAVLSLAL  GGCFSAVVGG  AAVGAKSVID  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYTPQISV  VGYNRHLLL  GQVATEGEKQ
101 FVGQIARSEQ  AAEGVYNYIT  VASLPRTAGD  IAGDTWNTSK  VRATLLGISP
151 ATQARVKIIT  YGNVTYVMGI  LTPEEQAQIT  QKVSTTVGVQ  KVIITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:

```

m936-1.seq
1  ATGAAACCCA  AACCGCACAC  CGTCCGCACC  CTGATTGCCG  CCATTTTCAG
51  CCTTGCCCTT  AGCGGCTGCG  TCAGCGCAGT  AATCGGAAGC  GCCGCCGTCG
101 GCGCGAAATC  CGCCGTCGAC  CGCCGAACCA  CCGGCCGCGA  AACCGACGAC
151 AACGTTATGG  CGTTGCGTAT  CGAAACCACC  GCCCGTTCCT  ATCTGCGCCA
201 AAACAACCAA  ACCAAAGGCT  ACACGCCCCA  AATCTCCGTC  GTCGGCTACA
251 ACCGCCACCT  GCTGCTGCTC  GGACAAGTCG  CCACCGAAGG  CGAAAAACAG
301 TTCGTCCGTC  AGATTGCACG  TTCCGAACAG  GCCGCCGAAG  GCGGTATACAA
351 CTATATTACC  GTCGCCTCCC  TGCCGCGCAC  TGCCGGCGAC  ATCGCCGGCG
401 ACACTTGGAA  CACATCCAAA  GTCCGCGCCA  CGCTGTTGGG  CATCAGCCCC
451 GCCACACAGG  CGCGCGTCAA  AATCGTTACC  TACGGCAACG  TAACCTACGT
501 TATGGGCATC  CTCACCCCG  AAGAACAGGC  GCAGATTACC  CAAAAAGTCA
551 GCACCACCGT  CGGCGTACAA  AAAGTCATCA  CCCTTACCA  AAATACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:

```

m936-1.pep
1  MKPKPHTVRT  LIAAIFSLAL  SGCVS AVIGS  AAVGAKSAVD  RRTTGAQTDD
51  NVMALRIETT  ARSYLRQNNQ  TKGYTPQISV  VGYNRHLLL  GQVATEGEKQ
101 FVGQIARSEQ  AAEGVYNYIT  VASLPRTAGD  IAGDTWNTSK  VRATLLGISP
151 ATQARVKIIV  YGNVTYVMGI  LTPEEQAQIT  QKVSTTVGVQ  KVIITLYQNYV
201 QR*

```

m936-1/g936-1 95.5% identity in 202 aa overlap

```

          10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVD RRTTGAQTDDNVMA LRIETT
          |||||:||||:| |||:| |||||:|||||:|||||:|||||:|||||
g936-1      MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGA KSVIDRRTTGAQTDDNVMA LRIETT
          10      20      30      40      50      60

          70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHL LLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g936-1      ARSYLRQNNQTKGYTPQISVVGYNRHL LLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
          70      80      90      100     110     120

          130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

1353

```

g936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130      140      150      160      170      180

              190      200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
g936-1      QKVSTTVGVQKVITLYQNYVQRX
              190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:

```

a936-1.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51 CCTTGCCCTC GCGGCTGCG TCAGCGCAGT CGTCGGCGGC GCGGCGGTCC
101 GCGCGAAATC CGCGTTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTAATGG CGCTGCGTAT CGAAACCACC GCGCGCTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTT GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGGTACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACAC TTGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAGTCATCA CCCTCTACCA AAACCTACGC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

```

a936-1.pep
1  MKPKPHTVRT LTA AVL SLAL GGC VSA VVG AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

a936-1/m936-1  97.0% identity in 202 aa overlap

              10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLIAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT
              |||||
a936-1      MKPKPHTVRTLTA AVL SLALGGCVSAVVGGA AVGAKSAVDRRTTGAQTDDNVMALRIETT
              10      20      30      40      50      60

              70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISVVGYNRHLLL GQVATEGEKQFVGQIARSEQAAEGVYNYIT
              |||||
a936-1      ARSYLRQNNQTKGYTPQISVVGYNRHLLL GQVATEGEKQFVGQIARSEQAAEGVYNYIT
              70      80      90      100     110     120

              130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              |||||
a936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130     140     150     160     170     180

              190     200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
a936-1      QKVSTTVGVQKVITLYQNYVQRX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:

```

g937.seq
1  atGAAAAATA TTCTCTTagt ATTTGTTAGC TTTGTGCCAT TATGTGTCCG
51 CACTGATCTG CCGCTGAata tCGAAGACAT AATGaccgAC AAGGGAAAAT
101 GGAAactGGA AACTTccctt acctacctgA acaGCGAAAA cagCCGCGCC
151 GCAC TTGCCT CACCGGTTTA CATTcAGACC GGCTCCGCTT CCTTTATCCC
201 CGTCCCGACC GAAATTCAGG AAAACGGCAG CAATACCGAT ATGCTCGCCG
251 GCACGCTCGG TTTGCGCTAC GGACTGAcgG GCAataccgA CATTACGGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAACCTGacg GCAACGGCAA

```

1354

```

351 AACCCGCAAC AAACGGATGT CCGACATATC CGCCGGCATC AGCCACACCT
401 TCCTtaAAGa cgGCAAAAAT CCCGCACTCA TCGCTTTCCT CGAAAGCACG
451 GTTTACGAAA AATCGCGCAA CAAAGCCTCG TCGGGAAAAT CGTGGCTCAT
501 CGGCGCCACC ACCTACAAAG CCATAGATCC GATTGTCCTT TCCCTACCG
551 CCGCTTACCG CATCAACGGC AGCAAAACCC TTTCAGACGA CGTCAAATAC
601 AAAGCAGGCA ATTACTGGAT GCTGAATCCC AACATCTCAT TTGCCGCCAA
651 CGACAGAATC AGCCTGACCG GAGGCATCCA ATGGCTGGGC AAACAGCCCG
701 ACCGCATAGA CGGCAAAAAA GAATCCGCAA GAAACACATC CACCTACGCC
751 CATTTCCGCG CAGGTTTCGG TTTCACCAA ACCGCGGCTT TAAACGCATC
801 CGCACGTTTC AACGTTTCAG GGCAAAGCAG TTCCGAAC TGAAATTGGGCG
851 TACAGCATAC ATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2888; ORF 937.ng>:

g937.pep

```

1 MKNILLVFVS FVPLCVRTDL PLNIEDIMTD KGKWKLETS TYLNSNSRA
51 ALASPVYIQT GSASFIPVPT EIQENGSTND MLAGTLGLRY GLTGNTDIY
101 SGSYLWHEER KLDGNGKTRN KRMSDISAGI SHTFLKDGKN PALIAFLEST
151 VYEKSRNKA SSKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTLDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2889>:

m937.seq

```

1 ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACTTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAgAAAaCGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGGCG TACGGAATGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACAG
351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCTTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAATCTCT CATTGCTGC
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCATTTTCG GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2890; ORF 937>:

m937.pep..

```

1 MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSENN
51 AELAAPVYIQ TGATSFIPIP TEIQENGSTN DMLVGTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLGNKSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTLDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 937 shows 86.9% identity over a 289 aa overlap with a predicted ORF (ORF 937.ng) from *N. gonorrhoeae*:

g937/m937

```

          10      20      30      40      50      59
g937.pep  MKNILL-VFVSFVPLCVRTDLPLNIEDIMTDKGKWKLETS TYLNSNSRAALASPVYIQ
          || || : : : : : : : : : : : : : : : : : : : : : : : : : :
m937      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETS TYLNSENNRAELAAPVYIQ
          10      20      30      40      50      60
g937.pep  TGSASFIPVPTTEIQENGSTNDMLAGTLGLRYGLTGNTDIYSGSYLWHEERKLDGNGKTR
          60      70      80      90      100     110     119

```

[illegible]

```

a937.seq
1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 ATATGGAACCT GGAACCTTCC CTTACTTACC TGAACAGCGA AAACAACCGC
151 GCCGAACCTG CCGCACCAGG TTACATCCAA ACCGGCGCAA CTTCGTTTAT
201 CCCCATCTCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCAGCTC CGGTTTGCGC TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG CACGGAAGAA CGCAAACTCG ACGGCAACGG
351 CAAAACCCGA AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCTTTAA AGACGACAAA AACCCCGCCC TAATCAGGTT TCTTGAAAGC
451 ACGGTTTACG AAAATTGCGC CAACAAGGCC TCGTCGGGAA ATCTCTGGCT
501 CATCGGCGCC AACACCTACA AAGCCATCGA CCCCCTGCTC CTTCTATTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCCTTTCAAG CAACACCAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCCAATATAT CCTTCGCGCG
651 CAACGACAGA ATACGCCTCA CGGGCGCAT CCAATTGGTG GGCAACGACG
701 CCGACCGTCT GGACGGCAAA AAGAATCCG CAAGAACAC ATCCACCTAT
751 GCCCATTTTG GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGACAGT TTCAACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTTTAA

```

a937.pap

1	MKRIFLPALP	AILPLSAYAD	LPLTIEDIMT	DKGKWKLETS	LTYLNSNNR
51	AELAAVPYIQ	TGATSFIPIP	TEIQENGSTN	DMLVGLTLGR	YGLTNGTDIY
101	GSGLYLWHEE	RKLDNGKTR	NKRMSDVSLG	ISHTFLKDDK	NPATISFLES
151	TVYKESRNKA	SSGKSWLIGA	TTYKAIDPVV	LSITAAYRIN	GSKTSSNTK
201	KAGNYWMLN	PNISFAANDR	ISLTGGQIQWL	GKQFDRDLHG	KESARNTSTY
251	AHFGAGGFGT	KTALLNASAR	FNVSGSSSE	LKFGVHTF*	

	10	20	30	40	50	60
m937.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
a937	:					
	10	20	30	40	50	60
	MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	70	80	90	100	110	120
m937.pep	TGATSFIPIPTEIQENGSNTDMLVGLTGLRYGLTGNTDIYSGSYLWHEERKLDGNSKTR					
a937	:					
	70	80	90	100	110	120
	TGATSFIPIPTEIQENGSNTDMLVGLTGLRYGLTGNTDIYSGSYLWHEERKLDGNGKTR					

1356

	130	140	150	160	170	180
m937.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a937						
	130	140	150	160	170	180
	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	190	200	210	220	230	240
m937.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a937						
	190	200	210	220	230	240
	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	250	260	270	280	290	
m937.pep	RESSRNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					
a937						
	250	260	270	280	290	
	KESARNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX					

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:

m939.seq (partial)

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCCTCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATATCGG
201 CATCCGCGAC GTAAACGCAC CC...
```

This corresponds to the amino acid sequence &lt;SEQ ID 2894; ORF 939&gt;:

m939.pep (partial)

```

1  MKRLTLFAFV LAAGAVSASP KADVEKGQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD VNAP...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:

a939.seq

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATATCGG
201 CATCCGCGAC GGTAAACGCA CCCACGGTTC GGCAGCTGTG ATGAACCGG
251 TGTAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTCTAT
301 GCCAAACAGC AGCCCAAATC CGGTGAAGCC AATCCTAAGG AAAATCCCGA
351 ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG
401 CGTGTATGTC CTGCCACGGT CCGAGCGGTG CCGGTATGCC GGGGGCGGGA
451 AGCGAAATTC AGGCTTATCC GCGTTTGGGC GGTCAGCATC AGGCATATAT
501 TGTGAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAAA AATACCATCA
551 TGGAAGATAT TGCAAACCGT ATGCTGAAG AAGATTGAA AGCGGTCGCC
601 AACTTTATCC AAGGTTTGGC TTAA
```

This corresponds to the amino acid sequence &lt;SEQ ID 2896; ORF 939.a&gt;:

a939.pep

```

1  MKRLTLFAFV LAAGAVSASP KADVEKGQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD GKRTHGSAV MKPVVMNLSQ QDILNVSAFY
101 AKQPKSGEA NPENPELGA KIYRGGLSDK KVPACMSCHG PSGAGMPGGG
151 SEIQAYPRLG GQHQAIVEQ MNAYKSGQRK NTIMEDIANR MSEDLLKAVA
201 NFIQGLR*
```

m939/a939 100.0% identity in 70 aa overlap

	10	20	30	40	50	60
m939.pep	MKRLTLFAFVLAAGAVSASPKADVEKGQVAATVCAACHAADGNSGIAMYPRLAAQHTAY					
a939						
	MKRLTLFAFVLAAGAVSASPKADVEKGQVAATVCAACHAADGNSGIAMYPRLAAQHTAY					



1357

```

                10      20      30      40      50      60
                70
m939.pep      IYHQTIGIRDVNAP
                |||||
a939          IYHQTIGIRDGKRTGHSAAVMKPVVMNLSDDQILNVSAFYAKQPKSGEANPKENPELGA
                70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

```

g950.seq
1  ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51 GGCCGCCGCG GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
251 AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

```

g950.pep
1  MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA
101 EGKCGEGKCG SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

```

m950.seq
1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGCGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

```

m950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

```

m950/g950      86.6% identity in 112 aa overlap

                10      20      30      40      50
m950.pep      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----
                |||||
g950          MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGCASKSAEGSCGASKSAEG
                10      20      30      40      50      60

                60      70      80      90      100
m950.pep      ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
                |||||
g950          SCGAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
                70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

```

a950.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGCGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>:

```
a950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from *N. meningitidis*

a950/m950 100.0% identity in 102 aa overlap

```

          10      20      30      40      50      60
a950.pep  MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
          |||||
m950       MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
          10      20      30      40      50      60

          70      80      90     100
a950.pep  EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
          |||||
m950       EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
          70      80      90     100
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2903>:

```
g951.seq
1  ATGATTATGT TACCCGCCCG TTCACTATT TTATCTGTCC TCGCAGCAGC
51  CCTGCTTGCC GGACAGGCGT ATGCTGCCGG CGCGGCGGAT GTGGAGCTGC
101 CGAAGGAAGT CGGAAAGGTT TTAAGGAAAC ATCGGCGTTA CAGCGAGGAA
151 GAAATCAAAA ACGAACGCGC ACGGCTTGCG GCAGTGGCGC AACGGGTCAA
201 CAGGGTGTTT ACGCTGTTGG GCGGTGAAAC GGCTTTGCAG AAAGGGCAGG
251 CGGGAACGGC TCTGGCAACC TATATGCTGA TGTGGAACG CACAAAATCC
301 CCCGAAGTCG CCGAACGCGC CTGGAAATG GCCGTGTCGC TGAACGCGTT
351 TGAACAGCGC GAAATGATT ATCAGAAATG GCGGCAGATC GAGCCTATAC
401 CCGGTGAGGC GCAAAAACGG GCGGGGTGGC TCGGGAACGT ATTGAGGGAA
451 GGGGGAATC AGCATCTGGA CCGGTGGAAG GAGGTGCTGG CGCAATCGGA
501 CGATGTGCAA AAACGCAGGA TATTTTGTCT GCTGGTGCAA GCCGCCGTGC
551 AGCAGGGTGG GGTGGCTCAA AAAGCATCGA AAGCGGTTCC CCGTGCGGCG
601 TTGAAGTATG AACATCTGCC CGAAGCGGCG GTTGCCGATG CCGTGTTCGG
651 CGTACAGGGA CGCGAAAAGG AAAAGGCAAT CGAAGCTTTG CAGCGTTTGG
701 CGAAGCTCGA TACGGAAATA TTGCCCCCA CTTTAATGAC GTTGCGTCTG
751 ACTGCACGCA AATATCCCGA AATACTCGAC GGCTTTTTCG AGCAGACAGA
801 CACCCAAAAC CTTTCGGCCG TCTGGCAGGA AATGGAAAT ATGAATCTGG
851 TTTCCCTGCG TAAGCCGATG GATGCCTATG CGCGTTTGA CGTGCTGTTG
901 GAACACAACC CGAATGCAAA CCTGTATATT CAGGCGGCGA TATTGGCGGC
951 AAACCGAAAA GAAGGTGCGT CCGTTATCGA CGGCTACGCC GAAAAGGCAT
1001 ACGGCAGGGG GACGGGGGAA CAGCGGGGCA GGGCGGCAAT GACGGCGGCG
1051 ATGATATATG CCGACCGCAG GGATTACGCC AAAGTCAGGC AGTGGTTGAA
1101 AAAAGTGTCC GCGCCGGAAT ACCTGTTCGA CAAAGCGCTG CTGGCGGCTG
1151 CCGCGGCTGC CGAATTGGAC GGAGGCCGGG CGGCTTTGCG GCAGATCGGC
1201 AGGGTGCGGA AACTTCCCGA ACAGCAGGGG CGGTATTTTA CGGCAGACAA
1251 TTTGTCCAAA ATACAGATGC TCGCCCTGTC GAAGCTGCCC GACAAACGGG
1301 AAGCCCTGAT CGGGCTGAAC AACATCATCG CCAAACTTTC GGCGGCGGGA
1351 AGCACGGAAC CTTTGGCGGA AGCATTGGCA CAGCGTTCCA TTATTACGA
1401 ACAGTTCGGC AAACGGGGAA AAATGATTGC CGACCTTGAA ACCGCGCTCA
1451 AACTTACGCC CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501 CTTTCCGATT CCAAACGTTT GGACGAGGGT TTCGCCCTGC TTCAGACGGC
1551 ATACCAATC AACCCGACG ATACCGCCGT TAACGACAGC ATAGGCTGGG
1601 CGTATTACCT GAAAGGCGAC GCGGAAAGCG CGTGCCCGTA TCTGCGGTAT
1651 TCGTTTGAAA ACGACCCCGA GCCCGAAGTT GCCGCCCAT TGGGCGAAGT
1701 GTTGTTGGCA TTGGGCAAC GCGATCAGGC GGTGACGTA TGGACGAGG
1751 CGGCACACCT TAGGGGAGAC AAGAAAATAT GCGGGGAGAC GCTCAAACGC
1801 TACGGAATCG CCTTGCCCGA GCCTTCCCGA AAACCCCGGA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>:

```
g951.pep
1  MIMLPARFTI LSVLAAALLA GQAYAAGAAD VELPKEVGKV LRKHRRYSEE
```

```

51 EIKNERARLA AVGERVNRVF TLLGGETALQ KGQAGTALAT YMLMLERTKS
101 PEVAERALEM AVSLNAFEQA EMIYQKWRQI EPIPGEAQKR AGWLRNVLRE
151 GGNQHLDGLE EVLAQSDDVQ KRRIFLLLVQ AAVQOGGVAQ KASKAVRRRA
201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL QRLAKLDEI LPPTLMTLRL
251 TARKYPEILD GFFEQDTQON LSAVWQEMEI MNLVSLRKP DAYARLNVLL
301 EHNPNANLYI QAAILAANRK EGASVIDGYA EKAYGRGTGE QRGRAAMTAA
351 MIYADRRDYA KVRQWLKQVS APEYLFDKGV LAAAAAELD GGRAALRQIG
401 RVRKLPEQQG RYFTADNLSK IQMLALSCLP DKREALIGLN NIIAKLSAAG
451 STEPLAEALA QRSIIYEQFG KRGKMIADLE TALKLTPDNA QIMNNLGYSL
501 LSDSKRLDEG FALLQTAYQI NPDDTAVNDS IGWAYYKGD AESALPYLRY
551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAAHLRGD KKIWRETLKR
601 YGIALPEPSR KPRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

```

m951.seq
1 ATGATTATGT TACCTAACCG TTTCAAAATG TTAAGTGTGT TGACGGCAAC
51 CTTGATTGCC GGACAGGTAT CTGCCGCCGG AGCGGGTGGC GGGGATATGA
101 AACAGCCGAA GGAAGTCGGA AAGGTTTCA GAAAGCAGCA GCGTTACAGC
151 GAGGAAGAAA TCAAAAACGA ACGCGCACGG CTTGCGGCAG TGGGCGAGCG
201 GGTTAATCAG ATATTTACGT TGCTGGGAGG GGAACCGGCC TTGCAAAAGG
251 GGCAGGCGGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGCACA
301 AAATCCCCCG AAGTCGCCGA ACGCGCCTTG GAAATGGCCG TGTGCGTGAA
351 CGCGTTTGAA CAGGCGGAAA TGATTTATCA GAAATGGCGG CAGATTGAGC
401 CTATACCGGG TAAGGCGCAA AAACGGGCGG GGTGGCTGCG GAACGTGCTG
451 AGGGAAGAGG GAAATCAGCA TCTGGACGGA CTGGAAGAGG TGTGCGTCA
501 GCGGACGAA GGACAGAAC GCAGGGTGT TTTATTGTTG GCACAAGCCG
551 CCGTGCAACA GGACGGGTTG GCGCAAAAG CATCGAAGC GGTTCGCCGC
601 GCGGCGTTGA AATATGAACA TCTGCCGAA GCGGCGGTTG CCGATGTGGT
651 GTTCAGCGTA CAGGACGCG AAAAGGAAA GGAATCGGA GCTTTCAGC
701 GTTGGCGAA GCTCGATACG GAAATATTGC CCCCCACTTT AATGACGTTG
751 CGCTGACTG CACGCAATA TCCCGAATA CTCGACGGCT TTTTCGAGCA
801 GACAGACACC CAAAACCTTT CGGCCGTCTG GCAGGAATG GAAATTATGA
851 ATCTGGTTT CCTGCACAG CTGGATGATG CCTATGCGCG TTTGAACGTG
901 CTGTTGGAAC GCAATCCGAA TGCAGACCTG TATATTGAG CAGCGATATT
951 GCGGCGAAAC CGAAAAGAG GTGCTCCGT TATCGACGGC TACCGCGAAA
1001 AGGCATACGG CAGGGGGACG GAGGAACAGC GGAGCAGGGC GGCCTAACG
1051 GCGGCGATGA TGTATGCCA CCGCAGGGAT TACGCCAAG TCAGGCAGTG
1101 GCTGAAAAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
1151 CCGCTGCGGC GGCTGTCGAG TTGGACGGCG GCAGGGCGGC TTTGCGGCAG
1201 ATCTGCGAGG TCGGAAACT TCCGAAACG CAGGGGCGGT ATTTTACGGC
1251 AGACAATTTG TCCAAAATAC AGATGCTCGC CTTGTCGAAG CTGCCCGATA
1301 AACGGGAGGC TTTGAGGGGG TTGGACAAGA TTATCGAAA ACCGCTGCC
1351 GGCAGTAATA CAGAGTTACA GGCAGAGGCA TTGGTACAGC GGTCAAGTTG
1401 TTACGATCGG CTTGGCAAGC GGAATAAAT GATTTAGAT CTTGAAAGGG
1451 CGTTACAGGCT TGCACCCGAT AACGCTCAGA TTATGAATA TCTGGGCTAC
1501 AGCCTGCTGA CCGATTCCAA ACGTTTGAC GAAGGTTTCG CCCTGCTTCA
1551 GACGGCATA CAAATCAACC CGGACGATAC CGCTGTCAAC GACAGCATAG
1601 GCTGGGCGTA TTACCTGAAA GCGCAGCGCG AAAGCGCGCT GCCGTATCTG
1651 CGGTATTCTG TTGAAAACGA CCCCAGGCC GAAGTTGCCG CCCATTGGG
1701 CGAAGTGTG TGGGCATTGG GCGAACGCGA TCAGGCGGTT GACGTATGGA
1751 CGCAGGCGGC ACACCTTACG GGAGACAAGA AAATATGGCG GGAACGCTC
1801 AAACGTCACG GCATCGCATT GCCCAACCT TCCGAAAAC CTGCGAATA
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

```

m951.pep
1 MIMLPNRFKM LTVLTATLIA GQVSAAGGGA GDMKQPKVGV KVFRRQORYS
51 EEEIKNERAR LAAVGERVNO IFLLGGETA LQKGQAGTAL ATYMLMLERT
101 KSPEVAERAL EMAVSLNAFE QAEMIYQKWR QIEPIPGKAQ KRAGWLRNVL
151 RERGNQHLDG LEEVLAQADE GQNRVFLLL AQAAVQDGL AQKASKAVRR
201 AALKYEHLPE AAVADVFSV QGREKEKAIG ALQRLAKLDT EILPPTLMTL
251 RLRTARKYPEI LDGFFEQDTQ QNLSAVWQEM EIMNLVSLHR LDDAYARLNV
301 LLERNFNADL YIQAAILAAN RKEGASVIDG YAEKAYGRGT EEQRSRAALT
351 AAMMYADRRD YAKVRQWLKQ VSAPEYLFDK GVLAATAAVE LDGGRAALRQ
401 IGRVRKLPEQ QGRYFTADNL SKIQMLALS LKPKREALRG LDKIIEKPPA
451 GSNTLQAEA LVQSVVYDR LGKRKMMISD LERAFRLAPD NAQIMNNGY
501 SLLTDSKRLD EGFALLQTAY QINPDDTAVN DSIWAYYK GDAESALPYL
551 RYSFENDPEP EVAHLGEVL WALGERDQAV DVWTQAAHLT GDKKIWRETL
601 KRHGIALPQP SRKPRK*

```

Computer analysis of this amino acid sequence gave the following results:

1360

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

m951.pep	10	20	30	40	50	60
	MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKVGVFRKQORYSEEEIKNERAR					
g951	10	20	30	40	50	
	MIMLPARFTILSVLAAALLAGQAYAA--GAADVLPKEVGVLRKHRRYSEEEIKNERAR					
m951.pep	70	80	90	100	110	120
	LAAVGERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
g951	70	80	90	100	110	
	LAAVGERVNRVFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
m951.pep	130	140	150	160	170	180
	QAEMIYQKWRQIEPIPGKAQKRAGWLRNVLRRERGNQHLDGLEEVLAQADEGQNRVFLLL					
g951	120	130	140	150	160	170
	QAEMIYQKWRQIEPIPGEAQKRAGWLRNVLREGGNQHLDGLEEVLAQSDDVQKRRIFLLL					
m951.pep	190	200	210	220	230	240
	AQAAVQDGLAQKASKAVRRAALKYEHLPAAVADVVFVQGREKEKAIGALQRLAKLDT					
g951	180	190	200	210	220	230
	VQAAVQGGVAQKASKAVRRAALKYEHLPAAVADAVFGVQGREKEKAIEALQRLAKLDT					
m951.pep	250	260	270	280	290	300
	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVQEMEIMNLVSLHRLDDAYARLNV					
g951	240	250	260	270	280	290
	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNL SAVQEMEIMNLVSLRKPDDAYARLNV					
m951.pep	310	320	330	340	350	360
	LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTTEEQRSAALTAAMMYADRRD					
g951	300	310	320	330	340	350
	LLEHNPANLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQGRRAAMTAAMIYADRRD					
m951.pep	370	380	390	400	410	420
	YAKVRQWLKKSVAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRLPEQQGRYFTADNL					
g951	360	370	380	390	400	410
	YAKVRQWLKKSVAPEYLFDKGVLA AAAA AELDGGRAALRQIGRVRLPEQQGRYFTADNL					
m951.pep	430	440	450	460	470	480
	SKIQLMALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD					
g951	420	430	440	450	460	470
	SKIQLMALSKLPDKREALIGLNNIIAKLSAAGSTEPLAEALAQRSIIYEQFGKRGKMIAD					
m951.pep	490	500	510	520	530	540
	LERAFRLAPDNAQIMNNLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
g951	480	490	500	510	520	530
	LETALKLTPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
m951.pep	550	560	570	580	590	600
	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL					
g951	540	550	560	570	580	590
	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLRGDKKIWRETL					
m951.pep	610					
	KRHGIALPQPSRKPRK					
g951	600	610				
	KRYGIALPEPSRKPRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2907>:

```
a951.seq
1  ATGTTACCCG CCGTTTCAC CATTTTATCT GTGCTCGCGG CAGCCCTGCT
51  TGCCGGGCGAG GCGTATGCCG CCGGCGCGGC GGATGCCAAG CCGCCGAAGG
101 AAGTCGGAAG GGTTCACAG AAGCAGCAGC GTTACAGCGA GGAAGAAATC
151 AAAAAACGAAC GCGCACGGCT TCGCGCAGTG GCGGAGCGGG TTAATCAGAT
201 ATTTACGTTG CTGGGAGGGG AAACCGCCTT GCAAAAGGGG CAGGCGGGAA
251 CGGCTCTGGC AACCTATATG CTGATGTTGG AACGCACAAA ATCCCCCGAA
301 GTCGCCGAAC GCGCCTTGGA AATGGCCGTG TCGCTGAACG CGTTTGAACA
351 GCGCGAAATG ATTTATCAGA AATGGCGGCA GATTGAGCCT ATACCGGGTA
401 AGGCGCAAAA ACGGGCGGGG TGGCTGCGGA ACGTGCTGAG GGAAGAGAGG
451 AATCAGCATC TAGACGGAAT GGAAGAAGTG CTGGCTCAGG CCGACGAAGG
501 ACAGAACCCG AGGGTGTTTT TATTGTTGGC ACAAGCCGCC GTGCAACAGG
551 ACGGGTTGGC GCAAAAAGCA TCGAAAGCGG TTCGCCGCGC GGCCTTGAGA
601 TATGAACATC TGCCCGAAGC GCGGTTTGCC GATGTGGTGT TCAGCGTACA
651 GGGACGCGAA AAGGAAAAGG CAATCGGAGC TTTGACGCGT TTGGCGAAGC
701 TCGATACGGA AATATTGCCC CCCACTTTAA TGACGTTGCG TCTGACTGCA
751 CGCAAATATC CCGAAATACT CGACGGCTTT TTCGAGCAGA CAGACACCCA
801 AAACCTTTTC GCGCTCTGGC AGGAAATGGA AATTATGAAT CTGGTTTCCC
851 TGCACAGGCT GGATGATGCC TATGCGCGTT TGAACGTGCT GTTGGAAACG
901 AATCCGAATG CAGACCTGTA TATTCAGGCA GCGATATTGG CCGCAAAACG
951 AAAAGAAGGT GCTTCCGTTA TCGACGGCTA CGCCGAAAAG GCATACGGCA
1001 GGGGACGGG GGAACAGCGG GGCAGGGCGG CAATGACGGC GGCATGATA
1051 TATGCCGACC GAAGGGATTA CACCAAAAGT AGGCAGTGGT TGAAAAAAGT
1101 GTCCGCGCCG GAATACCTGT TCGACAAAGG TGTGCTGGCG GCTCGGCGG
1151 CTGTGAGATT GGACGGCGGC AGGGCGGCTT TCGGCGAGAT CCGCAGGGTG
1201 CGGAAACTTC CCGAACAGCA GGGGCGGTAT TTTACGGCAG ACAATTGTTC
1251 CAAATACAG ATGTTGCGCC TGTCGAAGCT GCCCGACAAA CCGGAGGCTT
1301 TGAGGGGGTT GGACAAGATT ATCGAAAAAC CGCTGCGCGG CAGTAATACA
1351 GAGTTACAGG CAGAGGCATT GGTACAGCGG TCAGTTGTTT ACGATCGGCT
1401 TGGCAAGCGG AAAAAAATGA TTTGAGATCT TGAAGAGGCG TTCAGGCTTG
1451 CACCCGATAA CGCTCAGATT ATGAATAATC TGGGCTACAG CCTGCTTTCC
1501 GATTCCAAAC GTTTGGACGA AGGCTTCGCC CTGCTTCAGA CCGCATACCA
1551 AATCAACCCG GACGATACCG CTGTCAACGA CAGCATAGGC TGGGCGTATT
1601 ACCTGAAAGG CGACGCGGAA AGCGCGCTGC CGTATCTGCG GTATTCTGTT
1651 GAAACGACCC CCGAGCCCGA AGTTGCCGCC CATTGGGCGG AAGTGTGTTG
1701 GGCATTGGGC GAACGCGATC AGGCGGTTGA CGTATGGACG CAGGCGGCAC
1751 ACCTTACGGG AGACAAGAAA ATATGGCGGG AAACGCTCAA ACGTCACGGC
1801 ATCGCATTGC CCCAACCTTC CCGAAACCT CCGAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2908; ORF 951.a>:

```
a951.pep
1  MLPARFTILS VLAAALLAGO AYAAGAADAK PPKEVGKVF R KQORYSEEEI
51  KNERARLAAV GERVNQIFTL LGGETALQKG QAGTALATYM LMLERTKSPE
101 VAERALEMAV SLNAFEQAEM IYQKWRQIEP IPGKAQKRAG WLRNVLRERG
151 NQHLDGLIEV LAQADEGQNR RVFLLLAQAA VQDGLAQKA SKAVRRAALR
201 YEHLPEAAVA DVVFSVQGRE KEKAIGALQR LAKLDTIELP PTLMTLRLTA
251 RKYPEILDGF FEQTDTONLS AVQEMEIMN LVSLHRLDDA YARLNVLLER
301 NPNADLYIQA AILANRKEG ASVIDGYAEK AYGRGTGEQR GRAAMTAAMI
351 YADRRDYTKV RQWLKKVSAP EYLFDKGVLA AAAAVELDGG RAALRQIGRV
401 RKLPEQQGRY FTADNLSKIQ MFALSKLPDK REALRGLDKI IEKPPAGSNT
451 ELQAEALVQR SVVYDRLGKR KKMISDLERA FRLAPDNAQI MNNLGYSLLS
501 DSKRLDEGFA LLQTAYQINP DDTAVNDSIG WAYYLGDAE SALPYLRYSF
551 ENDPEPEVAA HLGVLWALG ERDQAVDVWT QAAHLTGDKK IWRETLKRHG
600 IALPQPSRKP RK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*

a951/m951 96.4% identity in 614 aa overlap

```

          10      20      30      40      50
a951.pep  MLPARFTILSVLAAALLAGQAYAAG--AADAKPPKEVGKVFRRKQORYSEEEIKNERAR
          ||| || :||:|:|:|:|:|: ||| | :| | | | | | | | | | | | | | |
m951      MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKVEVGKVFRRKQORYSEEEIKNERAR
          10      20      30      40      50      60
a951.pep  LAAVGERVNQIFTLGGETALQKGQAGTALATYMLMLERTKSPVAERALEMAVSLNAFE
          60      70      80      90     100     110
```

1362

```

|||||
m951      LAAGVERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
              70      80      90      100      110      120

          120      130      140      150      160      170
a951.pep   QAEMIQKWRQIEPIPGKAQKRAWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
          120      130      140      150      160      170
m951      QAEMIQKWRQIEPIPGKAQKRAWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
              130      140      150      160      170      180

          180      190      200      210      220      230
a951.pep   AQAAVQODGLAQKASKAVRRAALRYEHLPEAAVADVVSQGREKEKAIGALQRLAKLDT
          180      190      200      210      220      230
m951      AQAAVQODGLAQKASKAVRRAALRYEHLPEAAVADVVSQGREKEKAIGALQRLAKLDT
              190      200      210      220      230      240

          240      250      260      270      280      290
a951.pep   EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
          240      250      260      270      280      290
m951      EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
              250      260      270      280      290      300

          300      310      320      330      340      350
a951.pep   LLERNPNADLYIQAAILAANRKEGASVIDGYAEKAYGRGTGEQRGRAAMTAAMIYADRRD
          300      310      320      330      340      350
m951      LLERNPNADLYIQAAILAANRKEGASVIDGYAEKAYGRGTGEQRGRAAMTAAMIYADRRD
              310      320      330      340      350      360

          360      370      380      390      400      410
a951.pep   YTKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVKRLPEQQGRYFTADNL
          360      370      380      390      400      410
m951      YTKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVKRLPEQQGRYFTADNL
              370      380      390      400      410      420

          420      430      440      450      460      470
a951.pep   SKIQMFALSKLPDKREALRGLDKIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
          420      430      440      450      460      470
m951      SKIQMFALSKLPDKREALRGLDKIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
              430      440      450      460      470      480

          480      490      500      510      520      530
a951.pep   LERAFRLAPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK
          480      490      500      510      520      530
m951      LERAFRLAPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK
              490      500      510      520      530      540

          540      550      560      570      580      590
a951.pep   GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVWVQAHLTGDKKIWRETL
          540      550      560      570      580      590
m951      GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVWVQAHLTGDKKIWRETL
              550      560      570      580      590      600

          600      610
a951.pep   KRHGIALPQPSRKPRK
          600      610
m951      KRHGIALPQPSRKPRK
              610

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2909>:

```

g952.seq (partial)
1      ..TTGTCTTATC GTTTGAATGC TGCACCGATG TTTAACGATA ATCCTGTTGT
51     TTACGGAAAA ATCAAATTGC AGAGTTGGAA AGCGCGGCGG GATTTCATA
101    TTGTAAAGCA GGATTGGAT TTTTCCCTGCG GGGCGGCTTC GGTGGCGACG
151    CTTTTGAACA ATTTTACGG GCAAAGCTG ACGGAAGAAG AAGTGTGGGA
201    AAAACTGGGT AAGGAACAGA TGCGCGCGTC GTTTGAGGAT ATGCGGCGCA
251    TTATGCCCGA TTTGGGTTT GAGGCGAAAG GCTATGCCCT GTCTTTCGAA
301    CAGTCGCGCG AGTTGAAAAT CCCCCTCATC GTGTATCTGA AATACCGCAA
351    AGACGACCAT TTTTCGGTAT TGCGCGGAGT GGATGGCAAT ACGGTTTTCG
401    TTGCCGACCC GTCGCCGGGT CATGTTTCGA TGAGCAGGGC GCAGTTTTTG
451    GAGGCTTGCC AAACCCGTGA GGGAAATTG GCAGGCAAAA TTTTGGCGGT
501    CGTGCCGAAA AAAGCGGAGG CGATTTCAAA TAAATTGTTT TTCACACATC
551    ATCCCAAGCG GCAGACGGAG TTTGCAGTCG GACAGGTAAA ATGGTGGCGT

```

601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

g952.pep (partial)  
 1 ..LSYRLNAAAPM FNDNPVVYVK IKLQSWKARR DFNIVKQDLD FSCGAASVAT  
 51 LLNNFYGGQKL TEEVLEKLG KEQMRASFED MRRIMPDLGF EAKGYALSFE  
 101 QLAQLKIPVI VYLKYRKDDH FSVLRGVDGN TVLLADPSPG HVSMRAQFL  
 151 EAWQTREGNL AGKILAVVPK KAEAISNKL FTHHPKRQTE FAVGQVKKWR  
 201 AY\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

m952.seq  
 1 ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT  
 51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT  
 101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAG CGCGGCGGGA TTTCATATTT  
 151 GTAAAGCAGG ATTTGGATT TTTCTGTGGG GCGGCTTCGG TGGCGACGCT  
 201 TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA  
 251 AGCTGGATAA GGAGCAGATG CGCGCGTCTG TTGAGGATAT GCGGCGCATT  
 301 ATGCCTGATT TGGGTTTTGA GCGGAAGGCG TATGCCCTGT CTTTCGAGCA  
 351 GCTCGCGCAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG  
 401 ACGACCATTT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTGCTT  
 451 GCCGACCCGT CGCTGGGGCA TGTTCATAG AGCAGGCGCG AGTTTTTGGA  
 501 TGCTTGCGAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCTGTCA  
 551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC  
 601 CCAAACGCG AGACGGAGTT TACAGTCGGA CAAATCAGGC AAGCAGTGC  
 651 AGAGTAA

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

m952.pep  
 1 MMKFYVFL ACVVVLSYR LNAAPMFNDN PVVYKIKVQ SWKARRDFNI  
 51 VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKKLDKEQM RASFEDMRRI  
 101 MPDLGFQAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL  
 151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFFTQH  
 201 PKRQTEFTVG QIRQARAE\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952: 92.5% identity in 201 aa overlap

		10	20	30	40
g952.pep		LSYRLNAAAPMFNDNPVVYKIKLQSWKARRDFNIVKQDLDSCG			
m952		MMKFYVFLACVVVLSYRLNAAAPMFNDNPVVYKIKVQSWKARRDFNIVKQDLDSCG			
	10	20	30	40	50
	50	60	70	80	90
g952.pep	AASVATLLNNFYGGQKLTEEEVLEKLGKEQMRASFEDMRRIMPDLGFQAKGYALSFEQLAQ				
m952	AASVATLLNNFYGGQTLTEEEVLKKLDKEQMRASFEDMRRIMPDLGFQAKGYALSFEQLAQ				
	70	80	90	100	110
	110	120	130	140	150
g952.pep	LKIPVIVYLKYRKDDHFSVLRGVDGNTVLLADPSPGHVSMRAQFLEAWQTREGNLAGKI				
m952	LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVSMRAQFLDAWQTREGNLAGKI				
	130	140	150	160	170
	170	180	190	200	
g952.pep	LAVVPKKAETISNKLFFTHHPKRQTEFAVGQVKKWRAYX				
m952	LAVIPKKAETISNKLFFTHHPKRQTEFTVGQIRQARAE				
	190	200	210		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

a952.seq  
 1 ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT

1364

```

51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG AAAGGCGGGA TTTCAATATT
151 GTAAAGCAGG ATTTGGATT TTTCTGCGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCAGATT TGGGTTTGA AGCGAAAGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCACAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
401 ATGATCATTT CTCGGTATTG CGCGGGATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGTCA TGTTTCAATG AGCAGGGCGC AGTTTNGGA
501 TGCTTGGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCGGTCC
551 TGCCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACATCAT
601 CCCAAGCGGC AGACGGAGTT TGCAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

```

a952.pep
1 MMKFYVYVLL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
51 VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKLDKEQM RASFEDMRRI
101 MPDLGFCAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFFTHH
201 PKRQTEFAVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

```

a952/m952 97.7% identity in 218 aa overlap

a952.pep      10      20      30      40      50      60
MMKFYVYVLLACVVVLSYRLNAAPMFNDNPNVVYGKIKVQSWKERRDFNIVKQDLDFSCG
|||||
m952          10      20      30      40      50      60
MMKFYVYVLLACVVVLSYRLNAAPMFNDNPNVVYGKIKVQSWKARRDFNIVKQDLDFSCG

a952.pep      70      80      90      100     110     120
AASVATLLNNFYGQTLTEEEVLKLDKEQMRA SFEDMRIMPDLGFCAKGYALSFEQLAQ
|||||
m952          70      80      90      100     110     120
AASVATLLNNFYGQTLTEEEVLKLDKEQMRA SFEDMRIMPDLGFCAKGYALSFEQLAQ

a952.pep     130     140     150     160     170     180
LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVMSRAQFXDAWQTREGNLAGKI
|||||
m952         130     140     150     160     170     180
LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVMSRAQFLDAWQTREGNLAGKI

a952.pep     190     200     210     219
LAVVPKKAETISNKLFFTHHPKRQTEFAVGQIRQARAE
|||||
m952         190     200     210
LAVIPKKAETISNKLFFTHHPKRQTEFTVGQIRQARAE

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2915>:

```

g953.seq
1 ATGAAAAAAA TCATCTTCGC CGCGCTCGCA GCGGCAGCCG TCGGCACTGC
51 CTCCGCCACC TACAAAGTGG ACGAATATCA CGCCAACGTC CGTTTCGCCA
101 TCGACCACTT CAACACCAGC ACCAACGTCG GCGGTTTTTA CGGTCTGACC
151 GGTTCGCTCG AGTTCGATCA AGCAAAACGC GACGCAGAAA TCGACATCAC
201 CATTCCCGTC GCCAACCTGC AAAGCGGTTC GCAACCCCTC ACCGGCCACC
251 TGAAATCCGC CGACATCTTC GATGCCGCTC AATATCCGGA CATCCGCTTC
301 GTTCCACCA AATTCAACTT CAACGGCAAA AAACCTGTTT CCGTTGACGG
351 CAACCTGACC ATGCGCGGCA AAACGCCGCC CGTCAAACTC AAAGCCGAAA
401 AATTCAACTG CTACCAAAGC CCGATGGCGG AAACCGAAGT TTGCGGCGGC
451 GACTTCAGCA CCACCATCGA CCGACCAAAA TGGGGCGTGG ACTACCTCGT
501 TAACGCCGGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551 CAAAACAATA A

```



The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2917>:

This corresponds to the amino acid sequence <SEQ ID 2918; ORF 953>:

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*

m953/g953 93.0% identity in 187 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2919>:

a953.seq

1	ATGAAAAAAA	TCATCATCGC	CGCGCTCGCA	GCAGCCGCCA	TCGGCACTGC
1	CTCCGCCGCC	ACCTACAAAG	TGGACGAATA	TCAGCCCAAT	GCCCGTTTCT
51	CTATCGACCA	TTTCAACACC	AGGACCAACG	TCGGCGGTTT	TTACGGCTCTG
151	ACCGGTTCCG	TTGAGTTCGA	CCAAGCAAAA	CGCGACGGTA	AAATCGACAT
201	CACCATCCCC	TTTGCCAACC	TGCAAAAGCGG	TTTCAACACG	TTTACCGACC
251	ACCTGAAATC	AGGCCACATC	TTCGATGCCG	CCCAATATCC	GGACATCCGC
301	TTTGTTTCCA	CCAAATTCAA	CTTCAACCGC	AAAAAATCTGG	TTTCCGTTGA

1366

```

351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAAA CTCAAAGCCG
401 AAAAATTCAG CTGCTACCAA AGCCCGATGT TGAAAACCGA AGTTTGCGGC
451 GCGGACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2920; ORF 953.a>:

```

a953.pep
1  MKKIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHFNT STNVGGFYGL
51  TGSVEFDQAK RDGKIDITIP VANLQSGSQH FTDHLKSADI FDAAQYPDIR
101 FVSTKFNENG KKLVSVDGNI TMHGKTAPVK LKAKEFNCYQ SPMLKTEVCG
151 GDFSTTIDRT KWGMDYLVNV GMTKSVRIDI QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*

a953/m953 97.3% identity in 187 aa overlap

	10	20	30	40	50	60
a953.pep	MKKIIIAALAAAAIGTASAAATYKVDEYHANARFSIDHFNTSTNVGGFYGLTGSVEFDQAK					
m953	MKKIIFALAAAAISTASAAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
	10	20	30	40	50	60
a953.pep	RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKKLVSVDGNI					
m953	RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKKLVSVDGNI					
	70	80	90	100	110	120
a953.pep	RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKKLVSVDGNI					
m953	RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKKLVSVDGNI					
	70	80	90	100	110	120
a953.pep	TMHGKTAPVKLKAKEFNCYQSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI					
m953	TMHGKTAPVKLKAKEFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI					
	130	140	150	160	170	180
a953.pep	TMHGKTAPVKLKAKEFNCYQSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI					
m953	TMHGKTAPVKLKAKEFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI					
	130	140	150	160	170	180
a953.pep	QIEAAKQX					
m953	QIEAAKQX					

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:

```

m954.seq
1  ATGAAAAAGT TTTATTTTGT GCTGCTGGCG TTGGGTTTGG CAGCGTGTGG
51  GCAAGAACAA TCGCAGAAAG CTGATCGCGA GCAGTATTTT TTTGCCAATA
101 AATATCAATT TGCAGATGAG AAACAGGCTT TTTATTTTGA ACGCGCCGCC
151 CGTTTCCGTG TATTGCAACA AGGCCTTGCG GGGGATTTTG AGAGGTTTTT
201 AAAAGGAGAA ATACCTAATC AAGAAAATCT TGCAAAGTAT CGTGAAAATA
251 TTACTCAAGC AGTCGCTTAT TATGCGGACA CGAATGGAGA TGATGACCCA
301 TACCGCGTCT GCAAAACAGG TGCGCAAGAT GCAGAAATCC TGATGAAGAG
351 TATGGTAACA AGCGGTGGAG GCGGTACAAC TGATTAGAT AAGGAAAGTT
401 ATCAAATTA CCGAAATCA ATGCAAGAAT GCCGTAAC AATAACGGAA
451 GCTGAAGCCA ATTTGCCGAA AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:

```

m954.pep
1  MKKFYFVLLA LGLAACGQEQ SQKADAEQYF FANKYQFADE KQAFYFERAA
51  RFRVLQQGLG GDFERFLKGE IPNQENLAKY RENITQAVAY YADTNGDDDP
101 YRVCKQAAQD AEILMKSMVT SGGGGTTDLQ KESYQNYRKS MQECRKTITE
151 AEANLPKK*

```

a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

```
g957.seq (partial)
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGCGCG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGCGCGT TTGGTTGCGG
401 TTTTCGTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCGG GGGGatgaag gcaaacagtc tctgtgctcg
801 ctatgatgag gacggtCtgc CgcaAAAagt ctattggagt gtcgacaatg
851 gaaaaaaacc ccaagtgtc gaattattat tgaaaaacgg aaatcttttt
901 attgcccaat cttcgacggt aaccttgaaa acggtatggc taacgycgga
951 tatgcaaac tatcatgcgc aacaaacgtt gtatttggat ggg...
```

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

```
g957.pep (partial)
1  MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT EVPENPNFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALAIRLS
101 RLKKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGVSFDA AGRKGIGEDV
201 YEHLGCGYQM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MREIMPRGMK ANSLVVGYDA DGLPQKVYWS VDNKKPQSV EYYLKNGNLF
301 IAQSSTVTLK TDGVTADMQT YHAQOTLYLD G...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

```
m957.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGCGCG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCT TGCCGGAAT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGCGCGT TTGGTTGCGG
401 TTTTCGTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA
501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAAG
701 AGAGCAACCG AATTGCGTGC GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCGG AGGGATGAAG GCGAACAGTC TTGTGGTCTG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACC CGAGAGTTTC GAATATTATT TGAATAACCG AAATCTTTT
901 ATTGCACAA CTTCGACGCT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GCGGGCGGGA
1001 TTGTCCGCGA AGAGAAAACG GGAGACAGAC TGCTGATTT TCCTTTGAAC
1051 TTGAAAATT TGGAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGCG GGCAGGCGCG ACCTTTCTCA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

```
m957.pep
1  MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT EVKPNPNFV
51  AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALAIRLS
101 RLKKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFVNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGVSFDA AGRKGIGEDV
201 YEHLGCGYQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN
```

251 MRELMPRGMK ANSLVVGYDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF  
 301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN  
 351 LENLEKEVRR YAEAAARRSG GRRDLSH\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

	10	20	30	40	50	60
g957.pap	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNFAVAKLARLFNA					
m957	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFNA					
	10	20	30	40	50	60
g957.pap	70	80	90	100	110	120
	DRAVVIVKESMRTEESLAGAVDDGFLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
m957	DRAVVIVKESIRTEENLAGTVDDGFLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
	70	80	90	100	110	120
g957.pap	130	140	150	160	170	180
	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDPFSVNVYGGTAHGENYETTGEYRVV					
m957	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV					
	130	140	150	160	170	180
g957.pap	190	200	210	220	230	240
	WQPDGSVFDAAGRKGIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m957	WQPDGSVFDAAGRKGIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
g957.pap	250	260	270	280	290	300
	DSRDYVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSVDNGKKPQSVEYYLKNGNLF					
m957	DSRNSVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFYYYLKNGNLF					
	250	260	270	280	290	300
g957.pap	310	320	330			
	IAQSSTVTLKTDGVTADMOTYHAQQTLYLDG					
m957	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
m957	YAEAAARRSGGRRDLSHX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:

a957.seq

1	ATGTTTAAAA	AATTCAAACC	GGTACTGTTG	TCATTTTGTG	CACTTGTATT
51	TGCCTTTTGG	CTGGGAACGG	GTATTGCCTA	TGAGATTAAT	CCGCGTTGGT
101	TTTGTAGCGA	TACGGCAACT	GAAAATCCGA	ATGCTTTGTG	GGCGAAACTT
151	GCCCGCCTGT	TCCGAAATGC	CGACAGGGCG	GTTGTCATCG	TGAAGGAATC
201	GATCAGGACG	GAGGAAAGTC	TTGCCGGAGC	TGTGGATGAC	GGTCCGTTGC
251	AGTCGGAGAA	GGATTATCTT	GCACTCGCTG	TCCGGCTCAG	TCGTTTGAAA
301	GAAAAGGCGA	AATGGTTTCA	CGTAACGGAG	CAGGAACATG	GGGAAGAGGT
351	TTGGCTGGAT	TACTATATCG	GCGAGGGCGG	TTTGGTTGCG	GTTTCGCTTT
401	CGCAACGCTC	GCCGGAAGCG	TTTGTTAATG	CCGAATATCT	GTATCGGAAC
451	GATCGTCCGT	TTTCTGTAAA	TGTGTACGGC	GGAACGGTTC	ACGGGGAAAA
501	TTATGAAACG	ACAGGAGAAT	ATCGGGTTGT	TTGGCAACCG	GACGGTTCCG
551	TATTGTATGC	GTCGGGGCGC	GGGAAAATCG	GGGAAGATGT	TTATGAGCAT
601	TGCTCGGGT	GTTATCAGAT	GGCCCAGGTA	TATTTGGCGA	AATATCGGGA
651	TGTCGCGAAT	GATGAGCAGA	AGGTTTGGGA	CTTCCGCGAA	GAGAGTAACC
701	GGATTGCGTC	GGAATCGCGC	GATTCTGTGT	TTTATCAGAA	TATCGGGGAA
751	TTGATGCCCC	GAGGGATGAA	GGCAACAGT	CTTGTGGTCG	GCTATGATGC
801	GGACGGTCTG	CCGCAGAAAG	TCTATTGGAG	TTTCGACAAT	GGGAAAAAAC
851	GCCAGAGTTT	CGAATATTAT	TTGAAAAACG	GAAATCTTTT	TATTGCACAA
901	TCTTCGACGG	TAGCATTGAA	AGCGGATGGC	GTAACGGCGG	ATATGCAGAC

```

951 CTATCATGCG CAACAGACGT GGTATTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGACAGA CTGCCTGATT TTCCTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGGCAGGCGC GACCTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

```

a957.pep
1  MEKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGCGYQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a957/m957 96.3% identity in 377 aa overlap

a957.pep	10	20	30	40	50
m957	10	20	30	40	50
a957.pep	60	70	80	90	100
m957	60	70	80	90	100
a957.pep	120	130	140	150	160
m957	120	130	140	150	160
a957.pep	180	190	200	210	220
m957	180	190	200	210	220
a957.pep	240	250	260	270	280
m957	240	250	260	270	280
a957.pep	300	310	320	330	340
m957	300	310	320	330	340
a957.pep	360	370			
m957	360	370			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

```

g958.seq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCGGCACG CATTGCGCCG CCGATACCGT TCGGCGCGAA GAGGCGGACG

```

```

101  GCGGTGTCGC AGAAGGCGGT GCGCAGGGCG CGTCCGAATC CGCACAAGCT
151  TCCGATTGTA CCCTCGGTTC GACCTGCCTG TTTTGCAGTA ACGAAAGCGG
201  CAGCCCCGAG AGAACCAGAG CCGCCGTCCT AGGCAGCGGC GAAGCATCCG
251  TCCCCGAAGA CTATACGCGC ATTGTTGCCG ACAGGATGGA AGGACAGTCG
301  AAGGTTAAGG TCGCGCGCGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
351  AGTCTCTAAT ACCGATTGGG CGGATTACGA CCAGTCGGGC GACACCGTTA
401  CCGTAGGCGA CCGGTTTCGCC CTCCAACAGG ACGGTACGCT GATTCTGGGG
451  GAAACCTGTA CCTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAACTG
501  CCGTATGGAA ACCGAAACAAG GCGGACGGCG GCTGCAAAGC GTCAGCCGCA
551  CCGCCGAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCCAAATC
601  AACACCTGTT CCGCCGAGAG TCGCGGCTGG TATGTCAAGG CCGCCTCTGT
651  CGAAGCCGAT CCGGGAAAAG GCATAGGCGT TGCCAAACAC GCCGCCTTCG
701  TGTTCCGGCG CGTTCCCTTT TTCTATACGC CTTGGGCGGA CTTCCTCGCT
751  GACGGCAACC GCAAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCCGGTTC
801  GGACGGCGTT TCCCTTTCCG TCCCTATTA TTTCAACCTT GCCCCCAACT
851  TCGATGCCAC TTTCCGCCCC GGCATTATCG GCGAACCGCG CGCGACGTTT
901  GACGGCAACC TCCGTTACCT GCGTCCGAT TACAGCGGAC AGACCGACCT
951  GACCTGGTTG CCGCACGATA AGAAAAGCGG CAGGAACAAC CGCTATCAGG
1001 CAAAATGGCA GCACCGGCAC GACATTTCGG ACACGCTTCA GCGGGGTGTC
1051 GATTTCGAAC AAGTCTCCGA CAGCGGCTAC TACCGCGACT TTTACGGCGG
1101 CGAAGAAATC GCCGGCAACG TCAACCTCAA CCGCCGCGTA TGGCTGGATT
1151 ATGGCGGCAG GCGCGCGGGA GGCAGCCTGA ATGCCGCGCT TTCGTTTCAG
1201 AAATACCAGA CGCTGGCAAA CCAAAGCGGC TACAAAGACG AACCTTACGC
1251 CATCATGCCC CGCCTTTCTG CCGATTGGCA TAAAAACGCA GGCAGGGCGC
1301 AAATCGGCGT GTCCGCACAA TTTACCCGCT TCAGCCACGA CGGCCGCCAA
1351 GACGGCAGCC GACTGGTCGT GTATCCCGGT ATCAATGGG ATTTACAGCA
1401 CAGCTGGGGC TACGTCGCC CCAAACCTCG GCTGCACGCC ACTTATTACA
1451 GCCTCGACAG TTTCCGCGGC AAAGCATCCC GCAGCGTCGG CGCGCTTTTG
1501 CCGCTTGTCA ATATCGACGG CGGCACAACC TTCGAACGCA ATACGCGCCT
1551 GTTCGGCGGC GGAGTCGTGC AAACCATCGA GCGCGCGCTT TTCTACAAC
1601 ATATTCTTGC CAAATCTCAA AACGACCTGC CCAATTTTCA TTCGTCGGAA
1651 AGCAGCTTCG GCTACGGGCA GCTTTTCCGC GAAAACCTCT ATTACGGCAA
1701 CGACCGCATC AACGCCGCCA ACAGCCTTTC CACCGCGCTG CAGAGCCGTA
1751 TTTTGGACGG CGCGACGGGG GAGGAGCGTT TCCGCGCCGG TATCGGTCAG
1801 AAATTCTATT TCAAGGATGA TCGGCTGATG CTTGACGGCA GCGTCGGCAA
1851 AAATCCGCGC AGCCGTTCGG ACTGGGTGGC ATTCGCTCCG GCGCGCATAG
1901 GCGGGCGTTT CACCTCGAC AGCAGCATCC ACTACAACCA AAACGACAAA
1951 CGCGCCGAAC ATTACGCCGT CGGCGCAGGC TACCGCCCCG CCCCCGAAA
2001 AGTGTGTAAC GCCCGCTACA AATACGGGCG CAACGAAAAA ATCTACCTGC
2051 AGCGCGACGG TTCCTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
2101 GCACAATGGC CGCTGACGCG CAACCTGTCT GCCGTCGTCC GCTACAAC
2151 CGGTTTTTGA GCCAAAAAAC CGATAGAAAT GCTTGCCGGT GCAGAATACA
2201 AAAGCAGTTG CGGCTGCTGG GCGCGGGGCG TGTACGCCCA ACGCTACGTT
2251 ACCGCGGAAA ACACCTACAA AAACGCCGTC TTTTTTTCAC TTCAGTTGAA
2301 AGACCTCAGC AGCGTCGGCA GAAACCCCGC AGGCAGGATG GATGTCGCCG
2351 TTCCCGGCTA CATCCCGGCC CACTCTCTTT CCGCCGGACG CAACAAACGG
2401 CCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:

```

g958.pep
1  LARLFSLKPL VLALGFCFGT HCAADTVAAE EADGRVAEGG AQGASESAQA
51  SDLTGSLTCL FCSNESGSPE RTEAAVQSGS EASVPEDYTR IVADRMGQS
101 KVKVRAEGSV IIERDGAVLN TDWADYDQSG DVTVTGDRFA LQQDGLIRG
151 ETLYNLDDQO TGEAHNVNME TEQGGRRLLQ VSRTEMLGE GRYKLTETQF
201 NTCAGDAGW YVKAASVEAD RGKIGIVAKH AAFVFGGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYYFNL APNFDATFAP GIIGERGATF
301 DGQIRYLRPD YSGQTDLTWL PHDKKSGRNN RYQAKWQHRH DISDTLQAGV
351 DFNQVSDSGY YRDFYGGEEI AGNVNLNRRV WLDYGGRAAG GSLNAGLSVQ
401 KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSDGRQ
451 DGSRLVVYPG IKWDFSNSWG YVRPKLGLHA TYYSLDSFGG KASRSVGRVL
501 PVVNIDGGTT FERNTRLFGG GVVQTIEPRL FYNYPKSGT NDLPNFDSE
551 SSFGYQGLFR ENLYYGNDR I NAANSLSTAV QSRILDGATG EERFRAGIGQ
601 KFYFKDDAVM LDGSGVGNPR SRSDWVAFAS GGIGGRFTLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGKVLN ARYKYGRNEK IYLDQGSYF YDKLSQLDLS
701 AQWPLTRNLS AVVRYNYGFE AKKPIEMLAG AEYKSSCGCW GAGVYAQRVY
751 TGENTYKNAV FFSLQLKDLS SVGRNPAGRM DVAVPGYIPA HSLSAGRNRK
801 P*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:

```

m958.seq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTCTG
51  CTTCCGCGAC CATTCGCGCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA GCGTGTCCGA ACCCATACAG

```

```

151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTGCA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCGGT CCAAGGCAGC GGCAGAGCAT
251 CCATCCCCGA AGACTATACG CGCATGTGTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTGCTCG AACGCAACCG
351 GACGACCCCT AATACCGATT GGGCGGATTA CGACCACTCG GCGGACACCG
401 TTACCGCAGG CGACCGGTTC GCCCTCCAAC AGGACGGTAC GCTGATTTCGG
451 GGCAGAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGACAA
501 CGTCCGCRAT GAAATCGAAC AAGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCAGCCCT
651 TGTCCAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCCT
701 TCGTGTTCGG CGGCGTTCCT ATTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCTGCTT GTTCCCTCAC TGTCCGCCGG
801 TTCGACCGCG GTTCCCTTT CCGTCCCTA TTATTCAAC CTTGCCCCCA
851 ATCTCGATGC CACGTTCGCG CCCAGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGCG AGGTACGCTA CCTGCGGCGG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCATCGG CACGACATTT CCGACACGCT TCAGCGGGT
1051 GTCGATTTCA ACCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCGG CAGGGCGGCG GCGGCGAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAACCGTA
1251 TGCCCTCATG CCGCGCCTTT CGGTGAGTG GCGTAAAAAC ACCGGCAGGG
1301 CGCAAAATCG CGTGTCCGCA CAATTACCC GATTACGCGA CGACAGCCGC
1351 CAAGACGGCA GCCGCCTGGT CGTCTATCCC GACATCAAAT GGGATTTAG
1401 CAACAGCTGG GGCTATGTCC GTCCCAAAC CCGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
1501 CTGCCCATTG TCAACATCGA CAGCGGCGCA ACTTTGAGC GGAATACGCG
1551 GATGTTCCGG GGAGAAGTCC TGCAAACCCCT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTCTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTCTTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAGCC
1751 GTATTTTGGG CGGCGCGACG GGGGAAGAGC GTTCCGCGC CGGCATCGGT
1801 CAGAAATTCT ATTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGTCGG
1851 CAAAAAACCG CGCAACCGTT CCGACTGGGT GGCATTGGCC TCCGGCAGCA
1901 TCGGCAGCCG CTTTATCCTC GACAGCAGCA TCCACTACAA CAAAACGAC
1951 AAACGCGCCG AGAACTACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCCGCT ACAAAATACG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCCTAT TTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAAGCAG TTGCGGCTGC TGGGCGCGCG CCGTGACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTCG GCAGAAACCC CGCAGACAGG ATGGATGTCG
2351 CCGTTCCCGG CTATATCACC GCCCACTCTC TTTCCGCCGG ACGCAACAAA
2401 CGACCTGTA

```

This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

m958.pep

```

1 LARLFLSKPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
51 PLSLSLSTGC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
101 SQQVQRAEGN VVERNRRTL NTDWADYDQS GDTVTAGDRF ALQQDGLTIR
151 GETLTYNLEQ QTGEAHNVRM EIEQGGRRLO SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAVFVGGVP IFYTPWADFP
251 LDGNRKSGLL VPSLSAGSDG VLSVPYYFN LAPNLDTFA PSVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWOHR HDISDTLQAG
351 VDENQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSNLNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSVEWRKN TGRAQIGVSA QFTRFSDLSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNIDSGA TFERNTRMFG GEVLQTLLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGQLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKEYFKDDAV MLDGSGVKKP RNRSDWVAFS SGSIGSRFIL DSSIHNQND
651 KRAENYAVGA SYRPAQGVKL NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVL GAKEYSSCGC WGAGVYAQRY
751 VTGENTYKNA VFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

1372

m958/g958 89.3% identity in 802 aa overlap

m958.pep	10	20	30	40	50	60
	LARLFSLKPLVLALGLCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC					
g958	LARLFSLKPLVLALGLCFGTHCAA-DTVAEEADGRVAEGGAQGASESAQASDLTLGSTC					
	10	20	30	40	50	
m958.pep	70	80	90	100	110	120
	LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL					
g958	LFCSNESGSPERTEAAVQGSGEASVPEDYTRIVADRMEGQSKVKVRAEGSVIIERDGAVL					
	60	70	80	90	100	110
m958.pep	130	140	150	160	170	180
	NTDWADYDQSGDVTVTAGDRFALQQDGTILIRGETLTYNLEQQTGEAHNVMEIEQGGRRRLQ					
g958	NTDWADYDQSGDVTVTGDRFALQQDGTILIRGETLTYNLDQQTGEAHNVRMETEQGGRRRLQ					
	120	130	140	150	160	170
m958.pep	190	200	210	220	230	240
	SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKGIGVAKHAAAFVFGGVP					
g958	SVSRTAEMLGEGRYKLTETQFNTCSAGDAGWYVKAASVEADRGKIGVAKHAAAFVFGGVP					
	180	190	200	210	220	230
m958.pep	250	260	270	280	290	300
	IFYTPWADFPDGNRKSGLLVPSLSAGSDGVSLSVPYYFNLPNLDATFAPSVIGERGAV					
g958	IFYTPWADFPDGNRKSGLLVPSVSAGSDGVSLSVPYYFNLPNLDATFAPGIIGERGAT					
	240	250	260	270	280	290
m958.pep	310	320	330	340	350	360
	FDGQVRYLRPDYAGQSDLTWLPDCKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG					
g958	FDGQIRYLRPDYSGQDLTWLPDCKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG					
	300	310	320	330	340	350
m958.pep	370	380	390	400	410	420
	YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
g958	YYRDFYGGEEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVQKYQTLANQSGYKDEPYAIM					
	360	370	380	390	400	410
m958.pep	430	440	450	460	470	480
	PRLSVEWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH					
g958	PRLSADWHKNAGRAQIGVSAQFTRFSHDGRQDGSRLVVYPGIKWDFSNSWGYVRPKLGLH					
	420	430	440	450	460	470
m958.pep	490	500	510	520	530	540
	ATYYSLNRFSGQEARRVSRTLPIVNIDSGATFERNTRMFGGEVLQTLEPRLFYNYIPAKS					
g958	ATYYSLDSFGGKASRSVGRVLPVVNIDGGTTFERNTRLFGGGVVQTIEPRLFYNYIPAKS					
	480	490	500	510	520	530
m958.pep	550	560	570	580	590	600
	QNDLPNFDSESSFGYGQLFRENLYYGNDRINTANSLSAAVQSRILDGATGEERFRAGIG					
g958	QNDLPNFDSESSFGYGQLFRENLYYGNDRINAANSLSTAVQSRILDGATGEERFRAGIG					
	540	550	560	570	580	590
m958.pep	610	620	630	640	650	660
	QKFFYKDDAVMLDGSVGGKPNRSDWVAFASGSGSRFILDSSIHYNQNDKRAENYAVGA					
g958	QKFFYKDDAVMLDGSVGGKPNRSDWVAFASGGIGGRFTLDSSIHYNQNDKRAEHYAVGA					
	600	610	620	630	640	650
m958.pep	670	680	690	700	710	720
	SYRPAQGVNLNARYKYGRNEKIYKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF					
g958	GYRPAQGVNLNARYKYGRNEKIYQADGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF					
	660	670	680	690	700	710



1373

```

              730      740      750      760      770      780
m958 . pep    EAKKPIEVLAGEYKSSCGCWAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR
              |||||
g958          EAKKPIEVLAGEYKSSCGCWAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPAGR
              720      730      740      750      760      770

              790      800
m958 . pep    MDVAVPGYITAHSLSAGRNRKP
              |||||
g958          MDVAVPGYIPAHSLSAGRNRKPX
              780      790      800

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

```

a958 . seq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCGGCACG CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGGA AGCGTTCGGA GCGTGTCCGA ACCCATAACG
151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTCGA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAATCG
351 GACGACCCTC AATGCCGATT GGGCGGATTA CGACCAGTCG GGCGACACCG
401 TTACCGCAGG CGACCGGTTC GCCCTCCAAC AGGACGGTAC GCTGATTTCG
451 GGCAGAAACC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGTATG GAAACCGAAC ACGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCCGCTTC
651 CGTCGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CAGCCCGCCT
701 TCGTGTTCGG CGGCGTTCCC ATTTTCTACA CCCCTTGGGC GGACTTTCCG
751 CTTGACGGCA ACCGCAAAAG CGGCCTGCTC GTTCCCTCAC TGTCGCCGG
801 TTCGGACGGC GTTTCCTTT CCGTCCCTTA TTATTTCAAC CTTGCCCCCA
851 ATCTCGATGC CACGTTCGCG CCCGGCGTGA TCGGCGAACG CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGCCG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CCGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCACCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTC AACAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCGG CAGGCGCGCG GCGGCGAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAGC GGTACAAAG ACAACCGTA
1251 TGCCCTGATG CCGCGCCTTT CCGCCGATTG GCGCAAAAC ACCGGCAGGG
1301 CGCAAAATCG CGTGTCCGCC CAATTTACCC GCTTCAGCCA CGACAGCCGC
1351 CAAGACGGCA GCCGCCTCGT CGTCTATCCC GACATCAAAT GGGATTTCAG
1401 CAACAGCTGG GGTACGTCC GTCCCAAAC CCGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCGCAGCGCT CAGCCGCACT
1501 CTGCCATCG TCAACATCGA CAGCGGCATG ACCTTCGAAC GCAATACGCG
1551 GATGTTCCGG GCGCGAGTCC TGCAAAACCT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTGTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTTTT CGTGAAAAC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCGCCGCC GTGCAAGGCC
1751 GTATTTTGGG CGGCGCGACG GGGGAAGAGC GTTCCGCGC CGGCATCGGG
1801 CAGAAATTCT ACTCAAAAA CGACGCAGTC ATGCTTGACG GCAGTGTCCG
1851 CAAAAAACCG CGCAGCGGTT CCGACTGGGT GGCATTGCGC TCCAGCGGCA
1901 TCGGCGAGCG CTTTATCCTC GACAGCAGCA TCCAATAACA CCAAAACGAC
1951 AAACGCGCCG AGAACTACGC CGTCGGTGCA AGTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCCGCT ACAAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAGCAG TTGCGGCTGC TGGGCGCGG CGGTGTACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTGC GCAGAAACCC CGCAGACAGG ATGGATGTGC
2351 CCGTCCCGG CTATATCCCC GCCCACTCTC TTTCCGCCGG ACGCAACAAA
2401 CGGCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

```

a958 . pep
1  LARLFLKPL VLALGFCEFT HCAAADAVAA EETDNPTAGG SVRSVSEPIQ
51  PLSLSLSTC LFCNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
101 SQVQVRAEGN VVVERNRTTL NADWADYDQS GDTVTAGDRF ALQQDGTLLR
151 GETLTYNLEQ QTGEAHNVRM ETEHGGRRLLQ SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFVFGGVP IFYTPWADFP

```

```

251 LDGNRKSGLL VPSLSAGSDG VSLSVPPYFN LAPNLDTFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSLNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAQIGVSA QTFRSHDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNIDSGM TFERNTRMFG GGVLTQLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKNDV MLDGSVGKKP RSRSDWVAF SSGIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYLSKDSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRNYGF EAKKPIEVL GAEEKSSCGC WGAGVYAQRV
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 98.1% identity in 802 aa overlap

a958.pep	10	20	30	40	50	60
	LARLFS	SLKPLVL	ALGFCFG	THCAAADA	VAAEETDN	NPTAGGSV
m958	10	20	30	40	50	60
	LARLFS	SLKPLVL	ALGFCFG	THCAAADA	VAAEETDN	NPTAGESV
a958.pep	70	80	90	100	110	120
	LFCSNES	GSPERTEA	AVQGSGE	ASIPEDY	TRIVADR	MEGQSQV
m958	70	80	90	100	110	120
	LFCSNES	GSPERTEA	AVQGSGE	ASIPEDY	TRIVADR	MEGQSQV
a958.pep	130	140	150	160	170	180
	NADWADY	DQSGDVT	AGDRFAL	QQDGLT	IRGETLT	YNLEQQT
m958	130	140	150	160	170	180
	NTDWADY	DQSGDVT	AGDRFAL	QQDGLT	IRGETLT	YNLEQQT
a958.pep	190	200	210	220	230	240
	SVSRTAE	MLGEGHY	KLTTETQ	FNTCSAG	DAGWYV	KAAASVE
m958	190	200	210	220	230	240
	SVSRTAE	MLGEGHY	KLTTETQ	FNTCSAG	DAGWYV	KAAASVE
a958.pep	250	260	270	280	290	300
	IFYTPWA	DFPLDGN	RKSGLLV	PVSLSAG	SDGVSL	SVPPYFN
m958	250	260	270	280	290	300
	IFYTPWA	DFPLDGN	RKSGLLV	PVSLSAG	SDGVSL	SVPPYFN
a958.pep	310	320	330	340	350	360
	FDGQVRY	LRPDYAG	QSDLTWL	PHDKKSG	RNNRYQ	AKWQHRH
m958	310	320	330	340	350	360
	FDGQVRY	LRPDYAG	QSDLTWL	PHDKKSG	RNNRYQ	AKWQHRH
a958.pep	370	380	390	400	410	420
	YYRDFY	GNKEIAG	NVNLNRR	VWLDYGG	RAGGSL	NAGLSVL
m958	370	380	390	400	410	420
	YYRDFY	GNKEIAG	NVNLNRR	VWLDYGG	RAGGSL	NAGLSVL
a958.pep	430	440	450	460	470	480
	PRLSAD	WRKNTGR	AQIGVSA	QFTRFS	HDSRQD	GSRLVVY
m958	430	440	450	460	470	480
	PRLSVE	WRKNTGR	AQIGVSA	QFTRFS	HDSRQD	GSRLVVY
a958.pep	490	500	510	520	530	540
	ATYYSL	NRFSGQ	EARRVSR	TLPIVN	IDSGMT	FERNTRM
m958	490	500	510	520	530	540
	ATYYSL	NRFSGQ	EARRVSR	TLPIVN	IDSGMT	FERNTRM

1375

	490	500	510	520	530	540
a958.pep	550	560	570	580	590	600
m958	QNDLPNFDSESSFGYQOLFRENLYYGNDRI	TANSLAAVQSRILDGATGEERFRAGIG				
	550	560	570	580	590	600
a958.pep	610	620	630	640	650	660
m958	QKFYFKNDVMDGSGVGGKPRSRSDWVAFAS	SGISRFILDSSIHYNQNDKRAENYAVGA				
	610	620	630	640	650	660
a958.pep	670	680	690	700	710	720
m958	SYRPAQGGKVLNARYKYGRNEKIYKSDGSY	FYDKLSQLDLSAQWPLTRNLSAVVRYNYGF				
	670	680	690	700	710	720
a958.pep	730	740	750	760	770	780
m958	EAKKPIEVLAGAIEYKSSCGCWGAGVYAQR	YVTGENTYKNAVFFSLQLKDLSSVGRNPADR				
	730	740	750	760	770	780
a958.pep	790	800				
m958	MDVAVPGYIPAHSLSAGRNRKP					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

g959.seq  
 1 ATGAACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTGGG  
 51 CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC  
 101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC  
 151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA  
 201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG  
 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC  
 301 GTGATTTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2936; ORF 959.ng>:

g959.pep  
 1 MNIKHLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR  
 51 AQAEKAAR VGGKITDIDL EHDGRPHYD VEIVKNGQEY KVVVDARTGR  
 101 VISSRRDD\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

m959.seq  
 1 ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG  
 51 CATTTCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC  
 101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC  
 151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA  
 201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG  
 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC  
 301 GTGATTTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2938; ORF 959>:

m959.pep  
 1 MNIKHLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR  
 51 AQAEKAALR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR  
 101 VISSRRDD\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*

1376

m959/g959 95.4% identity in 108 aa overlap

```

      10      20      30      40      50      60
m959.pep  MNIKHLLLSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEKAALAR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g959      MNIKHLLLSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEKAALAR
          10      20      30      40      50      60

      70      80      90     100     109
m959.pep  VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g959      VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
          70      80      90     100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

```

a959.seq
1  ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51 CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2940; ORF 959.a>:

```

a959.pep
1  MNFKRLLLLTA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

```

      10      20      30      40      50      60
a959.pep  MNFKRLLLLTAATALMGISAPALAHHDGHGDDDHGHAHQHSKQDKIISRAQAEKAALAR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m959      MNIKHLLLSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEKAALAR
          10      20      30      40      50      60

      70      80      90     100     109
a959.pep  VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m959      VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
          70      80      90     100

```

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

```

m960.seq
1  ATGCAAGTAA ATATTCAGAT TCCCTGTATG CTGTACAGAC GCGGGAGTGT
51 TAAGCCCCC TTGTTTGAAG CTCCGCGGCT CTGCGGAGC TTCACCGACC
101 CCGTGTGCC CAAGCTCTCT GCTCCCGGCG GCTACATTGT CGACATCCCC
151 AAAGGCAATC TGAAAACCGA AATCGAAAAG CTGGCCAAAC AGCCCGAGTA
201 TGCCTATCTG AACAGCTCC AAGTAGCGAA AAACGTCAAC TGGAACCAGG
251 TGCAACTGGC TTACGATAAA TGGGACTATA AGCAGGAAGG CTTAACCAGA
301 GCCCGTGCAG CGATTATCGC GCTGGCTGTT ACCGTGGTTA CTGCGGGCGC
351 GGGAGTCGGA GCCGCACTAG GCTTAAACGG CGCAGCCGCA GCAGCGGCCG
401 ATGCCGCCCTT TGCCTCACTC GCTTCTCAGG CTTCCGTATC GCTCATCAAC
451 AATAAAGCG ATGTCGGCAA AACCTGAAG GAACTGGGCA GAAGCCGCAC
501 GGTAAAAAT CTGTTGTAG CGCGGCGAAC GGCAGGCGTA TCCAACAAAC

```

```

551 TCGGTGCCTC TTCCCTTGCC ACTTGAGCG AAACCCCTTG GGTAAACAAC
601 CTCAACGTGA ACCTGGCCAA TCGGGGCAGT GCCGCGCTGA TCAACACCGC
651 TGTTAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAAT ATCCTGGCGG
701 CATTGGTGAA TACCGCGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
751 GATCAGCACT ATGTCGCCCA CAAAATCGCT CATGCCGTAG CGGGCTGTGC
801 GGCTGCAGCG GCGAATAAGG GCAAAATGTCA GGACGGCGCG ATCGGTGCGG
851 CTGTGGGTGA GATTGTCGGG GAGGCTTTGG TTAATAATAC CGATTTTAGC
901 GATATGACCC CGGAACAATT AGATCTGGAA GTTAAGAAAA TTACCGCCTA
951 TGCCAAACTT GCGGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATACTGCTGC ACAAACCGCA CAAAACGCGG TAGAAAAATA TCGGTTTAAA
1051 GCTGTTGTAA CTGCTGCAAA AGTGGTTTAT AAGGTAGCCA GAAAAGGATT
1101 AAAAAACGGG AAAATCAACG TTAGAGATT AAAACAGACG TTGAAAGACG
1151 AAGGTTATAA TTTAGCCGAC AACCTGACCA CCTTATTCGA CGAAACATTG
1201 GATTGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTCG GAACAGAGCT
1251 GAATCGCGCT AATAAAGGGG AAGCGGCACA AAAGGTCAAG GAAGTTTATG
1301 AAAAAAATCG TCCTTATATC CCTAATAAAG GTGCTGTACC GAATATGAGT
1351 ACATACATGA AAAATAATCC TTTTGGAAAA CAGCTGGCTC AAATTCAGA
1401 AAAGACAACG CTTCCGACGC AGCAAGGGCA GTCTGTCTTC TTGGTAAAAA
1451 GAAACCAAGG GTTATTAAAA ACCGGTGATA GGTTTTATTT AGATGGCCAA
1501 CATAAAAAATC ATTTAGAGGT TTTTGATAAA AATGGGAAC TTAAGTTTGT
1551 TCTAAATATG GATGGTTCGC TTAACCAAAT GAAAACTGGG GCAGCAAAAG
1601 GTCGTAATTT AAACTTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

```

m960.pep
1  MQVNIQIPCM LYRRGSVKPP LFEAPRLLPS FTDPVVPKLS APGGYIVDIP
51  KGNLKTEIEK LAKQPEYAYL KQLQVAKNVN WNQVQLAYDK WDYKQEGLTR
101 AGAAIIALAV TVVTAGAGVG AALGLNGAAA AAADAFAFSL ASQASVSLIN
151 NKGDVGKTLK ELGRSRTVKN LVVAAATAGV SNKLGASSLA TWSETPWVNN
201 LNVNLNAGS AALINTAVNG GSLKDNLEAN ILAALVNTAH GEASIKIKGL
251 DQHYVAHKIA HAVAGCAAAA ANKKGKQDGA IGAAVGEIVG EALVKNTDFS
301 DMTPEQLDLE VKKITAYAKL AAGTVAGVTG GDVNTAAQTA QNAVENNAVK
351 AVVTAAKVVY KVARGLKNG KINVRDLKQT LKDEGYNLAD NLTLTFDETL
401 DWNDAKAVID IIVGTENLRA NKGEAAQVKV EVLEKNRPYI PNKGAVPNMS
451 TYMKNNPFGK QLAQISEKTT LPTQQGQSVF LVKRNQGLLK TGRFYLDGQ
501 HKNHLEVFDK NGNEKFVLNM DGSINQMKTG AAKGRKLNLK *

```

a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

```

m961.seq
1  ATGAGCATGA AACACTTTC AGCCAAAGTA CTGACCACAG CCATCCTTGC
51  CACTTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAAA
101 AAGCTGCCAC TGTGGCCATT GTTGCTGCCT ACAACAATGG CCAAGAAATC
151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCAA AAAGACGCAA CTGCAGCCGA TGTGAAGCC GACGACTTTA
251 AAGGTCTGGG TCTGAAAAAA GTCGTGACTA ACCTGACCAA AACCGTCAAT
301 GAAACAAAC AAAACGTCGA TGCCAAAGTA AAAGCTGCAG AATCTGAAAT
351 AGAAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCCG TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
451 AATATAACGA CATTGCTGA AGAGACTAAG ACAAAATATG TAAAAATTGA
501 TGAAAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
601 GCGCTCAAAA CCGCCAATGA AGCCAAACAG ACGGCCGAAG AAACCAAAACA
651 AAACGTCGAT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAGCCG
701 AAGCTGCCGC TGGCACAGCT AATACTGCAG CCGACAAGGC CGAAGCTGTC
751 GCTGCAAAAAG TTACCGACAT CAAAGCTGAT ATCGCTACGA ACAAAGCTGA
801 TATTGCTAAA AACTCAGCAC GCATCGACAG CTTGGACAAA AACGTAGCTA
851 ATCTGCGCAA AGAAACCCGC CAAGGCCTTG CAGAACAAGC CGCGCTCTCC
901 GGCTGTCTCC AACCTTACAA CGTGGGTCGG TTCAATGTAA CGGCTGCAGT
951 CGGCGGTAC AAATCCGAAT CGGCAGTCGC CATCGGTACC GGCTTCCGCT
1001 TTACCGAAAA CTTTGGCCGC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
1051 GGTTCCTCCG CAGCCTACCA TGTCGGCGTC AATTACGAGT GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

```

m961.pep
1  MSMKHFPKAV LTTAILATFC SGALAATSDD DVKKAATVAI VAAAYNNGQEI

```

1378

```

51  NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKK VVTNLTKTVN
101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LADTDAALDE TTNALNKLGE
151 NITTFAEETK TNIVKIDEKL EAVADTVDKH AEA FN DIADS LDETNTKADE
201 AVKTANEAKQ TAEETKQNV D AKV KAAETAA GKAEAAAGTA NTAADKAEAV
251 AAKVTDIKAD IATNKADIAK NSARIDSLDK NVANLRKETR QGLAEQAALS
301 GLFQPYNVGR FNVTAAGGY KESAVAIGT GFRFTENFAA KAGVAVGTSS
351 GSSAAYHVG V NYEW*

```

a961.seq not found yet  
a961.pep not found yet

g972.seq not found yet  
g972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:

```

m972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTC GArGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCAGGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTATAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAGAA AGCAAATGGG TAAGGTTCTG GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTGATCAG AGAAAGAAAA AGCTTAATTT AACTTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAAAC TGG TCAATTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAATTT GAACCTGATG AATTGGGGGT TATTGCTTTT AAAAATCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAAATGT
1251 AGATTATGAT TATTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:

```

m972.pep
1  LTNRGGAKLK TXSKSSERMS EVEYFSHFIS DGKGLLEIP QRRGKQDGVF
51  VDWSIFTFHE DTLKVS GCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFGXQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FPDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNE DSGKTFYVGR KKNRFRVRY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFICRKF NMPVPERFDQ RKKKLNLTFE
301 HKLHYAKNAV GKLNVFMIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVVHQNVDDY YF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:

```

a972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CGGGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

```

1379

```

251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTCG GAGGTGAGCG CAATACTGTT TTAGTTGAGT
401 TGAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCCTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTTTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAGAA AGCAAATGGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCGAAAG GTTGATCAG AGAAAGAAA CGCTTAATTT AACTTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAAACCTG TCAATTTTAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAGGCAG
1001 ATTCCGGGAT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAATG
1051 TTAAGGGACG GTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAATG GAACCTGATG AATTGGGGT TATTGCTTTT AAAAATCTG
1151 ACAAATTCGA TAGGGAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2948; ORF 972.a>:

```

a972.pep
1  LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGKKGKLEIP QRRGKQDGVF
51  VDWSIFTFHE DTLKLVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GKFYESMYR LGSDDVDYGE VHFGGQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNE DSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFPICRKF NMPVPERFDQ RKKTNLNLTFE
301 HKLHYAKNAV GKLVNFMIE MGFNDSEIVE LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVVHQNVDYD YF*

```

m972/a972 99.3% identity in 422 aa overlap

	10	20	30	40	50	60
m972.pep	LTNRGGAKLKTXXSKSSERMSEVEYFSHFISDGKKGKLEIPQRRGKQDGVFVDWSIFTFHE					
a972	LTNRGGAKLKTNSKSSERMSEVEYFSHFISDGKKGKLEIPQRRGKQDGVFVDWSIFTFHE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m972.pep	DTLLKVS GCPLFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDDVDYGE					
a972	DTLLKVS GCPLFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDDVDYGE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m972.pep	VHFGXQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RTITRIDLALDFFDGEYTPDQ					
a972	VHFGGQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RTITRIDLALDFFDGEYTPDQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m972.pep	ALLDHDNGFFDNSNQRPKSETIGTAWRNE DSGKTFYVGRKKNSRFVRVYEKGRQLGDKE					
a972	ALLDHDNGFFDNSNQRPKSETIGTAWRNE DSGKTFYVGRKKNSRFVRVYEKGRQLGDKE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m972.pep	SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFPICRKFKNMPVPERFDQRKKTLNLTFE					
a972	SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFPICRKFKNMPVPERFDQRKKTLNLTFE					
	250	260	270	280	290	300

1380

	310	320	330	340	350	360
m972 . pep	HKLHYAKNAVGKLVNFMIE	MGFDNSEIVESLKADSGFP	KGLEPEKYALEMLRDGLKH	GFI		
a972	HKLHYAKNAVGKLVNFMIE	MGFDNSEIVESLKADSGFP	KGLEPEKYALEMLRDGLKH	GFI		
	310	320	330	340	350	360
	370	380	390	400	410	420
m972 . pep	HEQPDIDLEIELDELGVIA	FKNSDKFDR	EKRFLSPDYDVE	KERKYQEYLSKVYHQ	NVDYD	
a972	HEQPDIDLEIELDELGVIA	FKNSDKFDR	EKRFLSPDYDVE	KERKYQEYLSKVYHQ	NVDYD	
	370	380	390	400	410	420

m972 . pep	YFX
a972	YFX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:

```

g973 . seq
1  ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCC
51  actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGGCTGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATGCCA TGATTACGCG
201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATCACCG
251 CCTACGTCAT CGATACCGCC CATTGCGCGT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTTGCGC CTGCGCGTTT
401 TCGTGCCCGA AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
501 TTTGGTCACC TTTGAAGACA TCATCGAGCa aatcgctcggg gacatCGAAG
551 ACGAGTTTGA CGAAGACGAA AGCGccgacg acatCCACTC cgTTTccgCC
601 GAACGCTGGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCTT
651 TTTCCGTACG GAatacggca gcaagaagc cgacaccatc ggcggctTGG
701 TCATTACAGG ATTGGGACAC CTGCCCGTGC GCGCGAATAA AGTCCTTatc
751 ggcgGTTTGC agttcacgct CGCCCGCGCC GACAACCGCC GCCTGCACAC
801 GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCcgc accgcggttT
851 CTGCacAGTT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:

```

g973 . pep
1  MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLROAHEQEV FDADTLTRLE
51  KVLDFAELEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFPN EQFHLKSVLR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTGLVT FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
201 ERWRIHAATE IEDINAFFGT EYGSEADTI GGLVIQELGH LPVRGEKVL I
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:

```

m973 . seq
1  ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCC
51  ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA GCAGGAAGTT TTTGATGCCG ATACGCTTTT AAGATTGGAA
151 AAAGTCCTCG ATTTTCCGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAG CGCATCACCG
251 CCTACGTTAT CGATACCGCC CATTGCGCGT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTTAACCCC GAGCAGTTCC ACCTCAAATC CATTCTCCGC CCCGCCGTCT
401 TCGTCCCGGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTATCGAC GAATACGGCG GCACATCCGG
501 CTTGGTCACC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
551 ACGAGTTTGA CGAAGACGAT AGCGCCGACA ATATCCATGC CGTTTCTTcm
601 GaACGcTGGC GCATCCATGC AGCTACCGAA ATCGAAGACA TCAACACCTT

```



1381

651 CTTCGGCAGC GAATACAGCA kCGAAGAAGC CGACACCATT GCGGCGCTGG  
 701 TCATTCAAGA GTTGGGACAT CTGCCCCGTGC GCGGCGAAAA AGTCCTTATC  
 751 GCGCGTTTGC AGTTACACCGT CGCACGCGCC GACAACCGCC GCCTGCATAC  
 801 GCTGATGGCG ACCCGCGTGA AGTAA

This corresponds to the amino acid sequence <SEQ ID 2952; ORF 973>:

m973.pep

1 MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLRLLE  
 51 KVLDFSDLEV RDAMITSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED  
 101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE  
 151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG BIEDEFDEDD SADNIHAVSS  
 201 ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIQELGH LPVRGEKVL  
 251 GGLQFTVARA DNRRLHTLMA TRVK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 973 shows 95.6% identity over a 274 aa overlap with a predicted ORF (ORF 973.ng) from *N. gonorrhoeae*:

m973/g973

m973.pep	10	20	30	40	50	60
	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
g973	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFAELEV					
	10	20	30	40	50	60
m973.pep	70	80	90	100	110	120
	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
g973	RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
m973.pep	130	140	150	160	170	180
	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVID EYGGTSGLVT FEDIIEQIVG					
g973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVID EYGGTSGLVT FEDIIEQIVG					
	130	140	150	160	170	180
m973.pep	190	200	210	220	230	240
	BIEDEFDEDD SADNIHAVSS ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIQELGH					
g973	DIEDEFDEDESADDIHSVSAERWRIHAATE IEDINAFGT EYGSSEADTI GGLVIQELGH					
	190	200	210	220	230	240
m973.pep	250	260	270			
	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
g973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2953>:

a973.seq

1 ATGGACGGCG CACAACCGAA AACAAATTT TTTGAACGCC TGATTGCCCG  
 51 ACTCGCCCGC GAACCGGATT CCGCCGAAGA CGTATTGACC CTGTTGCGCC  
 101 AAGCGCACGA ACAGGAAGTA TTTGATGCGG ATACGCTTTT AAGATTGGAA  
 151 AAAGTCCTCG ATTTTCTGA TTTGGAAGTG CGCGACGCGA TGATTACGCG  
 201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAA CGCATCACCG  
 251 CCTACGTTAT CGATACCGCC CATTGCGGCT TCCCGTCAT CGGTGAAGAC  
 301 AAAGACGAAG TTTTGGGTAT TTTGCACGCC AAAGACCTGC TCAAATATAT  
 351 GTTCAACCCC GAGCAGTTCC ACCTCAAATC GATATTGCGC CCTGCCGTCT  
 401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAGA GTTCCGCGAA  
 451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG  
 501 TTTGGTAACT TTTGAAGACA TCATCGAGCA AATCGTCGGC GACATCGAAG  
 551 ATGAGTTTGA CGAAGACGAA AGCGCGGACA ACATCCACGC CGTTTCCGCG

1382

```

601 GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
651 TTTCGGCAGC GAATACAGCA GCGAAGAAGC CGACACCATC GGCGGCCTGG
701 TCATTGAGGA ATTGGGACAC CTGCCCGTGC GCGGCGAAAA AGTCCTTATC
751 GCGGCTTTCG AGTTCACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

```

a973.pep
1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLRLLE
51 KVLDFSDLEV RDMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVILGILHA KDLLKYMFPN EQFHLKSILR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGGLVT FEDIEEQIVG DIEDEFDEDE SADNIHAVSA
201 ERWRIHAATE IEDINAFFFT EYSSEEADTI GGLVIQELGH LPVRGEKVL
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

m973/a973 97.8% identity in 274 aa overlap

	10	20	30	40	50	60
m973.pep	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
a973	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m973.pep	RDMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVILGILHAKDLLKYMFPN					
a973	RDMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVILGILHAKDLLKYMFPN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGGLVTFEDIEEQIVG					
a973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGGLVTFEDIEEQIVG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m973.pep	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
a973	DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFFFTGSSEEADTIGGLVIQELGH					
	190	200	210	220	230	240
	250	260	270			
m973.pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
a973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

```

g981.seq
1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCAC TCGCGCTGTC
51 TGCCGTGCGC GGTCAGGGCA AAGATGCCGC CGCGCCTGCC GCCAACCCCG
101 GCAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TAAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCCTCTG AACCAACGCG ATGCGGACGT TGTGATGTCG
301 GGCCTAACCA TTACCGACGA CCGCAAACAG TCTATGGATT TCAGCGACCC
351 GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTTCTCCGA AGATTGAAA AAGATGAACA AAGTCGGCGT GGTACCAGGC
451 CACACGGGCG ATTTCTCCGT TTCCAAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTCGAAAACG TCCCCTGAT TATCAAAGAA CTGAAAACG
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTATCGC CAATTATGTG
601 AAAAAACAAC CGGCCAAAGG AATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATCTACG CCAAATATTT TGCCAAAGAG GCGGACAGG CTGCGAAATA
801 A

```

1383

This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

```
g981.pep
1  MKKWIAAALA CSALALSACG GQKDAAPA ANPGKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWSLFPAL NNGDADVMS
101 GVTITDDRQK SMDFPSDPYE ITQVVLVPGK KKVSSSEDLK NMNKVGVTG
151 HTGDFSUSKL LGNDNPFIAR FENVPLIIEK LENGGLDSV SDSAVIANV
201 KNNPAKGMDF VTLPDFTTEH YGIAVRKGE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE GQAAK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

```
m981.seq
1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTGAGGGCA AAGATACCGC CGCGCTGCC GCCAACCCCG
101 ACAAGTGTGA CCGCGTGGCT TCCAACCGCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAATACTGA ATCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCGCGCTTA AACACGCGC ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCAACCAAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTTCTTCCGA AGATTGAAA AACATGAACA AAGTCGGCGT GGTAACCGGC
451 TACACGGGCG ATTTCTCCGT ATCCAAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAACG
551 GCGGCTTGA TTCCGTGGTC AGCGACAGCG CGGTCATGCG CAATTATGTG
601 AAAACAAATC CGGCAAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATTACG CCAATATTT TGAAAAGAA GACGACAGG CCGCAAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

```
m981.pep
1  MKKWIAAALA CSALALSACG GQKDTAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWSLFPAL NNGDADVMS
101 GVTITDDRQK SMDFPSDPYE ITQVVLVPGK KKVSSSEDLK NMNKVGVTG
151 YTGDFSUSKL LGNDNPFIAR FENVPLIIEK LENGGLDSV SDSAVIANV
201 KNNPAKGMDF VTLPDFTTEH YGIAVRKGE ATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE DGQAAK*
```

m981/g981 98.1% identity in 266 aa overlap

```

      10      20      30      40      50      60
981.pep  MKKWIAAALACSALALSACGGQKDTAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF
          |||
981      MKKWIAAALACSALALSACGGQKDAAPAANPGKVYRVASNAEFAPFESLDSKGNVEGF
      10      20      30      40      50      60

      70      80      90      100     110     120
981.pep  DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQKSMDFSDPYFE
          |||
981      DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQKSMDFSDPYFE
      70      80      90      100     110     120

      130     140     150     160     170     180
981.pep  ITQVVLVPGKKVSSSEDLKNNMKVGVTGYTGDFSUSKLLGNDNPFIARFENVPLIIEK
          |||
981      ITQVVLVPGKKVSSSEDLKNNMKVGVTGHTGDFSUSKLLGNDNPFIARFENVPLIIEK
      130     140     150     160     170     180

      190     200     210     220     230     240
981.pep  LENGGLDSVSDSAVIANVYKNNPAKGMDFVTLPDFTTEHYGIAVRKGEATVKMLNDAL
          |||
981      LENGGLDSVSDSAVIANVYKNNPAKGMDFVTLPDFTTEHYGIAVRKGEATVKMLNDAL
      190     200     210     220     230     240

      250     260
981.pep  EKVRESGEYDKIYAKYFAKEDGQAAKX
          |||
981      EKVRESGEYDKIYAKYFAKEGGQAAKX
      250     260
```

1384

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2959>:

```
a981.seq
1   ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTCAAGGTA AAGATGCCGC CGCGCCCGCC GCAAATCCCG
101 ACAAAAGTGA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCGCCTTG AACACGGCG ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCCTAG TCGTCCTCGT TCCGAAAGGC AAAAAATAT
401 CTTCTTCCGA AGATTGAAA AACATGAACA AAGTCGGCGT GGTAAACCGGC
451 TACACGGGCG ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCCTGAT TATCAAAGAA CTGGAACACG
551 GCGGCTTGGA TTCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAACAATC CGACCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAATATTT TGCAAAGAA GACGGACAGG CCGCAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

```
a981.pep
1   MKKWIAAALA CSALALSACG GQGKDAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101 GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKISSSEDLK NMNKVGVTG
151 YTGDFSVS KL LGNDNPKIAR FENVPLIIE LENGGLDSV SDSAVIANV
201 KNNPTKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL KKVRESGEYD
251 KIYAKYFAKE DGQAAK*
```

m981/a981 98.5% identity in 266 aa overlap

	10	20	30	40	50	60
m981.pep	MKKWIAAALACSALALSACGGQGKDTAAPANPDKVYRVASNAEFAPFESLDSKGNVEGF					
a981	MKKWIAAALACSALALSACGGQGKDAAPANPDKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
m981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKSMDFSDPYFE					
a981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKSMDFSDPYFE					
	70	80	90	100	110	120
m981.pep	ITQVVLVPKGKVSSEDLKNMNKVGVTGYTGDFSVS KLLGNDNPKIARFENVPLIIE					
a981	ITQVVLVPKGKISSSEDLKNMNKVGVTGYTGDFSVS KLLGNDNPKIARFENVPLIIE					
	130	140	150	160	170	180
m981.pep	LENGGLDSVSDSAVIANVKNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
a981	LENGGLDSVSDSAVIANVKNPTKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
m981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
a981	KKVRESGEYDKIYAKYFAKEDGQAAKX					
	250	260				

1385

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

```

g982.seq
1  atcgcacgcg aaaaaccttcg attcgacaat cgattcctcc aaaaaatggt
51  caacggcgTg aatatatttgc cggccgcCga ttgggtagcC ttgGGcgCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TAAAAGAAGT CGCGTCCAAA ACCAACgagCg
251 tagCCGgcga cggtagcact accgCCACCG TATTGGCACA ATCCATCGTT
301 GCCGAAGgca TGAATACGT TACCGCCGGC ATGAACCGA CCGATCTGAA
351 ACGCGGCATC GACAAAGccg ttgCCGCTtt ggttgAAGAg cTGA AAAACA
401 TCGCCAAACC TTGCGATACT TCCAAAGAAA TCGCCCAAGT CGGCTCGATT
451 TCCGCCAACT CCGACGAACA AGtcgGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGCG AAAGAAGgcg tgattacCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCCCCTTACT TTATCAACGA CGCGGAAAAA CAAATCGCCG GTCTGGACAA
651 TCCGTTTGTG TTGCTGTTTCG AAAAAAAAT CAGCAACATC CGCGACCTGC
701 TCGCCGTGTT GGAACAAGTG GCGAAAGCCA GCCGCCCGCT GTTGATATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATC CTGAAAACCG TTGCCGTCAA AGCccccggc tTCGGcGACC
851 GCCGCAAAGC GATgctgcaa gaCATCGCCA TCCTGACcgg cggcgTagtG
901 ATTTccGAAG Aagtcggcct GTCTTTGGAA AAagcgactT TGgacgaCTT
951 Gggtcaaacc aaACGcatCG AAATCGGtga agaaaacact ACCGTATcG
1001 acgGCTTCGG CGACGcagcC CAAAtcgaag cgCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCGAC CAGCGATTAC GACAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAATGCGCAG GAGGCGTGGC AGTGATCAA GTCCGCGCGG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGG AGACGCGCTG
1201 CACGCTACCC CGCGAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGCGCT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTAT TCGCGCCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGA GAACCCAGCG TTGGTGGTGAA
1401 CAAAGTGTG GAAGGCAAAG GCAactacgG TTACAACGCa ggctcCGGCG
1451 AATACGgcga CATGATCGGA ATGGGCGTAC TCGACCCTGC CAAAGTAACC
1501 CGTTCGCGC TGCAACACGC CGCGTCTAtc GCCGGTCTGA TGCTGACGAC
1551 CGATGCGATG ATTGCCGAAA TCCCTGAAGA AAAACCGGCT GTGCCCGATA
1601 TGGGGGAAT GGGCGGTATG GGCGGCATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

```

g982.pep
1  IASQNLRFDN RFLQKMVNGV NILPAADWVA LGAKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGTT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAAALVEE LKNIAPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KSLNELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LFDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVVNNIRGI LKTAVKAPG FGDRRKAMLQ DIAILTTGGV V
301 ISEEVLGSLE KATLDDLQGT KRIEIGEENT TVIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGVALL RARAALNLH TGNADQDAGV QIVLRAVES P
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYN A GSGEYDMIG MGVLDPAKVT
501 RSALQHAASI AGLMLTTDCM IAEIPEEKPA VPDMGGMGM GMM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

```

m982.seq
1  ATGGCAGCAA AAGACGTACA GTTCGCAAT GAAGTCGTC AAAAAATGTT
51  AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAGAAGT TCGGTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTGACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGCG AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCTG CTTTGGACAA

```

651	TCCGTTTGTA	TTGTTGTTCC	ACAAAAAAT	CAGCAACATC	CGCGACCTGC
701	TGCCTGTTTT	GGAACAAAGT	GCAAAAGCCA	GCCGTGCGCT	GTTGATTATC
751	GCTGAAGACG	TAGAAGGCCA	AGCCTTGCGC	ACTTTGGTGC	TGAACAACAT
801	CCGAGGCATC	CTGAAAACCG	TTGCCGTCAA	AGCCCCGTGC	TTCCGCGACC
851	CGCGCAAAGC	GATGTTGCAA	GCATCGCCCA	TCTGTACCGG	CTGCGCTGTG
901	ATTTCCGAAG	AAGTCGGTCT	GTCTTTGGAA	AAAGCGACTT	TGGACGACTT
951	GGGTCAAGCC	AAACGCATCG	AAATCGGTAA	AGAAAACACC	ACCATCATCG
1001	ACGGCTATCG	CGACGCAGCC	CAAACTCGAA	GCGCTGTTGC	CGAAATCCGC
1051	CAACAATTGC	AAACCGCAAC	CAGCGATTAC	GACAAGAGAA	AAC TGCAAGA
1101	CGCGCTGGCT	AAATTGGCAG	CGCGCGTGGC	AGTCATCAA	GTCCGCTGCC
1151	CGACCGAAGT	CGAAATGAAA	GAGAAAAAAG	ACCGCGTGGA	AGACGCGCTG
1201	CACGCTACCC	GCGCAGCCGT	TGAAGAAAGC	GTGGTTGCAG	GCGGCGGCGT
1251	AGCCCTGTTG	CGTGCCCCGT	CTGCTTTGGA	AAACCTGCAC	ACCGGCAATG
1301	CCGACCAAGA	CGTAGCGCTA	CAATCTGCTT	TGCGCCCGGT	TGAGTCTCCG
1351	CTGCGCCAAA	TCGTTGCCAA	CGCAGGCGCT	GAACCCAGCG	TGGTTGTGAA
1401	CAAAGTATTG	GAAGGCAAAG	GCAACTACGG	TTACAACGCT	GGCAGCGGCG
1451	AATACGGCGA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAGTACC
1501	CGTTCTGCGC	TGCAACACGC	CGCATCTATC	GCCGGCTTGA	TGCTGACCAC
1551	TGATTGTCAT	ATCCTGTGAA	TCCCCGAAGA	CAAACGGGCT	GTGCCTGATA
1601	TGGGCGGCAT	GGGTGGTATG	GQCGGCATGA	TGTA	

m982.seq

1	ATGGCAGCAA	AAGACGTACA	GTTCCGCAAT	GAAGTCCGTC	AAAAAATGGT
51	AAACGGCGTG	AACATTCTGG	CAAACGCCGT	CCGCGTAACC	TTGGGCCCCA
101	AAGGTCGGA	CTAGTCGTT	GACCCGCGAT	TCGGCGGGCC	GCACATCACC
151	AAAGACGGCG	TACCGCTCGC	CAAGAAGAAAT	GAACTGAAGT	ACAAGTTTGA
201	AAATATGGGC	CGCGAAATGG	TGAAAGAAGT	TGCGTCCAAA	ACCAACGACG
251	TGGCAGGCGA	CGGTACGACT	ACCGCCACCG	TACTGGCGCA	ATCCATCGTT
301	GCCGAAGGTA	TGAATATGTT	TACCGCAGGT	ATGAATCCGA	CCGACCTGAA
351	ACGCGGTATC	GATAAAGCCG	TCGCGCGTTT	GTTGTACGAA	CTGAAAACAA
401	TCGCCAAACC	TTGCGACACT	TCTAAAGAAA	TCGCCCAAGT	CGGCTCTATT
451	TCCGCCAACT	CCGACGAACA	AGTCGGCGCG	ATTATCGCCG	AAGCGATGGA
501	AAAAGTCGGC	AAAGAAGGCG	TGATTACCGT	TGAAGACGGC	AAGTCTTTGG
551	AAAACGAGCT	GGACGTAGTT	GAAAGTATGC	AGTTTCAGCG	CGCCTACCTG
601	TCTCCTTACT	TCATCAACGA	TGCGGAAAAA	CAAAATCGTG	CTTTGGACAA
651	TCCGTTTGTA	TTGTTGTTTC	ACAAAAAATC	CAGCAACATC	CGCGACCTGC
701	TGCCCTGTTT	TGAACAAGTG	GCAAAAGCCA	CGCGTCCGCT	GTTGATTATC
751	GCTGAAGACG	TAGAAGCGCA	AGCCTTGGCG	ACTTTGGTCG	TGAACAACAT
801	CCGAGGCATC	CTGAAAACCG	TTGCCGTCAA	AGCCCTTGGC	TTCGGCAGCC
851	GCCGCAAAGC	GATGTTGCAA	GACATCGCCA	TCCTGACCGG	CGGCGTGGTG
901	ATTTCCGAAG	AAGTCCGTCT	GTCCTTGGAA	AAAGCGACTT	TGGACGACTT
951	GGTTCAGGCC	AAACGCATCG	AAATCGGTAA	AGAAAACACC	ACCATCATCG
1001	ACGGCTTTGG	CGACGCAGCC	CAAATCGAAG	CGCGTGTGTC	CGAAATCCGC
1051	CAACAAATCG	AAACCGCAAC	CAGCGATTAC	GACAAAGAAA	AACTGCAAGA
1101	GCGCGTGGCT	AAATTGGCAG	GCGGGCTGGC	AGTCATCAAA	GTCGGTGGCC
1151	CGACCGAAGT	CGAAATGAAA	GAGAAAAAAG	ACCGCTGGA	AGACGCGCTG
1201	CACGCTACCC	CGCAGCCGCT	TGAAGAAGGC	GTGGTTGACG	CGGGCGGCGT
1251	AGCCCTGTTG	CGTGCCCGTG	CTGCTTTGGA	AAACCTGCAC	ACCGGCAATG
1301	CCGACCAAGA	CGCAGGCGTA	CAAAATCGTCT	TGCGCGCGCT	TGAGTCTCCG
1351	CTGCGCAAAA	TGTTTGCCAA	CGACGGCGGC	GACCCACGCG	TGGTTGTGAA
1401	CAAAGTATTG	GAAGGCAAAAG	GCAACTACGG	TTACAACGCT	GGCAGCGGAA
1451	AATACGGCGA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAGTAACC
1501	CGTTCTGCGC	TGCAACACGC	CGCATCTATC	GCCGCGCTTG	TGCTGACCAC
1551	TGATTGCTATG	ATCGCTGAAA	TCCCCGAAGA	CAAAACGGCT	GTGCCCTGATA
1601	TGGCGCGCAT	GGGTGGTATG	GCCGCGCATGA	TGTAA	

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m982/g982 95.8% identity in 544 aa overlap

m982.pep MAAKDVFQGNVEVRQKMGVNVILANAVRVTLGPKGRNVVDRAFGGPHITKDGVTVAKEI  
:::|: ||||| | :| ||||||||||||||||||

1387

g982	IASQNLRFDNRFLOKMVNGVNILPAADWVALGAKGRNVVVDRAFGGPHITKDGVTVAKEI
	10 20 30 40 50 60
	70 80 90 100 110 120
m982.pep	ELKDKFENMGAQMVKEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
g982	ELKDKFENMGAQMVKEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
	130 140 150 160 170 180
m982.pep	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
g982	DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
	190 200 210 220 230 240
m982.pep	KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
g982	KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
	250 260 270 280 290 300
m982.pep	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTG
g982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTG
	250 260 270 280 290 300
	310 320 330 340 350 360
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDFGDAAQIEARVAEIRQQIETATSDY
g982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
	370 380 390 400 410 420
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVG
g982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVG
	370 380 390 400 410 420
	430 440 450 460 470 480
m982.pep	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVGKNGYGYNA
g982	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVGKNGYGYNA
	430 440 450 460 470 480
	490 500 510 520 530 540
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGM
g982	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGM
	490 500 510 520 530 540
m982.pep	GGMMX
g982	GGMMX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:

a982.seq

1	ATGGCAGCAA	AAGACGTACA	ATTCGGCAAT	GAAGTCCGCC	AAAAAATGGT
51	AAACGGCGTG	AACATTTTGG	CAAACGCCGT	GCGCGTAACC	TTGGGTCCCA
101	AAGGCCGCAA	CGTGGTGGTT	GACCGCGCTT	TCGGCGGCC	GCACATCACC
151	AAAGACGGCG	TAACCGTCGC	CAAAGAAATC	GAAGTCAAAG	ACAAGTTTGA
201	AAATATGGGC	GCGCAAATGG	TGAAAGAAGT	CGCGTCCAAA	ACCAACGACG
251	TGGCGGGCGA	CGGTACGACT	ACCGCCACCG	TATTGGCGCA	ATCCATCGTT
301	GCCGAAGGTA	TGAAATACGT	TACCGCCGGT	ATGAACCCGA	CCGACCTGAA
351	ACGCGGTATC	GACAAAGCCG	TCGCCGCTTT	GGTTGAAGAG	CTGAAAAACA

1388

```

401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTTCGACG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGCGAAAAA CAAATCGCCG GCTTGACAA
651 TCCGTTTGTG TTGCTGTTTCG AAAAAAAT CAGCAATATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCCAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATT CTGAAAACCG TTGCCGTTAA AGCTCCGGGC TTCGGCGACC
851 GCCGCAAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901 ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAGGCC AAACGCATCG AAATCGGTAA AGAAAAACCC ACCATCATCG
1001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AACTGGCAG GCGGCGTGGC AGTAATCAAA GTCGGTGGCG
1151 CGACCGAAGT GGAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGTGTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CCGCCCCGTG CCGCTCTGGA AAACCTGCAC ACCGGCAATG
1301 CAGACCAAGA CGCAGGCGTA CAAATCGTCT TCGCGCCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGTTGTGAA
1401 CAAAGTGTG GAAGGCAAAG GCAACTATGG TTACAACGCT GGCAGCGCG
1451 AATACGGCGA CATGATCGAA ATGGGCGTAC TCGACCCGCG CAAAGTAACC
1501 CGTTCCGCGC TGCAACACGC CCGCTCTATC GCCGGCCTGA TGCTGACCAC
1551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

```

a982.pep
  1 MAAKDVQFGN EVRQKMVNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
 51 KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGTT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAVAALVEE LKNIAPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KSLLENLDV V EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV L LFDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVVNNIRGI L KTVAVKAPG FGDRRKAMLQ DIAILTGTV
301 ISEEVGLSLE KATLDDLQQA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALENLH TGNADQDAGV QIVLRAVES P
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYN A GSGEYDMIE MGVLDPAKVT
501 RSALQHAASI AGLMLTTDCM IAEIPEDKPA MPDMGGMGGM GGMM*

```

m982/a982 99.3% identity in 544 aa overlap

```

              10      20      30      40      50      60
m982.pep      MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVDRAFGGPHITKDGVTVAKEI
              |||
a982           MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVDRAFGGPHITKDGVTVAKEI
              10      20      30      40      50      60

              70      80      90      100     110     120
m982.pep      ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIIVAEQMKYVTAGMNPTDLKRG I
              |||
a982           ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIIVAEQMKYVTAGMNPTDLKRG I
              70      80      90      100     110     120

              130     140     150     160     170     180
m982.pep      DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
              |||
a982           DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
              130     140     150     160     170     180

              190     200     210     220     230     240
m982.pep      KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
              |||
a982           KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
              190     200     210     220     230     240

```



1389

	250	260	270	280	290	300
m982.pep	AKASRPLLIIAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGGVV					
a982	AKASRPLLIIAEDVEGEALATLVVNNIRGILKTAVKAPGFGDRRKAMLQDIAILTGGTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m982.pep	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
a982	ISEEVGLSLEKATLDDLGOAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
a982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m982.pep	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSSVVVNKVLEGKNGYGYNA					
a982	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSSVVVNKVLEGKNGYGYNA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGMGM					
a982	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGMGM					
	490	500	510	520	530	540
m982.pep	GGMMX					
a982	GGMMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986.seq

```

1  GTGTTCAAAA AATACCAATA CTTGCTTTG GCGGCACTGT GTGCCGCCTT
51  GCTGGCAGGC TCGGAAAAGG CAGGCAGCTT TTTCGGTGCG GACAAAAAAG
101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAAGACGA CGGCAGTGTC
151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGCG AAGGCCCGGC
201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCG
251 GCAATGCCGA AACCGATTCC GACCCGCTTG CCGACAGCGA CCCGTTCTAC
301 GAATTTTCA AACGCCTCGT CCCGAACATG CCCGAAATCC CCCAAGAAGA
351 AGCAGATGAC GCGCGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAA
401 ACGGCTACAT CTTGACCAAT ACCCAGCTCG TTGCCGGTAT GGCAGATATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TACCCGTCGT CAAAATCGGC AATCCCAAAA ATTTGAAACC GGCAGATGG
601 GTCGCTGCCA TCGGCGCGCC CTTGCGCTTT GACAACAGCG TGACCGCCGG
651 CATCGTGTCG GCCAAAGGCA GAAGCCTGCC CAACGAAAgc tACACACCCT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAATTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGt cgTCGGCATC AATTCGCAA TATACAGCCG
801 CAGCGgcgga ttCATGGGCA TCTCCTTTGC CATCCCGATT GACGTTGCCA
851 TGAATGTCGC CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAGGA AGTATCCTAC GGTTCGGCAC AGTCGTTCCG
951 TCTGGATAAA GCCAGCGGCG CATTGATTGC CAAAATCCTT CCCGGCAGCC
1001 CCGCAGAACG TGCCGGCCTG CAGCGGGGCG ACATCGTCTT CAGCCTCGAC
1051 GCGGAGAGAA TACGTTCTTC CGGCGACCTT CCCGTCATGG TCGGCGCCAT
1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAAA GGCGAAGAAA
1151 TCACAATCAA AGCCAAGCTG GGCAACGCCg ccgagcATAC CGGCgcacTA
1201 TCCAAAAACAG ATGAAgcccc ctacaccgAA CAGCAATCCG GTACGTTCTC
1251 GGTCAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGca
1301 aacacctcgt cgtcgtacgg gtttccgacg cggcagaacg cGCAGGCTTA

```

1390

1351 AGgcgcggcg acgaaatcct cgcggtcggg caagtccccg tcaatgacga  
 1401 agccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC  
 1451 TGGTCAtgcg ccgTGGCAAC ACGCTGTTCA TCGCATTAAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

g986.pep

1 VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV  
 51 SMLLPDFAQL VQSEGPVAVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY  
 101 EFFKRLVPM PEIPQEEADD GGLNFGSGFI ISKNGYILT THVVAGMGS  
 151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW  
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL  
 251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQ L KNTGKVQRGQ  
 301 LGVIIQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD  
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS  
 401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGKHLVVVR VSDAAERAGL  
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLVMRRGN TLFIALNLQ\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

m986.seq

1 GTGTTCAAAA AATACCAATA CCTCGCTTG GCAGCACTGT GTGCAGCCTC  
 51 GCTGGCAGGC TGCACAAGG CAGGCAGCTT CTTCGTGGCG GACAAAAAAG  
 101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAAGACGA CGGCAGCGTC  
 151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCGGGC  
 201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCG  
 251 GCAATGCCGA AAACGATTCC GACCCGATTG CCGACAACGA CCCGTCTAC  
 301 GAATTTTCA AACGCCTCGT CCGAATATG CCCGAAATCC CCCAAGAAGA  
 351 AGCAGATGAC GCGCGATTGA ACTTCGTTT GGGCTTCATC ATCAGCAAAG  
 401 ACGGCTACAT CCTGACCAAT ACCCAGTCG TTACCGGCAT GGGCAGTATC  
 451 AAAGTCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTT  
 501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC  
 551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG  
 601 GTCGCCGCCA TCGGCGCGCC CTTGCGCTTC GACAACAGCG TGACCGCCGG  
 651 CATCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT  
 701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG  
 751 TTCAACTTAA AAGGACAGGT CGTCGCGATC AACTCGCAAA TATACAGCCG  
 801 CAGCGCGGGA TTCATGGGCA TTTCTTCGCG CATCCCGATT GACGTGCGCA  
 851 TGAATGTCGC CGAACAGCTG AAAAAACCG GCAAAGTCCA ACGCGGACAA  
 901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGGCAC AATCGTTCGG  
 951 TTTGGACAAA GCCGCGGCG CACTGATTGC CAAAATCCTG CCCGCGAGCC  
 1001 CCGCAGAACG TGCCGCGCTG CAGGCGGGCG ACATCGTCCT CAGCCTCGAC  
 1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT  
 1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAAA GCGGAAGAAA  
 1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA  
 1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC  
 1251 GGTGCAATCC GCAGGCATTA CCCTCAGAC ACATACCGAC AGCAGCGGCG  
 1301 GACACCTCGT CGTCGTACGG GTTTCGACG CGGCAGAACG CGCAGGCTTG  
 1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA  
 1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC  
 1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

m986.pep..

1 VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV  
 51 SMLLPDFAQL VQSEGPVAVN IQAAPAPRTQ NGSGNAENDS DPIADNDPFY  
 101 EFFKRLVPM PEIPQEEADD GGLNFGSGFI ISKNGYILT THVVTGMGSI  
 151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW  
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL  
 251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQ L KNTGKVQRGQ  
 301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD  
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS  
 401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGGHLVVVR VSDAAERAGL  
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ\*

Computer analysis of this amino acid sequence gave the following results:

1391

Homology with a predicted ORF from *N. gonorrhoeae*

m986/g986 97.0% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	:     :    :     :     :     :     :     :     :     :					
g986	VFKKYQYFALALCAALLAGCEKAGSFFGADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPNMPEIPQEEADD					
	:     :     :     :     :     :     :     :     :					
g986	VQSEGPVVNIQAAPAPRTQNGSGNAETDSDPLADSDPFYEFFKRLVPNMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	:     :     :     :     :     :     :     :     :					
g986	GGLNFGSGFIISKNGYILTNTHVVAGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	:     :     :     :     :     :     :     :     :					
g986	TEELPVVKIGNPKNLKPGEWVAAIGAPFGFNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLENLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	:     :     :     :     :     :     :     :     :					
g986	INPGNSGGPLENLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300

1392

	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
g986	LGVIIQEVSYGLAQSFGLDKASGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
g986	PVMVGAITPGKEVSLGVWRKGEEITIKAKLGNAAEHTGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQHTDSSGGHLVVVRVSDAAERAGLRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
g986	AGITLQHTDSSGGHLVVVRVSDAAERAGLRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
g986	VPLLVMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2971>:

```

a986.seq
1  GTGTTCAAAA AATACCAATA CCTCGCTTGT GCAGCACTGT GTGCCGCCTC
51  GCTGGCAGGC TGCGACAAAG CCGGCAGCTT TTTCGGTGCG GACAAAAAAG
101 AAGCATCCTT TGTAGAACGC ATCAAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGTCCAAGTG GTTCAAAGCG AAGGCCCGGC
201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCC GCGCACCCAA AACCGCAGCA
251 GCAATGCCGA AACCAGATTCC GACCCGCTTG CCGACAGCGA CCCGTCTTAC
301 GAATTTTCA AACGCCTCGT CCCGAACATG CCCGAAATCC CCCAAGAAGA
351 AGCAGATGAC GNGGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTATAT TCTGACCAAT ACGCAGTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCTGCT TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCCGCCA TCGGCGCGCC CTTCCGCTTC GACAACAGCG TGACCGCCGG
651 CNTCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
701 TACATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAAA TATACAGCCG
801 CAGCGGCGGA TTCATGGGCA TTTCTTTCG CATCCCGATT GACGTTGCCA
851 TGAATGTGCG CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGGCAC AATCGTTCGG
951 TTTGGACAAA GCCGCGCGCG CACTGATTGC CAAAATCCTG CCGGCAGCC
1001 CCGCAGAACG TGCCGGCCTG CGGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCAGCCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAAA GCGGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCAATCC GCAGGCATTA CCCTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTTCCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2972; ORF 986.a>:

```

a986.pep
1  VFKEYQYLAL AALCAASLAG CDKAGSFFGA DKKEASFVER IKHTKDDGSV
51  SMLLPDFVQL VQSEGPVVN IQAAPAPRTQ NGSSNAETDS DPLADSDPFY
101 EFFKRLVPNM PEIPQEEADD GGLNFGSGFI ISKDGYYLTN THVVTGMGSI
151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGXVS AKGRSLPNES YTPFIQTQDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGO

```

1393

301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL RAGDIVLSLD  
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS  
401 SKTDEAPYTE QQSGTFSVES AGITLQHTD SSGGHLVVVR VSDAERAGL  
451 RRGDEILAVG QVPVND EAGF RKAMDKAGN VPLLIMRRGN TLFIALNLQ\*

m986/a986 98.2% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
a986	VFKKYQYLALCAASLAGCDKAGSFFGADKKEASFVERIKHTKDDGSVSMLLPDFVQL					
	10	20	30	40	50	60
m986.pep	VQSEGPAVVNIQAAPARTQNGSGNAENDSDPIADNPFYEFFKRLVPMPEIPQEEADD					
a986	VQSEGPAVVNIQAAPARTQNGSSNAETDSDPLADSDPFYEFFKRLVPMPEIPQEEADD					
	70	80	90	100	110	120
m986.pep	VQSEGPAVVNIQAAPARTQNGSGNAENDSDPIADNPFYEFFKRLVPMPEIPQEEADD					
a986	VQSEGPAVVNIQAAPARTQNGSSNAETDSDPLADSDPFYEFFKRLVPMPEIPQEEADD					
	70	80	90	100	110	120
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
a986	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
a986	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTIVA					
a986	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGXVSAKGRSLPNESYTPFIQTIVA					
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTIVA					
a986	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGXVSAKGRSLPNESYTPFIQTIVA					
	190	200	210	220	230	240
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
a986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
a986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
a986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
a986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
m986.pep	PVMVGAITPGKEVSLGVWRKGEETIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
a986	PVMVGAITPGKEVSLGVWRKGEETIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEETIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
a986	PVMVGAITPGKEVSLGVWRKGEETIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
m986.pep	AGITLQHTDSSGGHLVVVRVSDAERAGLRRGDEILAVGQVPVND EAGFRKAMDKAGN					
a986	AGITLQHTDSSGGHLVVVRVSDAERAGLRRGDEILAVGQVPVND EAGFRKAMDKAGN					
	430	440	450	460	470	480
m986.pep	AGITLQHTDSSGGHLVVVRVSDAERAGLRRGDEILAVGQVPVND EAGFRKAMDKAGN					
a986	AGITLQHTDSSGGHLVVVRVSDAERAGLRRGDEILAVGQVPVND EAGFRKAMDKAGN					
	430	440	450	460	470	480
m986.pep	VPLLIMRRGNTLFIALNLQX					
a986	VPLLIMRRGNTLFIALNLQX					
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
a986	VPLLIMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:

g987.seq

1 ATGAAAACAC GCAGCCTCAT TTCCCTTTTA TGCTCCTTC TCTGTTTCATG

1394

```

51  TTCTTCATGG TTGCCCCCAG TGAAGAAGC GACGGAAAGC CGTCATTTTA
101 ATACTTCCAA ACCTGTCTCT CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGACATCTAC CTGCTCGACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATTGGG CGCAACGaCA TTTCCGGCAG GCTGCTGTTC
301 AACCTCATGT ACCTTGCCGC agaacgcGGC GTGCGCGTAC GCCTGCTGTT
351 ggacgacaAC AACAcgcgcg gcttgacga tctcctGCTC GCCCTCGACA
401 GGCAATCCAA TactaagtG CGCCTGTTCA ACCCCTcgt CCTACGCAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCgcCTCA ACCGCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGCGGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACATCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACGGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT GATCAGCGAC AGCCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GAGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCTACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTACGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCACAACCA TGCCGTCCCC GCCACAAAAG ACAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGacg gCAAACGCAT
1251 CTTCAATCGG TCATTCAACC TCGACCCCGG TTCCGCACGG CTCATAACCG
1301 AAATGGGCGT CGTCAATCGAA AGCCCAAAA TCGCAGAACA GATGGAGCGC
1351 AccctCGCGC AtacCACACC CGAATACGCC TACCGCGTTA CCCTCGACAA
1401 ACACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCC TCGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

```

g987.pep
1  MKTRSLISLL CLLLCSSSW LPPLEERTES RHFNTPSKPVL LDNILQIRHT
51  PHNNGLSDIY LLDDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLMYLAAERG VRVRLLLDDN NTRGLDDLL ALDSHPNI*V RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD SPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSIFYVPT KSGTDALAKL VQDGDIVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVIE SPKIAEQMER
451 TLADTTPEYA YRVTLDKHNR LQWHPATRK TYPNEPEAKL WKRIAARKLS
501 LLPIEGLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

```

m987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCTTTTA TGCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCCAG TGAAGAAGC GACGGAAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCAG GCTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTT GCCCTCGACA
401 GGCAATCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCgcCTCA ACCGCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GATTTGGACA TCCTCGCCAC CGGCAGCGTC GTCGCGGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
851 GAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC

```

1395

```

901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTTCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTTCTG
1051 ACCAACTCGC TGCAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCACGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGT TCGTTCAACC TCGACCCCGG TTCGCGCGGT CTCAACACCG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCACACC CGCCTACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACC CGA AGCCAAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

```

m987.pep
  1 MKTRSLISLL CLLLCSCSSW LPPLEERTES RHFNTSKPVR LDNILQIRHT
 51 PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERG VRVRLLEDN NTRGLDLLLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLTD FRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHAHNA TRIIRSGDIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGCIDW QSVRTRLISD DPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPAYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIA AKILS
501 LLPIEGLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m987/g987 97.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
g987	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVLLDNILQIRHTPHNGLSDIY					
	10	20	30	40	50	60
m987.pep	70	80	90	100	110	120
	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNVLVYLAERGVRVRLLEDN					
g987	LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNMYLAERGVRVRLLEDN					
	70	80	90	100	110	120
m987.pep	130	140	150	160	170	180
	NTRGLDLLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFFRLNRRMHNKSFTADNRATI					
g987	NTRGLDLLLLALDSHPNIXVRLFNPFVLRKWRALGYLTDFFRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
m987.pep	190	200	210	220	230	240
	LGGRNIGDEYFKVGEDTVFADLDILATGSVGEVSHDFDRYWASHAHNATRIIRSGDIG					
g987	LGGRNIGDEYFKVGEDTVFADLDILATGSVGEVSHDFDRYWASHAHNATRIIRSGNIG					
	190	200	210	220	230	240
m987.pep	250	260	270	280	290	300
	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR					
g987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDSPAKGLDRDR					
	250	260	270	280	290	300
m987.pep	310	320	330	340	350	360
	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGDVTVLTNSLQATDVA					

1396

```

g987      |||||
          RKPP|IAGRLQDALKQPEKSV|LVSPYFVPTKSGT|DALAKLVQDGIDVT|VLTNSLQATDVA
          310      320      330      340      350      360

          370      380      390      400      410      420
m987.pep  AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKR|FIG
          |||||
g987      AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKR|FIG
          370      380      390      400      410      420

          430      440      450      460      470      480
m987.pep  SFNLDPRSARLNT|EMGVVIESPKIAEQMERT|LADTTPAYAYRV|TLDRHNRLQWHD|PATRK
          |||||
g987      SFNLDPRSARLNT|EMGVVIESPKIAEQMERT|LADTTPEYAYRV|TLDKHNRLQWHD|PATRK
          430      440      450      460      470      480

          490      500      509
m987.pep  TYPNEPEAKLWKRIA|AAKILSLPIEGLLX
          |||||
g987      TYPNEPEAKLWKRIA|AAKILSLPIEGLLX
          490      500

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

```

a987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTCATG
51  TTCTTCATGG TTGCCCCCAC TGGAAGAAGC GACGGAAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTGGAACG ACCCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCCG ACTGCTGTTT
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTC GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTC AACCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGTACCT GACCGACTTC CCGCGCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCTCTAC CAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCT GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGG TCATTCAACC TCGACCCCGG TTCGCGACGG CTCAATACTG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAAGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

```

a987.pep
1  MKTRSLISLL C|LLLCSCSSW LPPLEERTES RHFNTSKPVR LDN|LQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLA|AERG VRVRL|LLDDN NTRGLD|DLLL ALDSHPNIEV RLFPFVLRK
151 WRALGY|LTDF PRLNR|RMHMK SFTADNR|ATI LGGRNIGDEY FKVGEDTVFA
201 DLDI|LATGSV VGEVSH|DFDR YWASHSA|HNA TRIIRSGNIG KGLQALGYND
251 ETSR|HALLRY RETVEQ|SPLY QKIQTGR|IDW QSVQTR|LSD DPAKGLDRDR
301 RKPP|IAGRLQ DALKQPE|SV YLVSPYF|VPT KSGTDALAKL VQDGIDVTVL

```



1397

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS  
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPARSAR LNTEMGVVIE SPKIAEQMER  
 451 TLADTSPEYA YRVTLDRHNR LQWHPATRK TYPNEPEAKL WKRIAAILLS  
 501 LLPIESLL\*

m987/a987 98.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSCSSWLPPEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
a987						
	10	20	30	40	50	60
	70	80	90	100	110	120
m987.pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
a987						
	70	80	90	100	110	120
	130	140	150	160	170	180
m987.pep	NTRGLDDLLALDHPNIEVRLFPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
a987						
	130	140	150	160	170	180
	190	200	210	220	230	240
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG					
a987						
	190	200	210	220	230	240
	250	260	270	280	290	300
m987.pep	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVTRRLISDDPAKGLDRDR					
a987						
	250	260	270	280	290	300
	310	320	330	340	350	360
m987.pep	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNLSLQATDVA					
a987						
	310	320	330	340	350	360
	370	380	390	400	410	420
m987.pep	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
a987						
	370	380	390	400	410	420
	430	440	450	460	470	480
m987.pep	SFNLDPARSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNRQLQWHPATRK					
a987						
	430	440	450	460	470	480
	490	500	509			
m987.pep	TYPNEPEAKLWKRIAAILLSLLPIEGLLX					
a987						
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:

g988.seq  
 1 ATGAATAAAA ATATTAAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT

1398

```

51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGgaATGGA
101 TAATCGAATT GTTGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACGCGAGC TGTGATTAC GGAAGacgag tATGTCTTTT TTGAACGCCG
201 TCTGAaggCG atgCGCGGG AcggtCAGGT TTTAATCAAC CGCCgaggcg
251 CagtTTGCGc gGCggacaag ctgGATTTGG TCAAATGccg Cgtcaggcg
301 catAAgGAcg gtttcggctt cgcCGTGCCG CTCATGCCGA TGGACGAAGG
351 GGATTTCTGT TTATACGAAC GCCAgatgcg tggTgcatG CAcggcgaca
401 ccgttACCGT CCGTCTGCG ggtatggaCC GCAGGGGccg ccgcGAAggg
451 acgtttctGG ATATTGTGCA ACGCGCGCAA AGCAAAGTTG TCGGCCGTTT
501 CTATATGGAT AGGGCGGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTGTGGAA CCGGACGCG TGGCGGTTT CAAACCCGAA
601 TCCGGTCAGG TTATCGTCGG CAAAATTGAG GTTTATCCCG AGCAAAACCG
651 GCCTGCAGTG GCAAAAATCA TTGAAGTTT GGGCGATTAT GCCGACAGCG
701 GGATGGAAt cgAAATTGCC GTGCGCAAGC ATCATTGGCC GCaccgaTTC
751 AGTGAagcgt gtGcCAAATC CGgaaAAAA ATtcccagacc ATGTACGCAA
801 AAGCGATTG AAAGGCCGCG TCGATTGTG CGACCTTCTT TTGGTAACGA
851 TAGACGCGCA AACGGCGCG GATTCGACG ACGCGGTGTT TGCCGAAAAA
901 GTCGGACGCA ATTACCGCCT GGTCGTGGCG ATTGCGGATG TCAGCCATTA
951 TGTCCGCCCT GACGATGCGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
1001 GCGTGTATTT CCCGCGCGT ATGATTCCGA TGCTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTATC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCTGA CCTACAACCA AGTTTGAAAA
1201 TGGCTTTCAG ACGGCATCGG GAATCCGCAC AAAGCCCAA TCGACACGCT
1251 TTACAAGCTG TTTAAATTT TGCAGAAAAA ACGTCTGGCG CGCGGGCGG
1301 TGGAGTTGA AAGCGTCGAA ACCCAGATGA TTTTCGACGA CAACGCCAAA
1351 ATCGAAAAA TTGTCCCGT CGTCCGCAAC gatGCCACA AGCTGATTGA
1401 AGAATGTATG CTGGCGCGCA ATGTTTGC GC CGGATT TT CTGTTGAAAA
1451 ACAACATAC GGCTTTGTTT CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1501 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGCGCG
1551 CGCGGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GAACAATTCA
1601 AAGGCAGGCC GGATGCGGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAGCAGGCGG TTTACGAACC GCATTGCGAA GGGCATTTCG GTTTGGCTTA
1701 TGAAGCATAC GCCCACTTTA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTCCACCG TGCCATCAAA GCCGTATTGA ACCGGAAAAC CTACACGCCA
1801 AACAAAAGCT GGCAGGCTTT GGGCGTGCAT ACTTCGTTTT GCGAACGCGG
1851 TGCCGACGAT GCTGGCGCG ATGTGAAAAA CTGGCTGAAA ACTTATTATA
1901 TGCGCGATAA GGTGCGTGAA ATATTGAAG GcaaaatCtc ccggggtgtg
1951 gcaaaTtttg gaATATTTGT CACTTTGGAC GATATccata tgcacggtct
2001 ggtacaTATC AGCGatttgg gcgaAGATTA TTTCaacttc cgccccgAAA
2051 TCATGGCAAT CGAAGGCGAA CGCAGCGGCA TCCGTTTCAA TATGGGGGAC
2101 AGGGTTGCCG TCCGGGTCGC GCGTGCCGAT TTGGATGATG GAAAAATCGA
2151 CTTTGTCTTA ATTGCGGGAG AAAGCGGCAG GCGGCGGAAG GTCAAATTAT
2201 CCGCATCTGC CAAACCGGCA GGGGCGGCGG GGAAGGGGAA ATCGAAAAAC
2251 ACCGCCGAGA AAAAAACAGC CCGATGCGGC AAAGTAAGGG GAAGGGCGGT
2301 GCCTGCCGTT GCCGAATCGG GGA AAAAGGC AAAGAAACCG GTTCCGATTA
2351 AGGTCAAAAA ACGGAAAGGC AAATCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

```

1  MNKNIKSLNL REKDPFLSRE KQRYEHPLPS REWIIELLER KGVPSKIESL
51  ARELSITEDE YVFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVEA
101 HKDGFGEFAV LMPMDEGDFV LYERQMRGVM HGDVTVTRPA GMDRRGRREG
151 TFLDIVERAQ SKVVGRFYMD RGVAILPED KRLNQSIVLE PDGVARFKPE
201 SGQVIVGKIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHRF
251 SEACAKSAKK IPDHVRKSDL KGRVDLCDLP LVTIDGETAR DFDDAVFAEK
301 VGRNYRLVVA IADVSHYVRP DDAIDADAQE RSTSVYFPRR MIPMLPENLS
351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSDGIGNPH KAQIDTLYKL FKILQKKRLA RGAVEFESVE TQMI FDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQLGL LGLQLGGGDN PSPKDYAALA EQFKGRPD AE LLQVMMLRSM
551 QQAVYEPHCE GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNRKTYTP
601 NKSWQALGVH TSFCERRADD AGRDVENWLK TTYMRDKVGE IFEGKISRGV
651 ANFGIFVTL DDIHIDGLVHI SDLGEDYFNF RPEIMAIEGE RSGIRENMGD
701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSKT
751 TAEKKTARCG KVRGRGVPVAV AESGKKAKKP VPIKVKRKG KS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

```

m988.seq (partial)
1  ..ACAGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
51 CTATATGGAT AGGGGCGTGG CGATTTTGGG GCCGGAAGAC AAGCGTCTGA
101 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
201 GCCGGCAGTG GCAAAAATCA TCGAAGTTT GGGCGATTAT GCCGACAGCG
251 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTGGCC GCACCAATTC
301 AGTGAAGCGT GTGCCAAAGC TGCAGAAAAA ATCCCGTCC ATGTACGCAA
351 AAGCGATTG AAAGGCCGCG TCGATTTCGC CGACCTGCCT TTGGTAACGA
401 TAGACGGCGA AACGGCGCGC GATTTCGACG ACGCGGTGTT TGCCGAAAAA
451 GTCGGACGCA ATTACCGTCT GGTCTGGCG ATTGCGGATG TCAGCCATTG
501 TGTCGCCCTT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551 GCGTATATTT CCCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601 AACGGCATT GTCGCTCAA TCCGATGTC GAGCGTTTGT GTATGGTGTG
651 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTACC
701 CCGCCGTAAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGAAAA
751 TGGATTTTCA ACGGCATCGA CCATCCGTAC AAAGCCCAAA TCGACACCTT
801 TTACAAATC TTCAAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGCGCGG
851 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGATGA CAACGGCAAA
901 ATCGAAAAA TCGTCCCCGT TGTCGCAAC GATGCCACA AGCTGATTGA
951 AGAATGTATG CTGGCGGCGA ATGTTTGC GCAGGATTTC CTGTTGAAAA
1001 ACAAGCATA GGCCTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1051 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1101 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTC GAACAATTCA
1151 AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1201 CAGCAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCCTA
1251 CGAAGCATA GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1301 CCGTACACCG CGCCATCAAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1351 AAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1401 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1451 TGCGCGATAA GGTGCGCGAA GTATTGGAAG GTAAAATCTC CGGCATGACC
1501 AGTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
1551 GCATATCAGC GATTGGGCG AAGACTATTT CAACTCCGC CCCGAAATCA
1601 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTCAACAT GGGGGACAGG
1651 GTTGCCGTCC GGGTCGCCCG TGCCGATTG GATGACGAA AAATCGATTT
1701 TGTCCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
1751 CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAAACCGCC

```

1400

1801 GCCGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC  
 1851 TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAAG  
 1901 TAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)

1 ..TVLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE  
 51 SGQVIVGEIE VYPEQNRPAV AKIEVLGDY ADGMEIEIA VRKHHLPHQF  
 101 SEACAKAAKK IPVHVRKSDL KGRVDLRDLP LVTIDGETAR DFDDAVFAEK  
 151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTSVYFPRR VIPMLPENLS  
 201 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPVMRSH ARLTYNQVWK  
 251 WISDGIDHPY KAQIDTLYKL FKILQKKRFE RGAVEFESVE TQMIFDDNGK  
 301 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK  
 351 LATLREQLGL LGLQLGGGDN PSPKDYAALV EQFKGRPDAE LLQVMMLRSM  
 401 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP  
 451 KKSQWALGVH TSFCERRADD ASRDVENWLK TTYMRDKVGE VFEGKISGMT  
 501 SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRFNMGDR  
 551 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGKPKTA  
 601 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKRKGK S\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

m988.pep				10	20	30
				TVLDIVERAQSKVVGRFYMDRGVAILEPED		
g988	LYERQMRGVMHGD	TVTVRPA	MDRRGRREGT	FLDIVERAQSKVVGRFYMDRGVAILEPED		
	130	140	150	160	170	180
m988.pep		40	50	60	70	80
		KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA				
g988		KRLNQSIVLEPDGVARFKPESGQVIVGKIEVYPEQNRPAVAKIEVLGDYADSGMEIEIA				
	190	200	210	220	230	240
m988.pep		100	110	120	130	140
		VRKHHLPHQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLP				
g988		VRKHHLPHRFSEACAKSAKKIPDHVRKSDLKGRVDL				
	250	260	270	280	290	300
m988.pep		160	170	180	190	200
		VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRR				
g988		VGRNYRLVVAIADVSHYVRPDDAIDADAQERSTSVYFPRR				
	310	320	330	340	350	360
m988.pep		220	230	240	250	260
		ERLCMVCDMVVTYAGNIKEYRFYPVMRSHARLTYNQVWK				
g988		ERLCMVCDMVVTYAGNIKEYRFYPVMRSHARLTYNQVWK				
	370	380	390	400	410	420
m988.pep		280	290	300	310	320
		FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRN				
g988		FKILQKKRLARGAVEFESVETQMIFDDNGKIEKIVPVVRN				
	430	440	450	460	470	480
m988.pep		340	350	360	370	380
		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGDN				
g988		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGDN				

1401

	490	500	510	520	530	540
	400	410	420	430	440	450
m988.pep	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
g988	LLQVMMLRSMQQAVYEPHCEGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNRRKTYTP					
	550	560	570	580	590	600
	460	470	480	490	500	509
m988.pep	KKSQWQALGVHTSFCERRADDASRDVENWLKTYIMRDKVGVEFEGKIS-GMTSFGIFVTLT					
g988	NKSQWQALGVHTSFCERRADDAGRDVENWLKTYIMRDKVGEIFEGKISRGVANFGIFVTLT					
	610	620	630	640	650	660
	510	520	530	540	550	569
m988.pep	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRENMGDRVAVRVARADLDDGKIDFVL					
g988	DIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRENMGDRVAVRVARADLDDGKIDFVL					
	670	680	690	700	710	720
	570	580	590	600	610	629
m988.pep	IAGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGKVRGRGASAAESRKKAKKP					
g988	IAGESGRRRKVKLSASAKPAGAAGKGKSKTTAEKKTARCGKVRGVPVAESGKKAKKP					
	730	740	750	760	770	780
	630	640				
m988.pep	VPIKVKKRKGKXS					
g988	VPIKVKKRKGKXS					
		790				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2983>:

```

a988.seq
1   ATGAATAAAA ATATTAAATC TTAAATTTA CGGGA AAAAG ACCCGTTTTT
51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTGCCCCAGT CGGGAATGGA
101 TAATCGAGCT GCTTGAACGT AAAGGCGTAC CATCCAAGAT TGAAGCTTTG
151 GTACGCGAAT TGTGCGATTAA GGAAGAAGAG TACGAATTTT TCGAACGTCG
201 TCTGAAGGCG ATGGCGCGGG ACGGTCAGGT TTTAATCAAC CGTCGGGGCG
251 CGGTTTGCGC GCGGCACAAA TTGGATTGGG TCAAATGCCG TGTCAAGGCG
301 CACAAAGACC GCTTCGGTTT CGCCGTGCCG CTCACGCCCG CCAAAGACGG
351 TGATTTTGTG TTGTACGAAC GCCAGATGCG CGGCATTATG CACGGCGATA
401 TTGTCACGTG TCGTCCTGCC GGCATGGACG GTAGGGGCGG CCGCGAAGGG
451 ACGGTTCTGG ATATTGTCTGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
501 CTANATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
601 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
651 GCCGGCAGTG GCAAAAATCA TCGAAGTTT GGGCGATTAT GCCGACAGCG
701 GCATGGAGAT TGA AATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
751 AGTGAAGCGT GTGCCAAAGC CGGAAAAAA ATTCCCGACC ATGTACGCAA
801 AAGCGATTGG AAAGGCCGCG TCGATTTGCG CGACCTGCCT TTGGTAACGA
851 TAGACGGCGA AACGGCTCGA GATTTTGACG ATGCGGTGTT TGCCGAGAAA
901 ATCGGACGCA ATTACCGTCT GGTGCTGGCG ATTGCCGATG TCAGCCATTA
951 GTGCCGCCCC GATGACGCTA TCGACACGGA CGCTCAGGAA CGCAGCACCA
1001 GTGTTTACTT CCCGCGCCGC GTGATTCCCA TGTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCTCATGTC GAGCGTTTGT GTGTGGTGTG
1101 CGATATGGTT ATCACTTACG CGGGCAATAT CAAAGAATAC CGCTTCTACC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCTGA CCTACAACCA AGTTTGAAAA
1201 TGGCTTTTCA GCGGCATCGA GCATCCGTTT AAAACCCAAA TCGACACGCT
1251 TTCAAATC TTCAAATCC TTCAGAAAAA GCGTTTTCGAA CGCGGGGCGG
1301 TGGAGTTTGA CAGCATCGAA ACCCAAATGC TTTTCGACGA CAACGGTAAA
1351 ATTGAAAAA TCGTCCCGGT GTGCCGCAAC GATGCCACA AGCTGATTGA
1401 AGAATGTATG TTGGCGGCAA ACGTTTGCGC AGCGGATTTT CTGTTGAAAA
1451 ACAAGCATAC CGCATTGTTC CGCAACCATT TGGGGCCAC GCCCGAAAAA
1501 CTCGCCGCT TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GGACAGTTCA

```

1402

```

1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAACAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCCCTA
1701 CGAAGCATA CCCCACCTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTACACCG CGCCATCAAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1801 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1851 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA
1901 TGCGCGATAA GGTCGGCGAA GTATTGGAAG GTAAAAATCTC CGGCATGACC
1951 AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
2001 GCATATCAGC GATTTGGGCG AAGACTATTT CAACTTCCGC CCCGAAATCA
2051 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCACAT GGGGGACAGG
2101 GTTGCCGTCC GGGTCGCCCCG TGCCGATTG GATGACGGAA AAATCGATTT
2151 TGTCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
2201 CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAAACCGCC
2251 GCCGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
2301 TGCCGCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG
2351 TAAAAAACG GAAAGGCAAA TCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2984; ORF 988.a>:

```

a988.pep
  1 MNKNIKSLNL REKDPFLSRE KQRYEHLPLS REWIIELLER KGVPSKIEAL
  51 VRELSIKEEE YEFFERLKA MARDGQVLIN RRGAVCAADK LDLVKCRVKA
 101 HKDRFGFAVP LTPAKDGDFV LYERQMRGIM HGDIVTVRPA GMDGRGRREG
 151 TVLDIVERAQ SKVVGRFXMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
 201 SQQVIVGEIE VYPEQNRPAV AKIIEVLGDY AD SGMEIEIA VRKHHLP HQF
 251 SEACAKAAKK IPDHVRKSDL KGRVDLRDLP LVTIDGETAR DFDDAVFAEK
 301 IGRNYRLVVA IADVSHYVRP DDAIDTDAQE RSTSVYFPRR VIPMLPENLS
 351 NGICSLNPHV ERLCVVCDMV ITYAGNIKEY RFYPAVMRSH ARLTYNQVWK
 401 WLSGGIEHPF KTQIDTLYKL FKILQKKRFE RGAVEFDSIE TQMLFDDNGK
 451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
 501 LAALREQLGL LGLQLGGGDN PSPKDYAALA GQFKGRPDAE LLQVMMLRSM
 551 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP
 601 KKSQWALGVH TSFCERRADD ASRDVENWLK TTYMRDKVGE VFEGKISGMT
 651 SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAEGER SGIRFNMGDR
 701 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGPCKTA
 751 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKRKGK S*

```

m988/a988 97.0% identity in 641 aa overlap

```

                                     10      20      30
m988.pep                               TVLDIVERAQSKVVGRFYMDRGVAILEPED
                                     |||
a988      LYERQMRGIMHGDIVTVRPA GMDGRGRREGTVLDIVERAQSKVVGRFXMDRGVAILEPED
               130      140      150      160      170      180

               40      50      60      70      80      90
m988.pep      KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA
               |||
a988      KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA
               190      200      210      220      230      240

               100      110      120      130      140      150
m988.pep      VRKHHLP HQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLP LVTIDGETARDFDDAVFAEK
               |||
a988      VRKHHLP HQFSEACAKAAKKIPDHVRKSDLKGRVDLRDLP LVTIDGETARDFDDAVFAEK
               250      260      270      280      290      300

               160      170      180      190      200      210
m988.pep      VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRRVIPMLPENLSNGICSLNPDV
               :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a988      IGRNYRLVVAIADVSHYVRPDDAIDTDAQERSTSVYFPRRVIPMLPENLSNGICSLNPHV
               310      320      330      340      350      360

               220      230      240      250      260      270
m988.pep      ERLCMVCDMVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL
               |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a988      ERLCVVCDMVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWLSGGIEHPFKTQIDTLYKL

```

1403

	370	380	390	400	410	420
m988.pep	280	290	300	310	320	330
a988	340	350	360	370	380	390
m988.pep	400	410	420	430	440	450
a988	460	470	480	490	500	510
m988.pep	520	530	540	550	560	570
a988	580	590	600	610	620	630
m988.pep	640	650	660	670	680	690
a988	700	710	720	730	740	750
m988.pep	760	770	780	790	800	810
a988	820	830	840	850	860	870
m988.pep	880	890	900	910	920	930
a988	940	950	960	970	980	990

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

g989.seq

```

1   ATGACCCCTT TCACACTGAA AAAAACCCTC CTGCTGCTCG GCACTGCCTT
51  TGCCGCCGCA TCTGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCCG ACGCGTCGAC CATCTTCTAC
151 AATCCCGCCG GCCTGACCAA ACTCGACAGC AGCCAGATT TCCGTCAACGC
201 CAACATCGTG CTGCCCAGCA TTCATTATGA AGCAGATTCC GCCACCGACT
251 TTACCGGGCT TCCCGTCCAA GGTCTAATAA ACGGCAAAAT CACCAAAACC
301 ACGGTCGCAC CCCACATTTA CGGCGCATAC AAAGTCAACG ACAATCTGAC
351 CGTGGGCTTG GCGGTGTACG TCCCCTTCGG CTCTGCCACC GAATACGAAA
401 AAGATTCGT GTTGGCCAC AACATCAACA AACTCGGTCT GACCAGCATC
451 GCCGTCGAAC CTGTCGCCGC GTGGAACCTC AACGAACGCC ATTCCTTCGG
501 CGCAGGCATC ATCGCCCAAC ATAATTCCGC CGAACTGCGC AAATATGCCG
551 ACTGAGGAAT CCCAAAAAAA GCGCAAATGC TGCAAGCAAC ACCTTCTAAT
601 CCTACTGCCG CTGCTCAAA TCAAGGCCGAC GGACACGCCG ATGTCAAAGG
651 CAGCGATTGG GCGCTCGGCT ACCAACTGGC GTGGATGTGG GACATCAACG
701 ACCGCGCGCG CGTGGGCGTG AACTACCGTT CCAAAGTTTC ACACACGCTC
751 AAAGGCGATG CCGAATGGGC GGCAGACGGC GCGGCGGCGA AACAACAGTG
801 GAATGACAAT ATGCTCACAC CGCTCGGTTA CACGGCGAAT GAAAAAGCCA
851 GTGTCAAAAT CGTAACGCCT GAGTCTTTGT CCGTACACGG CATGTACAAA

```

1404

```

901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAACCTGGA CGCGCCACAG
951 CCGCTTCAAT AAGGCGGAAC TGTTTTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCGC ACCACCATCA CCCCCAATG GCGCAACACC
1051 TACAAAGTCG GCTTGGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAACCGCC TGTCCGCAAC GCCGACTacC
1151 GCATGAACAG CCGCCCGAC GGAACCGCA TCTGGTTCTC CGCCGGCATG
1201 AAATACCATA TCGGCAAAAA CCACGTCGTC GATGCCGCCT ACACCCCAT
1251 CCACATCAAC GACACCAGCT ACCGCACGGC GAAGGCAAGC GGAACGATG
1301 TGACAGCAA AGGTGCGTCT TCGCACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAAA TAA

```

-- This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

```

g989.pep
1 MTPFTLKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
51 NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNDNLTVGL GVVVPFGSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAWKL NERHSFGAGI IAQHNSAELR KYAD*GIPKK AQMLQATPSN
201 PTAQAQIKAD GHADVKGSDW GVGQLAWMW DINDRARVGV NYRSKVSHTL
251 KGDAEWAADG AAKQQWNDN MLTPLGYTAN EKASVKIVTP ESLSVHGMKY
301 VSKADLFGD VTWTRHSREN KAEFFFEKEK NIANGKSDR TTITPNWRNT
351 YKVLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWFSAGM
401 KYHIGKNHVV DAAYTHIHIN DTSYRTAKAS GNDVDSKGAS CARFKNHADI
451 IGLQYTYKFK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

```

m989.seq
1 ATGACCCCTT CCGCACTGAA AAAAACCCTC CTGCTGCTCG GCACTGCCTT
51 TGCCGCCGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCGG CCGCAGAAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAACTCG ACAGCAGCCA
201 GATTTCCGTC AACGCCAACA TCGTGCTGCC CAGCATTCAT TATGAGGCGG
251 ATTCCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTT GAAAAGCGGC
301 AAAATCACCA AAACCACGGT CGCGCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGCGGT GTACGTCCCC TTCGGCTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGG AACTCAACGA
501 CCGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAAC
551 TGCGCAATA TGCCGACTGG GGGATTAAGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAAACTAA CCGTGTAGCC GAAGCTCAA AAATTGAGG
651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAATAC
751 CGTTCCAAAG TCTCGCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
801 CGGCGCGCGC GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAAACGGCT
851 ACACGGCGAA TGAAAAAGCC CGCGTTAAAA TCGTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTTCGGCGA
951 CGTAACTTGG ACGCGCCACA GCCGCTTCGA TAAGGCGGAA CTGGTTTTTG
1001 AAAAAGAAAA AACCGTCGTC AAAGGCAAAT CCGACCGCAC CACCATCACC
1051 CCAACTGGC GCAACACCTA CAAAGTCGGC TTCGGCGGTT CTTATCAAAT
1101 CAGCGAACCG CTGCAACTGC GCGCCGGCAT CGCTTTTGAC AAATCGCCCG
1151 TCCGCAACGC CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
1201 TGGTTCTCCG CCGGTATGAA ATACCATATC GGTA AAAACC ACGTCGTCGA
1251 TGCCGCCTAC ACCCATATCC ACATCAACGA CACCAGCTAC CGCACGGCGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG GCGCGTCTTC CGCACGTTTC
1351 AAAAACCACG CCGACATCAT CCGTCTGCAA TACACCTACA AATTCAAATA
1401 A

```

This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

```

m989.pep
1 MTPSALKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEADA
51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNDRHS FGAGIIAQHT SAELRKYADW GIKSKAEILT
201 AKFPKPNGVA EAAKIQADGH ADVKGSWGF GYQLAWMWDI NDRARVGVNY
251 RSKVSHTLKG DAEWAADGAA AKAMWSTMLA ANGYTANEKA RVKIVTPESL
301 SVHGMKYKVD KADLFGDVTW TRHSRFDKAE LVFEKEKTVV KGKSDRTTIT

```



1405

351 PNWRNTYKVG FGGSYQISEP LQLRAGIAFD KSPVRNADYR MNSLPDGNRI  
 401 WFSAGMKYHI GKNHVVDAA YTHIHINDTSY RTAKASGNDV DSKGASSARF  
 451 KNHADIIGLQ YTYKFK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

g989/m989 90.0% identity in 468 aa overlap

	10	20	30	40	50
g989.pep	MTPFTLKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAA-----DASTIFYNPAGL				
m989	MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL				
	10	20	30	40	50
	60	70	80	90	100
g989.pep	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNKGIKTTTAVPHIYGAYKVNDN				
m989	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNKGIKTTTAVPHIYGAYKVNDN				
	70	80	90	100	110
	120	130	140	150	160
g989.pep	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHN				
m989	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNRHSFGAGIIAQHT				
	130	140	150	160	170
	180	190	200	210	220
g989.pep	SAELRKYADXGIPKKAQMLQATPSNPTA---AAQIKADGHADVKGSDWGVGYQLAWMWDI				
m989	SAELRKYADWGIKSAEILTAKPPKNGVAEAAKIADGHADVKGSDWGFYQLAWMWDI				
	190	200	210	220	230
	240	250	260	270	280
g989.pep	NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKQOWNMMLTPLYTANERKASVKIVTPES				
m989	NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKAMWS-TMLAANGYTANERKARVKIVTPES				
	250	260	270	280	290
	300	310	320	330	340
g989.pep	LSVHGMKYVSDKADLFQDVTWTRHSRFEKAEKNIANGKKSDDRTTITPNWRNTYK				
m989	LSVHGMKYVSDKADLFQDVTWTRHSRFDKAEKLVFEKEKTVVKGK-SDRTTITPNWRNTYK				
	300	310	320	330	340
	350	360	370	380	390
g989.pep	VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
m989	VGFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
	360	370	380	390	400
	410	420	430	440	450
g989.pep	AYTHIHINDTSYRTAKASGNDVDSKGASCARFKNHADIIGLQYTYKFKX				
m989	AYTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX				
	420	430	440	450	460

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

a989.seq  
 1 ATGACCCCTT CCGCACTGAA AAAAACCGTC CTACTGCTCG GCACTGCCTT  
 51 TGCCGCCGCA TCCGCACAAG CCTCCGGCTA CCACTTCGGC ACACAGTCGG  
 101 TCAACGCGCA AAGCACGGCA AATGCCGCCG CCGCAGAAGC CGCCGACGCA  
 151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAACTCG ACAGCAGCCA  
 201 GATTTCGCTC AACGCCAACA TCGTGCTGCC CAGCATTCAT TATGAGGCGG  
 251 ATTCCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTT GAAAAGCGGC

1406

```
301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTAG GCTTGGGCGT GTACGTCCCC TTCGGTTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGA AACTCAACGA
501 ACGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAGC
551 TCGCGCAAATA TGCCGACTGG GGGATTATGG AAAAAGCGAA AGCACTAAAA
601 GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA
651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGGG
701 TGTGGGACAT CAACGACCGT GCGCGCGTGG GCGTGAAC TA CCGTTCCAAA
751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGCGGCGAG ACGACGCAAT
801 GGCGAAACAG TTATGGGATG CAAACAAACT CGCACTGCTC GGCTACACGC
851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTTGTCCGTA
901 CACGGTATGT ACAAAGTGTC CGACAAAGCC GACCTGTTTC GCGACGTAAC
951 TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAAGTGGTT TTTGAAAAAG
1001 AAAAAACCAT CGTCAACGGC AAATCCGACC GCACCACCAT CACCCCCAAC
1051 TGGCGCAACA CCTCAAAGT CGGCTTCGGC GGTCTTATC AAATCAGCGA
1101 ACCGCTGCAA CTGCGCGCCG GCATCGCTTT TGACAAATCG CCCGTCCGCA
1151 ACGCCGACTA CCGCATGAAC AGCCTGCCCC ACGGCAACCG CATCTGGTTC
1201 TCCGCCGGCA TGAAATACCA TATCGGCAAA AACCACGTCG TCGATGCCCG
1251 CTACACCCAC ATCCACATCA ACGACACCAG CTACCGCACG GCGAAGGCAA
1301 GCGGCAACGA TGTGGACAGC AAAGGCGCGT CTTCCGCACG TTTCAAAAC
1351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

```
a989.pep
1  MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEAADA
51  STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYK VNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERHS FGAGIIAQHT SAELRKYADW GIMEKAKALK
201 ETPPNPTKAA QIKADGHADV KGS DWGFGYQ LAWMWDINDR ARVGVNYRSK
251 VSHTLKGD AE WAADDAMAKQ LWDANKLALL GYTPSEKARV KIVTPESLSV
301 HGMVKVSDKA DLEGDVTWTR HSRFDKAE LV FEKEKTIVNG KSDRTTITPN
351 WRNTYKVGFG GSYQISEPLQ LRAGIAFDKS PVRNADYRMN SLPDGNRIWF
401 SAGMKYHIGK NHVVDAA YTH IHINDTSYRT AKASGNDVDS KGASSARFKN
451 HADIIGLQYT YKEK*
```

m989/a989 93.1% identity in 467 aa overlap

```
10 20 30 40 50 60
m989.pep MTPSALKKTVLLLGTAFAAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989 MTPSALKKTVLLLGTAFAAAASQASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL
10 20 30 40 50 60

70 80 90 100 110 120
m989.pep TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989 TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
70 80 90 100 110 120

130 140 150 160 170 180
m989.pep LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNRHSFGAGIIAQHT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989 LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHT
130 140 150 160 170 180

190 200 210 220 230 240
m989.pep SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGFGYQLAWMWDI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989 SAELRKYADWGIMEKAKALKETPPNPT---KAAQIKADGHADVKGSDWGFGYQLAWMWDI
190 200 210 220 230

250 260 270 280 290 299
m989.pep NDRARVGVNYRSKVSHTLKGD AEWAADGAAAKAMW-STMLAANGYTAN EKARVKIVTPES
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989 NDRARVGVNYRSKVSHTLKGD AEWAADDAMAKQLWDANKLALLGYTPSEKARVKIVTPES
```

1407

	240	250	260	270	280	290
m989.pep	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAE	LVFEKEKTVVKGKSDRTTITPNWRNTYKV				
a989	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAE	LVFEKEKTVVKGKSDRTTITPNWRNTYKV				
m989.pep	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
a989	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
m989.pep	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
a989	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

```

m990.seq
1  ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCCG
51  CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATTACAAT AGCGGCATCC TCGCCGTCGA
201 TAATATGCCC GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
251 TAAAGCAGGC GGTAAAAAGT CAATTACAGG ATTTATACAA AACAAGACCG
301 GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGCACA
351 GTTTGGAACA AAATTTAGTA CGCTCAAACA GACGATGCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCCAC GTCGCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TACGCTGGAA
601 ACTTCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAAGTGAC
651 CGTCCATAAG GATTATGCGG GCGGCGCGGA TTCTCTGTTT GGCTACGACG
701 TCGGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTGGGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
801 CCGGCGCAAA CTGATTGCGG CAAAAACGGC GGATTCCGGT TCGTTTGCCT
851 TTAAACAAAA TTACCGGCAG GGAATGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGACGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTTGGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCGCA TCCGTCCCGT
1051 CAAAAATTGT GGCTGCGCTT CATCGGCGGC CGGTCGCATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GGTGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GACTGGCAAT CGGCGTGATG
1201 GCGGCGAGGG CCGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTGAT TTGTATGGTT ATGGCGGGGG TGTATTATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
1401 AACCAAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCAT TGTCGGAAAA GGCAATAATG TGCGGTTTTA CCTACAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCGC
1601 GCATTCGGGC AAAAACCCGT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTAAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGGC
1751 GGTTCGGTAT TGAAGCCGCT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TATGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990.pep

1408

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQQKNYN SGILAVDNMP VVKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLKQTMP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEF ALTFEDKVSQ
251 QSGVVLERRP ENLKTLDGRK LIAAKTADSG SFQFKQNYRQ GLYELLKQOC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIIRGGA AADGWRKGVQ IGGEVFVRQN EGSRLAIGVM
401 GGRAGQHASV NGKGAAGSD LYGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKXIRINDE NRAERYKTKG WTASVEGGYN ALVAEGIVGK GNNVRFYLPQ
501 QAQFTYLGVN GGFTDSEGT VGLLGSQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

```

a990.seq
1 ATGTTCCAGAG CTCAGCTTGG TTCAAATACT CGTTCACCA AAATCGGCGA
51 CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGCG ACTTCCCATT
101 ATTTTCCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATAACAAT AGCGGCATAC TCGCCGTCGA
201 TAATATGCCC GTTGTTAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTTAAGAAG CAATTACAGG ATTTATACAA AACAAAGACC
301 GAAGCTTGGG AAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGAACA
351 GCTTGACCA AAATTTAGTA TACTCAAACA GAAAACCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCAC GTCCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCTT TTGGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCTGAAC ACGAAAGATG AAAAATGAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751 CAATCCGCGC TGGTTTGGGA ACGCCGGCCG GAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCCTTTGCGT
851 TTAACAAAA TTACCGGCAG GACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAATACT TTGTTGGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAATTGT GGCTGCGCTT CATCGGCGGC CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GGCGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTGT ACGGCAAAAT GAAGGCAGCC GGCTGGCAAT CCGCGTGATG
1201 GCGGCGAGG CTGGCAGCA CGCATCAGT AACGCAAG GCCTGCGGC
1251 AGGCAGTTAT TTGCATGTTT ATGGCGGGG TGTATTGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGTACAA
1401 AACCAAGGT TGGACGGCTT CTGTGAAGG CGGCTACAAC GCGCTGTGG
1451 CGGAAGGCGT TGTCGAAAAA GGCAATAATG TGCGGTTTTA CCGCAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCGAGCG TCAGTGGCAA AGCCGCGCGG
1601 GCATTCGGGC AAAAACCCTT TTTGCTTTC GTACGGTGT CAATCTTCAG
1651 CCTTTGCGG CTTTAAATGT TTTGCACAGG TCAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751 GTTTCGGCAT TGAAGCCGGT TGGAAAGGCC ATATGTCCG CCGCATCGGA
1801 TACGGCAAAA GGACGGACGG CGACAAAGAA GCCGATTGT CCGTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

```

a990.pep
1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQQKNYN SGILAVDNMP VVKYITDITY GDNLDKAVKK QLQDLYKTRP
101 EAWAENKKRT EEAYIEQLGP KFSILKQKNP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHMLE
201 TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDEP ALTFEEKVSG
251 QSGVVLERRP ENLKTLDGRK LIAAEKADSN SFQFKQNYRQ GLYELLKQOC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIIRGGA AADGRRKGVQ IGGEVFVRQN EGSRLAIGVM

```

WO 99/57280

1409

401 GGRAGQHASV NGKGGGAAGSY LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY  
 451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGVVGK GNNVRFYLQP  
 501 QAQFTYLGVN GGFTDSEGTA VGLLGSGQWQ SRAGIRAKTR FALRNGVNLQ  
 551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG  
 601 YGKRDTGDKE AALSLKWL\*F

m990/a990 96.0% identity in 619 aa overlap

	10	20	30	40	50	60
m990.pep	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN					
a990	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN					
	70	80	90	100	110	120
m990.pep	SGILAVDNMPVVKYITEKYGADLKQAVKSQLQDLYKTRPEAWAENKKRTEEAYIAQFGT					
a990	SGILAVDNMPVVKYITDTYGDNLKDAVKKQLQDLYKTRPEAWAENKKRTEEAYIEQLGP					
	130	140	150	160	170	180
m990.pep	KFSTLKQTMFDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
a990	KFSILKQKNPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
	190	200	210	220	230	240
m990.pep	MTLKDSLWEPRRHSDIHTLETSDNARIRLNTKDEKLTVHKDYAGGADFLFGYDVRESDEP					
a990	MTLKDSLWEPRRHSDIHMLETSDNARIRLNTKDEKLTVHKAYQGGADFLFGYDVRESDEP					
	250	260	270	280	290	300
m990.pep	ALTFEDKVSGQSGVVLERRPENLKTLDGRKLIAAKTADSGSFQKQNYRQGLYELLKQC					
a990	ALTFEEKVSGQSGVVLERRPENLKTLDGRKLIAAEKADSNSFAFKQNYRQGLYELLKQC					
	310	320	330	340	350	360
m990.pep	EGGFCLGVQRLAIPAEAVLYAQQAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
a990	EGGFCLGVQRLAIPAEAVLYAQQAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
	370	380	390	400	410	420
m990.pep	RSHQNIRGGAADGWRKGVQIGGEVFRQNEGSRLAIGVMGGRAGQHASVNGKGAAGSD					
a990	RSHQNIRGGAADGRRKGVQIGGEVFRQNEGSRLAIGVMGGRAGQHASVNGKGAAGSY					
	430	440	450	460	470	480
m990.pep	LYGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
a990	LHGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
	490	500	510	520	530	540
m990.pep	ALVAEGIVGKGNVRFYLQPPAQFTYLGVNGGFTDSEGTAVALGSGQWQSRAGIRAKTR					
a990	ALVAEGVVGKGNVRFYLQPPAQFTYLGVNGGFTDSEGTAVALGSGQWQSRAGIRAKTR					
	550	560	570	580	590	600
m990.pep	FALRNGVNLQPPFAAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					
a990	FALRNGVNLQPPFAAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					

1410

	550	560	570	580	590	600
	610	620				
m990.pep	YGKRTDGDKEAALSLKWLF	X				
a990	YGKRTDGDKEAALSLKWLF	X				
	610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

```

g992.seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGCGCGTTG  GGTATACGG
101 GATATGACAG  TGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GGCACGTGAG  GGGACGTGGG  TTTGACGCGG  CCCGTTCCGC  GACGGGCATC
201 GCGGAAATCC  GGCCACAGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGATACCCCT  TCACGTCATC  GACGGCGACG  GCGCGAAACA  TAAATTCGG
301 ATGGCGTATA  TCGACGCACC  GGAGATGAAA  CAGGCTTACG  GTACACGTTT
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAGGG  TAGGAAAGTC  AGTGTACGTG
401 TGTTTGAAAC  CGACCGCTAT  CAGCGCGAAG  TGGCGCAGGT  ATCCGCCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATT
501 TAAAGTTTAT  GCTAAAGAAC  AGCAGGATAA  GCGGGATTTT  GCCGACTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAATCCGC  AAGCGCCGTG  GCGGTACCGC  CGGGCAGGCA  GGAGCGCGCG
651 GGGCAATAAG  GATTGGATGG  ATTCCGTGGG  CGAATGGTTG  GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

```

g992.pep
1  MFRRHRHLKN  MQIKKIMKWL  PVALSLLGAL  GYTGVDSEAV  RTAVAVLDVL
51  GTAGDVGFDA  PVRRRASAKS  GHSYTGTVSK  VYDGDTHLVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDNLNMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDSVGEWL  GIW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

```

m992.seq
1  ATGTTTCAGAC  GGCATCGGCA  TTTGAAAAAT  ATGCAGATTA  AAAAAATCAT
51  GAAATGGCTT  CCCGTCGCCC  TGTCGCTTTT  GGGTGCCTTG  GGTATACGG
101 GGTACGGCAG  CGAGGCGGTG  CGGACGGCGG  TTGCCGTACT  CGACGTACTC
151 GCGCGGCGAG  GGGACGCGGG  TTCCGACGCG  CCCGCCCGCC  GCCGAGCATC
201 GCGGAAATCC  GGCCACCGCT  ACACAGGCAC  GGTGTCCAAA  GTCTATGACG
251 GCGACACCCCT  TCACGTTATC  GACGGCGACG  GCGCGAAACA  CAAATCCGG
301 ATGGCGTATA  TCGACGCGCC  GGAGATGAAA  CAGGCTTACG  GCACGCGTTC
351 GCGCGACAAC  CTGCGCGCGG  CGGCGGAAGG  CAGGAAAGTC  AGCGTGCCTG
401 TGTTTCGATC  CGACCGCTAC  CAGCGCGAAG  TGGCGCAGGT  TTCTGTCGGC
451 AAAACCGATT  TGAACCTGAT  GCAGGTGCAG  GACGGGGCGG  CGTGGCATT
501 TAAAGTTTAT  GCTAAAGAAC  AGCAGGATAA  GCGGGATTTT  GCCGATTATG
551 CCGACGCTCA  AATTCAGGCG  GAAAGGGAAC  GCAAAGGATT  GTGGAAAGCT
601 AAAAATCCGC  AAGCGCCGTG  GCGGTACCGC  CGAGCAGGCA  GGAGCGCGCG
651 GGGCAATAAG  GATTGGATGG  ATGCCGTGGG  CGAATGGTTG  GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

```

m992.pep
1  MFRRHRHLKN  MQIKKIMKWL  PVALSLLGAL  GYTGVDSEAV  RTAVAVLDVL
51  GAAGDAGSDA  PARRRASAKS  GHRYTGTVSK  VYDGDTHLVI  DGDGAKHKIR
101 MAYIDAPEMK  QAYGTRSRDN  LRAAAEGRKV  SVRVFETDRY  QREVAQVSAG
151 KTDNLNMQVQ  DGAAWHYKSY  AKEQQDKADF  ADYADAQIQ  ERERKGLWKA
201 KNPQAPWAYR  RAGRSGGGNK  DWMDAVGEWL  GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992 96.1% identity in 233 aa overlap

WO 99/57280

1411

```

      10      20      30      40      50      60
m992.pep  MFRRHRHLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA
          |||||
g992      MFRRHRHLKNNMQIKKIMKWL PVALSLLGALGYTGYDSEAVRTAVAVLDVLGTAGDVGFDA
          |||||

      70      80      90      100     110     120
m992.pep  PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN
          |||||
g992      PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN
          |||||

      130     140     150     160     170     180
m992.pep  LRAAAEGRKVSVRVFD TDRYQREVAQVSVGKTD LNLMMQVQDGAAWHYKSYAKEQQDKADF
          |||||
g992      LRAAAEGRKVSVRVFD TDRYQREVAQVSVGKTD LNLMMQVQDGAAWHYKSYAKEQQDKADF
          |||||

      190     200     210     220     230
m992.pep  ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRS GGGNKDWM DAVGEWLGIWX
          |||||
g992      ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRS GGGNKDWM DAVGEWLGIWX
          |||||

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

```

a992.seq
1  ATGTTTCAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAAATCAT
51  GAAATGGCTT CCCGTCGCCT TGTCGCTTTT GGGTGCCTTG GGTATACGG
101 GGTACGGCAG CGAGGCGGTG CGGACGGCGG TTGCCGTACT CGACGTACTC
151 GCGCGCGCAG GGGACGCGGG TTCCGACGCG CCCGCCGCC GCCGAGCATC
201 GCGCAATCC GGCACCCGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGACACCCT TCACGTTATC GACGGCGACG GCGCGAAACA CAAATCCGG
301 ATGGCGTATA TCGACGCGCC GGAGATGAAA CAGGCTTACG GCACGCGTTC
351 GCGCGACAAC CTGCGCGCGG CGGCGGAAGG CAGGAAAGTC AGCGTCCGCG
401 TGTTCGACAC CGACCGCTAC CAGCGCGAAG TGGCGCAGGT TTCTGTCGCG
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGCGG CGTGGCATTG
501 TAAAGTTAT GCTAAAGAAC AGCAGGATAA GCGCGATTTT GCCGATTATG
551 CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGGAAGCT
601 AAAAATCCGC AAGCGCCGTG GCGGTACCGC CGGCGAGGCA GGAGCGGCGG
651 GGGCAATAAG GATTGGATGG ATGCCGTGGG CGAATGGTTG GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

```

a992.pep
1  MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGYGSEAV RTAVAVLDVL
51  GAAGDAGSDA PARRRASAKS GHRYTGT VSKVYDGD TLHVIDGDGAKHKIR
101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFD TDRY QREVAQVSVG
151 KTDNLMMQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQAE ERERKGLWKA
201 KNPQAPWAYR RAGRS GGGNK DWM DAVGEWL GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/m992 100.0% identity in 233 aa overlap

```

      10      20      30      40      50      60
a992.pep  MFRRHRHLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA
          |||||
m992      MFRRHRHLKNNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA
          |||||

      70      80      90      100     110     120
a992.pep  PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN
          |||||
m992      PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN
          |||||

      130     140     150     160     170     180

```

1412

```

a992.pep      LRAAAEGRKVSVRVFDTRDYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF
|||||
m992          LRAAAEGRKVSVRVFDTRDYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF
              130      140      150      160      170      180

              190      200      210      220      230
a992.pep      ADYADAQIQAEERERKGLWKAKNPQAPWAYRRRAGRSGGGNKDWMDDAVGEWLGIX
|||||
m992          ADYADAQIQAEERERKGLWKAKNPQAPWAYRRRAGRSGGGNKDWMDDAVGEWLGIX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

```

g993.seq
1      CTGAAAGTCG TATTGGGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51     CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATTCGG ATGGTGGAAA
101    TTACCGGGCA GTATCTGCAC TATATTGCC AAATGGAAGC CTATCAGTTT
151    GATTTGGCGG CGGAATATCT TTTGATGGCG GCAATGCTGA TTGAAATCAA
201    ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCCG
251    ACCCGCGTGC CGAGTTGGTG CGCCGCTCTG TTGCCCTACGA GCAAATGAAA
301    CTGGCGGCGC AGGGTTTGGA CGCGCTGCCG CGTGCGGGAC GGGATTTCGC
351    GTGGGCTTAC CTGCCGCTGG AAATTGCAGC CGAGACGAAG CTGCCCGAGG
401    TTTACATCGC CGATTGTATG CAGGCATGGT TGGGCATTCT TTCTCGGGCA
451    AAACATACGC GCAGCCACGA AGTAATCCAA GAAACCCTTT CCGTGCGCGC
501    GCAAATGACG GCAATCCTGC GCCGTTTGAA CGAACACGGG ATATGCAGGT
551    TTCACGCCCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GATCGTCAAC
601    TTCATCGCCC TGTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651    GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701    ATTCAGACGG CATTTTCGGC ACACGGGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

```

g993.pep
1      LKVVLSFQG PLDLLLYLIR KQIDVLDIP MVEITGQYLH YIAQMEAYQF
51     DLAAEYLLMA AMLIEIKSRL LLPRTAEVED EEADPRAELV RRLLAYEQMK
101    LAAQGLDALP RAGRDFAWAY LPLEIAAETK LPEVYIADLM QAWLGILSRA
151    KHTRSHEVIQ ETLSVRAQMT AILRRLNEHG ICRFHALFNP EQGAAYVIVN
201    FIALLELAKE GLVGIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

```

m993.seq
1      TTGAAAGTCG TATTGGGCAG CTTCCAAGGC CCTTTGGATC TACTGCTGTA
51     TCTGATCCGC AAACAGAATA TCGACGTACT GGATATTCGG ATGGTGAAGA
101    TTACCGAGCA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151    GATTTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201    ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAAGCCG
251    ACCCGCGTGC CGAGTTGGTG CGCCGCTCTG TGGCTTACGA ACAGATGAAG
301    CTGGCGGCGC AGGGTTTGGA CGCGCTGCCG CGAGCCGGAC GGGATTTCGC
351    GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCAGG CTGCCCGAAG
401    TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTTT GTCTCGGGCA
451    AAACACACGC GCAGCCACGA AGTAATCAA GAAACCATCT CCGTGCGCGC
501    GCAAATGACG GCAATCCTGC GCCGTTTGAA CGGACACGGA ATATGCAGGT
551    TTCACGACCT GTTCAATCCC AAACAGGGCG CGGCTTACGT GGTCTGCAAC
601    TTCATCGCAC TGTGGAGCT TGCCAAAGAA GGATTGGTCA GAATCGTGCA
651    GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701    ATTCAGACGG CATTTCCGGC ACACGAGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

```

m993.pep
1      LKVVLSFQG PLDLLLYLIR KQIDVLDIP MVKITEQYLH YIAQIETYQF
51     DLAAEYLLMA AMLIEIKSRL LLPRTETVED EEADPRAELV RRLLAYEQMK
101    LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLGILSRA
151    KHTRSHEVIK ETISVRAQMT AILRRLNGHG ICRFHDLFNP KQGAAYVVVN
201    FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*



1413

m993/g993 93.1% identity in 248 aa overlap

	10	20	30	40	50	60
m993.pep	LKVVLSFGQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	ITYQFDLAAEYLLMA			
g993	LKVVLSFGQGPLDLLLYLIRKQ	NIDVLDIPMVEITGQYLHYIAQ	MEAYQFDLAAEYLLMA			
	10	20	30	40	50	60
	70	80	90	100	110	120
m993.pep	AMLIEIKSRLLLPRTETVEDEE	ADPRAELVRRLLAYEQMKLAAQ	GLDALPRAGRDFAWAY			
g993	AMLIEIKSRLLLPRTETVEDEE	ADPRAELVRRLLAYEQMKLAAQ	GLDALPRAGRDFAWAY			
	70	80	90	100	110	120
	130	140	150	160	170	180
m993.pep	LPLEIAVEAKLPEVYITDLTQ	AWLGILSRAKHTRSHEVIKETIS	SVRAQMTAILRRLNKG			
g993	LPLEIAAETKLPEVYIADLMQ	AWLGILSRAKHTRSHEVIQETLS	SVRAQMTAILRRLNEHG			
	130	140	150	160	170	180
	190	200	210	220	230	240
m993.pep	ICRFHDLFNPQGAAYVVVNFIA	LLELAKEGLVRIVQEDGFGEIRIS	LNHEGAHSDGISG			
g993	ICRFHALFNPQGAAYVVVNFIA	LLELAKEGLVGIVQEDGFGEIRIS	LNHEGAHSDGIFG			
	190	200	210	220	230	240
	249					
m993.pep	TRGGRDVF					
g993	TRGGRDVF					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

a993.seq

```

1  CTGAAAGTCG TATTGAGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATCCG ATGGTGAAGA
101 TTACCGAACA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTTGCGCG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAAC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCGCTG TGGCTTACGA GCAGATGAAG
301 CTGCGCGCAC AAGGTTTGA TGCCTTCCT CGTCCGGGCC GGGATTTCGC
351 ATGGGCATAC CTGCCACTGG AAATTGCCGT CGAAGCCAAG CTGCCCCGAG
401 TCTATATTAC CGACTTGACG CAGCGCTGGC TGAGTATTTT GTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTTATCAA GAAACCATCT CCGTGC GCGC
501 GCAAAATGACG GCAATCCTGC GCCGTTTGAA CAAACACGGG ATATGCAGGT
551 TTACGACCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GGTCTGCAAC
601 TTCATCGCAC TGTGGAGCT TGCCAAAGAA GGTTTGGTCG GAATCGTACA
651 GGAAGTCGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCCGGC ACACGGGGCG GGC GCGATGT GTTCTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 3006; ORF 993.a&gt;:

a993.pep

```

1  LKVVLSFGQ PLDLLLYLIR KQIDVLDIP MVKITEQYLH YIAQIETYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTETVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLSILSRA
151 KHTRSHEVIK ETISVRAQMT AILRRLNKHG ICRFHDLFNP EQGAAYVVVN
201 FIALLELAKE GLVGIVQEVG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

	10	20	30	40	50	60
a993.pep	LKVVLSFGQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	ITYQFDLAAEYLLMA			
m993	LKVVLSFGQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQ	ITYQFDLAAEYLLMA			

1414

	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
m993	70	80	90	100	110	120
a993.pep	130	140	150	160	170	180
m993	130	140	150	160	170	180
a993.pep	190	200	210	220	230	240
m993	190	200	210	220	230	240
a993.pep	249					
m993	249					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

g996.seq

```

1 ATGAACAGAA GAACCTTCCT CCTCGGCGCA GGC GCGTTGC TTCTTACCGC
51 CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTCCC GAAGGAAGCA
101 CCGTGCTTGC CTTGGGCGAT TCGCTCACCT TCGGCTACGG AGCAAACCCC
151 GCGGAATCCT ACCCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACGTCCGC GCAAGCCCTA TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAAA CCCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TGCACAAAGT TCCCGAGGAG CAGACCCGCG CCAATATCGC
351 GAAATCATC GAAACCGTGC AAAAGGAAAA CATCCCGGCC GTCCTCGTCG
401 GCGTGCCGCA CATCACTG GCGCGTTGT TCGGGCATTG GAGCGACCAT
451 CCGCTGTATG AGGATTGTG CAGGAATAC GGCATTCCGT TGTTCGGCGG
501 CCGCTGGGCG GAAATTTTGG GCAATAATA TCTGAAATCC GACCAATATC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTCG CCGAAATTTT GAATCAATTT
601 TTGAGAAAAC ATGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

g996.pep

```

1 MNRRTFLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51 GESYPAQLQK LTGWNIVNGG VSGDTSQAAL SRLPALLARK PKLVIVGIGG
101 NDFLRKVPPEE QTRANIAKII ETQKENIPA VLVGVPHITL GALFGLHSDH
151 PLYEDLSEFY GIPLFGGAWA EILGNLNLKS DQIHANGKGY RKFAENLNQF
201 LRKHGFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

m996.seq

```

1 ATGAACAGAA GAACCTTCCT CCTCGGCGCA GGC GCGTTGC TGCTTACCGC
51 CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTCCC GAAGGAAGCA
101 CCGTACTTGC CTTGGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCCCT
151 GCGGAATCCT ACCCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACATCTGC CCAAGCCCTG TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAAA CCCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TGCACAAAGT TCCCAAGGAG CAGACCCGCG CCAATATCGC
351 GAAATCATC GAAACCGTGC AGAAGGAAAA CATCCCGGCC GTCCTCGTCG
401 GCGTGCCGCA CATCACTG GGTGCGTTGT TCGGGCATTG GAGCGATCAT
451 CCGCTGTATG AGGATTGTG CAGGAATAC GGCATTCCGC TGTTCGGCGG
501 CCGCTGGGCG GAAATTTTGG GCGATAATA TCTGAAATCC GACCAATATC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTTG CCGAAGATTG GAATCAATTT
601 TTGAGAAAAC AGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>:

m996.pep

```

1 MNRRTFLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51 GESYPAQLQK LTGWNIVNGG VSGDTSQAAL SRLPALLARK PKLVIVGIGG

```

1415

101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLS DH  
 151 PLYEDLSEY GIPLFGGAWA EILGDN NLKS DQIHANGKGY RKFAEDLNQF  
 201 LRKQGFR

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

m996/g996 98.1% identity in 207 aa overlap

m996.pep	10	20	30	40	50	60
	MNRRTELLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					
g996	10	20	30	40	50	60
	MNRRTELLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					
m996.pep	70	80	90	100	110	120
	LTGWNIVNGGVSGD TSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
g996	70	80	90	100	110	120
	LTGWNIVNGGVSGD TSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
m996.pep	130	140	150	160	170	180
	ETVQKENIPAVLVGVPHITL GALFGHLS DHPLYEDLSEYGIPLFGGAWAEILGDN NLKS					
g996	130	140	150	160	170	180
	ETVQKENIPAVLVGVPHITL GALFGHLS DHPLYEDLSEYGIPLFGGAWAEILGNN NLKS					
m996.pep	190	200				
	DQIHANGKGYRKFAEDLNQFLRKQGFR					
g996	190	200				
	DQIHANGKGYRKFAENLNQFLRKHGFRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

a996.seq

```

1  ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGGTTGC TCCTTACCGC
51  CTGCGGCAGA AAATCCGCC GAACCCACGC CAAAATTCCC GAAGGAAGCA
101 CCGTACTTGC CTGGGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCCC
151 GCGCAATCCT ACCCGCGCA ACTGCAAAA CTGACGGGT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACATCCGC CCAAGCCCTG TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAA CCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TCGCAGAA GTCCCAAGGAG CAGACCCGCG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AGAAGGAAA CATCCCGGCC GTCCCTCGTCG
401 GCGTGCCGCA CATTACCTTG GCGCGTGTG TCGGGCATTG GAGCGATCAT
451 CCGCTGTATG AGGATTGTG CGAGGAATAC GGCATTCCGC TGTTCGGCGG
501 CCGCTGGGCG GAAATTTTG GCGATAATA TCTGAAATCC GACCAATCC
551 ACGCCAACGG CAAAGCTAT CGGAAATTG CCGAAGATT GAATCAATT
601 TTGAGAAAAC AGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

a996.pep

```

1  MNRRTELLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51  GESYPALQK LTGWNIVNGG VSGD TSAQAL SRLPALLARK PKLVIVGIGG
101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLS DH
151 PLYEDLSEY GIPLFGGAWA EILGDN NLKS DQIHANGKGY RKFAEDLNQF
201 LRKQGFR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

a996/m996 100.0% identity in 207 aa overlap

a996.pep	10	20	30	40	50	60
	MNRRTELLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					

1416

```

|||||
m996  MNRRTELLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFYGANPGESYPALQK
      10      20      30      40      50      60
a996.ppep  LTGWNIVNGGVSGDTSQAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
      70      80      90      100     110     120
m996  LTGWNIVNGGVSGDTSQAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
      70      80      90      100     110     120
a996.ppep  ETVQKENIPAVLVGVPHITLALFGHLSHDPLYEDLSEYGIPLFGGAWAEILGDNNLKS
      130     140     150     160     170     180
m996  ETVQKENIPAVLVGVPHITLALFGHLSHDPLYEDLSEYGIPLFGGAWAEILGDNNLKS
      130     140     150     160     170     180
a996.ppep  DQIHANGKGYRKFAEDLNQFLRKQGRX
      190     200
m996  DQIHANGKGYRKFAEDLNQFLRKQGR
      190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCGCGC TTGTCGCCCG CCGTCACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCCG CAGGCGGGCG GAAGGGCGCG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGGCGTGT TGCGCCTGAT GAAAACCATC GGTTCGAGCC
251 CCCGTGCCCG CTTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAAGTCTTGT
401 CCGATATGTC CGATTGTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAAT
501 GCAGTTTGGG CAGCCCTTGG TCTGGGGCGC GCTCAACACG CCTTTGGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCGCCTTGG CCGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGAAAAGTC
751 CTCGTCAACG GCGAAGCCTT CGATGCCGCC ATACTTGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCTGTC CCGCCCGCTG ACCGGCATtg CCGACggcAC
951 ggcaCaatgG CTGCTTTgcc cgGGGCAGGC tccggactgc CcccaaAacg
1001 aagTCTCCCG cGTCAttagc GTTCCGAcc GCGtcggcgC Gtttgcaaac
1051 cga...

```

This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>:

```

g997.pep (partial)
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51  GNTDGFGLD NGQHILLGAY RGVLRMLKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPSAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVL
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA ILATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGIADGTAQW LLCPGQAPDC PQNEVSAVIS VSDRVGAFAN
351 R....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3015>:

```

m997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCGAGG CTGTCCGCCG CCGTCACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCCCG CAGGCGGGCG GCAGGGCGCG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGGCGTGT TGCGCCTGAT GAAAACCATC GGTTCGAGCC
251 CCCGTGCCCG CTTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGTG CACCGACTGC ATTCAAAGCC AAAGTCTTGT
401 CCGATATGTC CGATTGTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTGAT
501 GCAGTTTGGG CAGCCCTTGG TTTGGGGCGC GCTCAACACG CCTTTGGAAA

```

1417

```
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAGCAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCTTGG CGGATCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCTCCCGGA CCGGAAAGTG
751 CTCGTCAACG GCGAAGCTTT CGATGCCGCC GTCCCGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCG TCCGCTTGGC GCGCCCGCTG ACCGGCCTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCAGGCT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGCGGG ACAAAGCCCA CGCCGACCTC AAACGCATCC TTCCGCATT
1101 GGGCGAACC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCGCC GACTTGTCTG GGTTCACCG GCACCGCATC
1201 TTCCCGCGCG GCGACTACCT CCACCGGAC TACCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

```
m997.pep
1 MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51 GNTDGGFGLD NGQHILLGAY RGVLRMLKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRAPTAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVLT
201 KKS GSDYLLP KQDLGAI VAE PALADLQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTQW LLCRGRGLP ENEVSAVISV SDRVGAFAFNR
351 AWADKAHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRHRI
401 FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

g997/m997 96.0% identity in 351 aa overlap

	10	20	30	40	50	60
g997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGGFGLD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g997.pep	NGQHILLGAYRGVLRMLKTI GSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
m997	NGQHILLGAYRGVLRMLKTI GSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g997.pep	ARRVPSAFKALLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFKALLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g997.pep	PLETASLRVLCNVLSGVLT KKS GSDYLLPKQDLGAI VAE PALAELQRLGADIRLETRVC					
m997	PLETASLRVLCNVLSGVLT KKS GSDYLLPKQDLGAI VAE PALADLQRLGADIRLETRVC					
	190	200	210	220	230	240
	250	260	270	280	290	300
g997.pep	RLNTLPDGKVLVNGEAFDAA ILATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY					
m997	RLNTLPDGKVLVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY					
	250	260	270	280	290	300
	310	320	330	340	350	
g997.pep	AEPVRLPAPLTGIADGTAQWLLCPGQAPDCPQNEVSAVISVSDRVGAFAFNR					
m997	AEPVRLPAPLTGLADGTQWLLCRGRGLPENEVSAVISVSDRVGAFAFNR					
	310	320	330	340	350	

1419

```

m997      PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC
           190      200      210      220      230      240

           250      260      270      280      290      300
a997.pep  RLNTLPDGKVLVNGEPFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRVHAITTVYLRY
           |||
m997      RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRVHAITTVYLRY
           250      260      270      280      290      300

           310      320      330      340      350      360
a997.pep  AEPVRLPAPLTGLADGTQWLLCRGRLGLFENEVSAVISVSDRVGAFANRAWADKVHADL
           |||
m997      AEPVRLPAPLTGLADGTQWLLCRGRLGLFENEVSAVISVSDRVGAFANRAWADKAHADL
           310      320      330      340      350      360

           370      380      390      400      410      420
a997.pep  KRILPHLGEPEAVRVITEKRATTAADAPPPDLNHLRHRIFPAGDYLHPDYPATLEAAVQ
           |||
m997      KRILPHLGEPEAVRVITEKRATTAADAPPPDLNHLRHRIFPAGDYLHPDYPATLEAAVQ
           370      380      390      400      410      420

           430
a997.pep  SGFASAEACLQSLSDAVX
           |||
m997      SGFASAEACLQSLSDAVX
           430

```

g999.seq Not found yet

g999.pep Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

```

m999.seq
1  ATGAATATGA AAAAATTGAT TTCCGCAATT TGTGTTTCAA TTGTTTATC
51  AGCCTGCAAC CAACAATCAA AACGGCACA AGCCGAAGAA CCTGTCCAAA
101 GTATCCAGGC TGCTGATTGT ACCGCCCAA TGGACATCAC AGTTGAACAA
151 TATCTCATCA ATTTGGAGCA AGCATTAAA ACTCAGAACG TCTCAACAAA
201 AATCCATAAT AAAAATATTG TCAAGACCGA TTGTGTTTAT GACCTTACTT
251 TGGTAATGGA TTTTGGGGCG ATTGCGCTCA AACTGGACGA GCAGCAAAAA
301 ATTAGAGCTA TCTCAGTAGG CTACATTTTA AAAACCGACG GAGAGAAAGG
351 ACAAATCTA GTCAATAATG CCATAAATGG ATTACACAGT ATTCAGGCAG
401 TTCTGTCTTT AACTACCACA GACAAATTGG GCGAATCGGA AGCAGGAAAA
451 CAACTTTTTA CAGCTTAAAC CGAAGTCGTC AAAGAATCCA ATCAGACAGG
501 AGCAACAGCG CAAAAGACG TTCCGGCAGA TGGTATTTTA TATAGCGTTG
551 TTTTGA AAAAGCAAAC ACCATTGCAA TAATCGGCAG AAAACAACCC
601 TAA

```

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>:

```

m999.pep
1  MNMKKLISAI CVSIVLSACN QOSKTAQAE PVQSIQAADC TAPMDITVEQ
51  YLINLEQAFK TQNVSTKIHN KNIVKTDGKY DLTLMDFGA IALKLDEQOK
101 IRAISVGYIL KTDGEKGQNL VNNAINGLHS IQAVLSLTTT DKLGESEACK
151 QLFTALTEVV KESNQTGATA QKDVPADGIL YSVVFEKETN TIAIIGRKQP

```

a999.seq Not found yet

a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.

1418

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

```
a997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCCGGC TTGTCCGCCG CCGTTACCTT GCGCGGCAC GCGACGTTA
101 CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GCAGGGCGCG CGCACTGGCC
151 GGAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ATATTTTACT
201 CGGCGCATAC CGGGGCGTGT TGCGCCTGAT GAAACCATC GGTTCAGACC
251 CCCATGCCGC CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCTGCCC GCG CCCCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAACGCTTG
401 CCGATATGTC CGATTTGCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGG CAGCCCTTGG TTTGGGGCGC GCTCAACACG CCTTTGGAAG
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCCCTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAGC GCGCATATGC CGTCTGAACA CCCTCCCGGA CGGGAAAGTG
751 CTCGTCAACG GCGAACCTTT CGATGCCGCC GTCCCGCGCA CCGCGCCCTA
801 CCACGCCGCG GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAT CACGCCATCA CCACCGTCTA TCTGCGCTAT
901 GCCGAACCCG TCCGCTTGCC TGCCCGGCTG ACCGGAAGTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCAAGCT CGGACTGCCT GAAACGAAG
1001 TGTCCGCGGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAACCGG
1051 GCGTGGGCGG ACAAAGTTCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GGGCGAACC CCGAAGGCAC CCGAAGGCAC GTTCAGACGG
1151 CAGCCGATGC CCCGCCCGCG GATTGTGCTG GGTTCGACCG GCACCGCATC
1201 TTCCCGCGCG GCGACTACCT CCACCCAGAC TACCCGCGCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

```
a997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLEAGR QAGGRARALA
51  GNTDGFGLD NGQHILLGAY RGVLRMKTI GSDPHAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHLGGVLL ARRVPFAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWALNT PLETASLRVL CNVLSGVL
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRIC RLNTLPDGKV
251 LVNPEPFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTVQW LLCRGRGLP ENEVSAVISV SDRVGAFAFR
351 AWADKVHADL KRILPHLGEF EAVRVITEKR ATTAADAPPP DLSWLHRHRI
401 FPAQDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

a997/m997 98.2% identity in 437 aa overlap

	10	20	30	40	50	60
a997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARALAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
a997.pep	NGQHILLGAYRGVLRMKTI GSDPHAAFLRVPLHWHMHGGLQFRALPLPAPLHLGGVLL					
m997	NGQHILLGAYRGVLRMKTI GSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHLGGVLL					
	70	80	90	100	110	120
a997.pep	ARRVPFAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWALNT					
m997	ARRAPFAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWALNT					
	130	140	150	160	170	180
a997.pep	PLETASLRVLCNVLSGVLTKKSQSDYLLPKQDLGAIVAEPAELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSGVLTKKSQSDYLLPKQDLGAIVAEPAELQRLGADIRLETRIC					
	190	200	210	220	230	240
a997.pep	PLETASLRVLCNVLSGVLTKKSQSDYLLPKQDLGAIVAEPAELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSGVLTKKSQSDYLLPKQDLGAIVAEPAELQRLGADIRLETRIC					

## CLAIMS

1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
3. A protein having 50% or greater homology to a protein according to claim 1.
4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
5. An antibody which binds to a protein according to any one of claims 1 to 3.
6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
14. A composition according to claim 11 for use as a pharmaceutical.
15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.



16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.

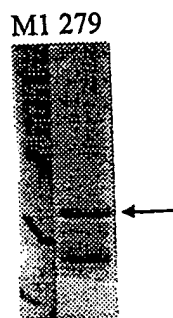
17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.

18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

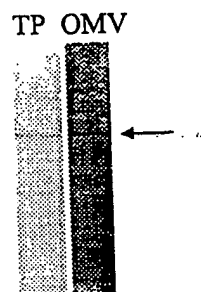
Fig. 2

279 (10.5 kDa)

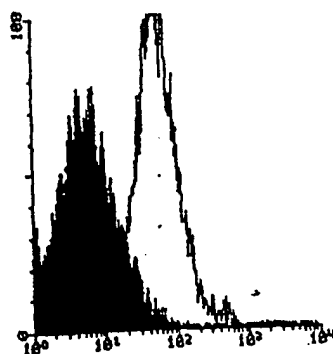
## A) PURIFICATION



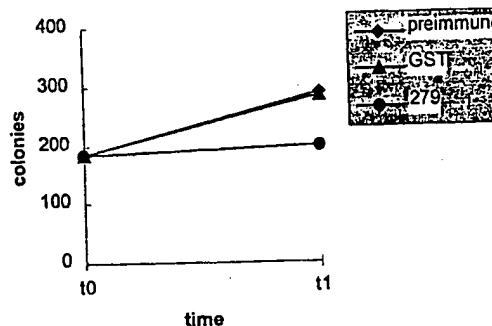
## B) WESTERN BLOT



## C) FACS



## D) BACTERICIDAL ASSAY

E) ELISA assay: positive

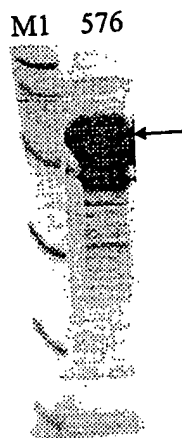
## 279

The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that protein 279 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 3

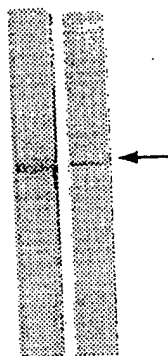
576 (27.8 kDa)

## A) PURIFICATION

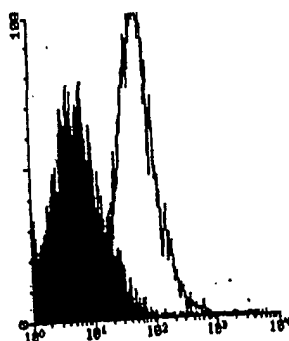


## B) WESTERN BLOT

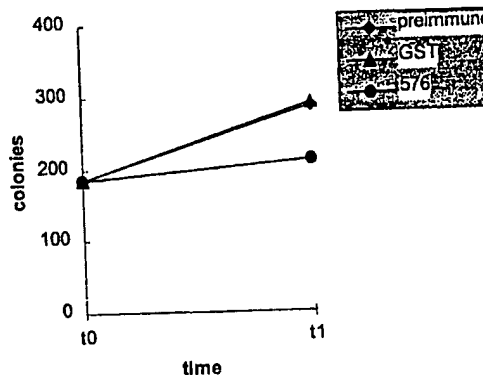
TP OMV



## C) FACS



## D) BACTERICIDAL ASSAY

E) ELISA assay: positive

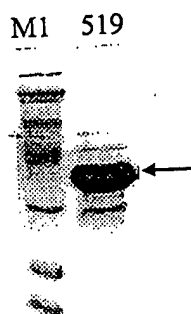
## 576

The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 576 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 4

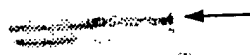
519 (33 kDa)

## A) PURIFICATION

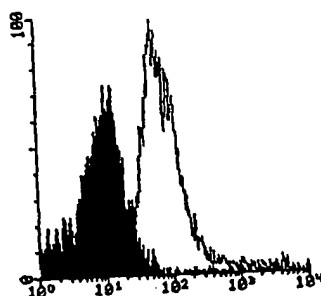


## B) WESTERN BLOT

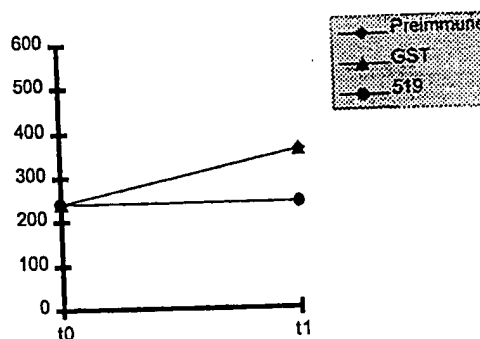
TP OMV



## C) FACS



## D) BACTERICIDAL ASSAY

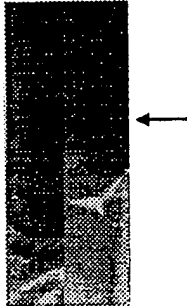
E) ELISA assay: positive

## 519

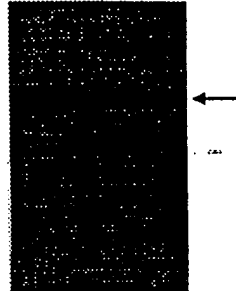
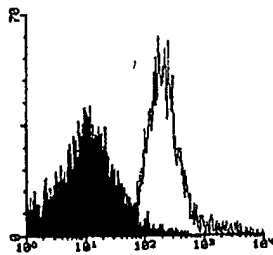
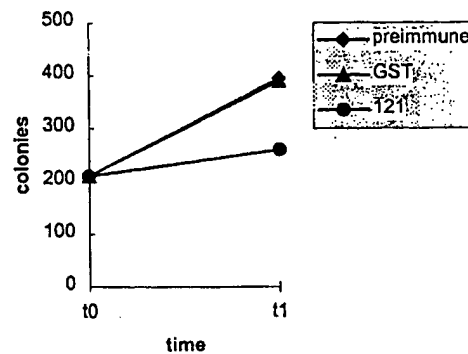
The predicted gene 519 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 519 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

**121 (40 kDa)****A) PURIFICATION**

M1 121

**B) WESTERN BLOT**

TP OMV

**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****121**

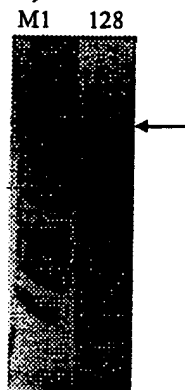
The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

**Fig. 5**

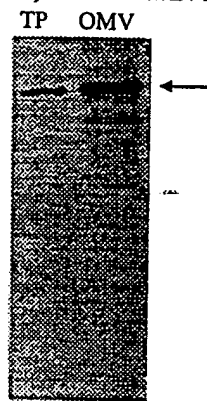
128 (101 kDa)

Fig. 6

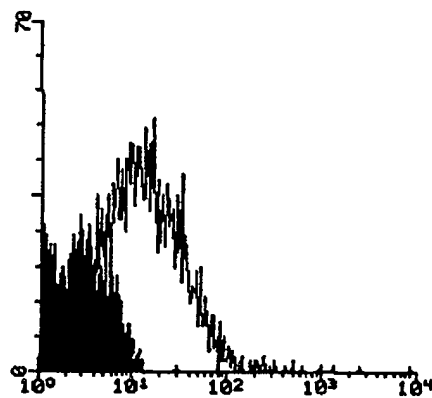
## A) PURIFICATION



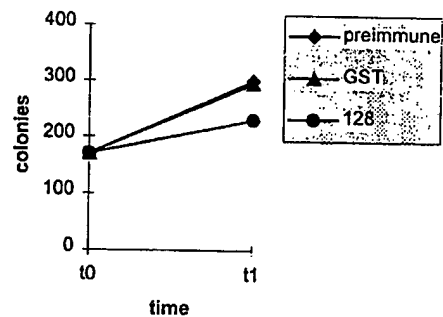
## B) WESTERN BLOT



## C) FACS



## D) BACTERICIDAL ASSAY



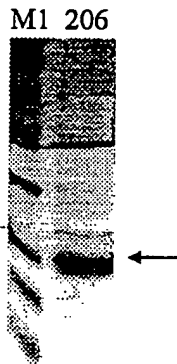
## E) ELISA assay: positive

## 128

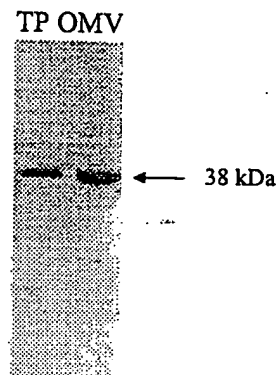
The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 7

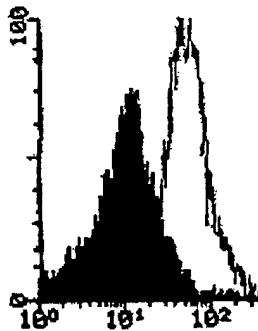
## A) PURIFICATION



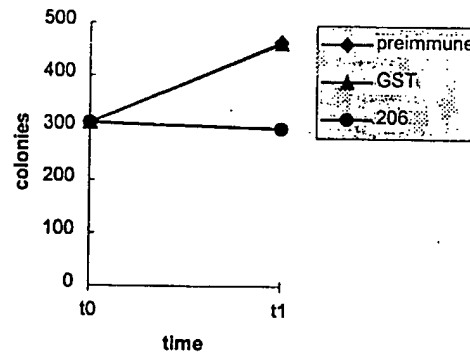
## B) WESTERN BLOT



## C) FACS



## D) BACTERICIDAL ASSAY



## E) ELISA assay: positive

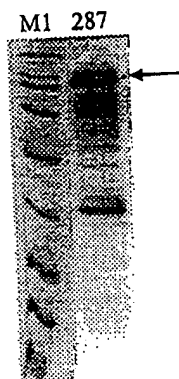
## 206

The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worthnoting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a recative band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C) is shown the FACS analysis, in panel D) the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

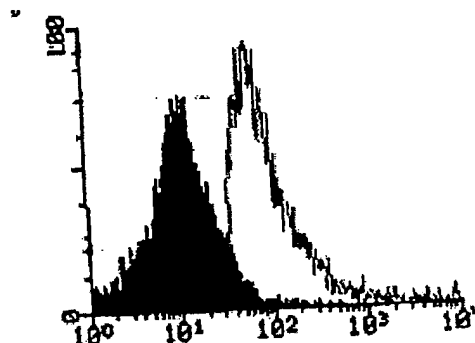
Fig. 8

287 (78 kDa)

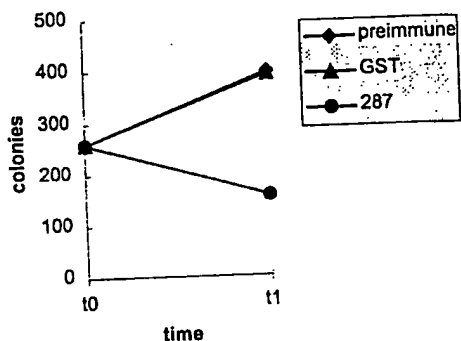
## A) PURIFICATION



## B) FACS



## C) BACTERICIDAL ASSAY

D) ELISA assay : positive

## 287

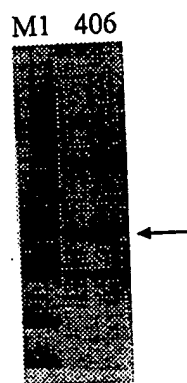
The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A).



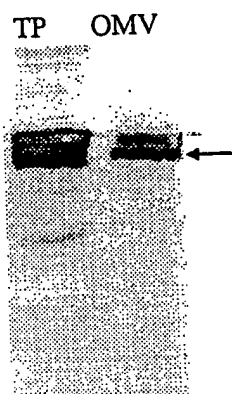
406 (33 kDa)

Fig. 9

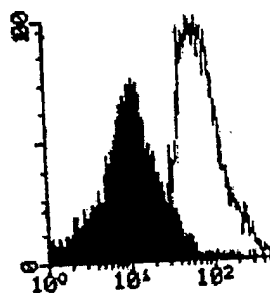
## A) PURIFICATION



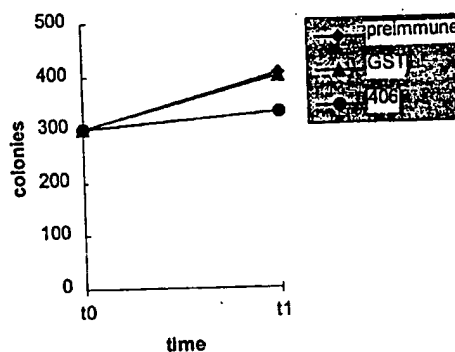
## B) WESTERN BLOT



## C) FACS



## D) BACTERICIDAL ASSAY

E) ELISA assay : positive

## 406

The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

9/30

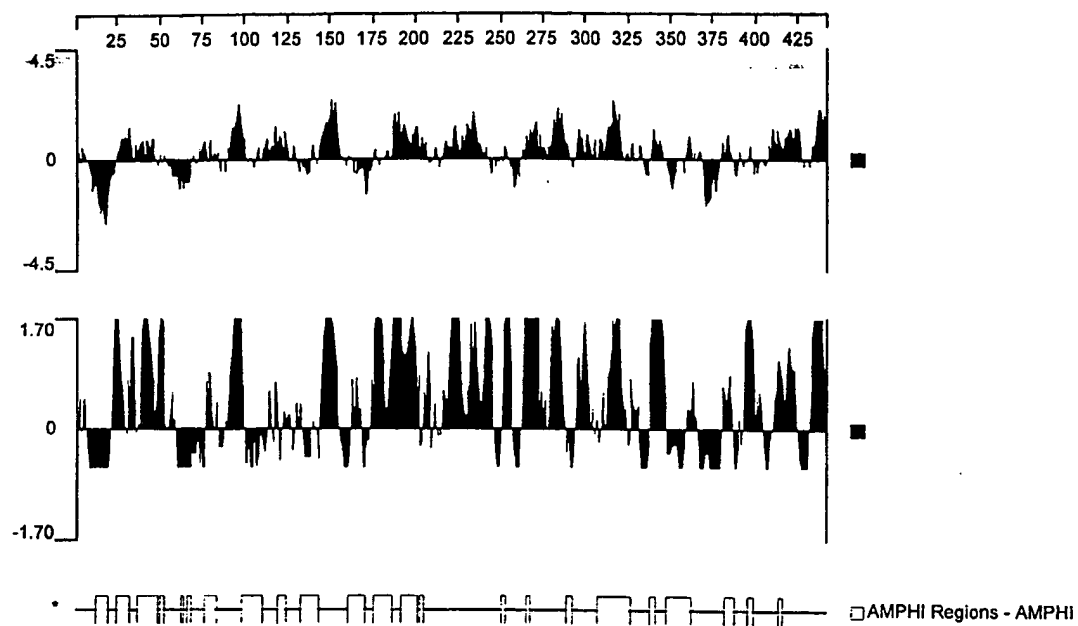
919Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 10

10/30

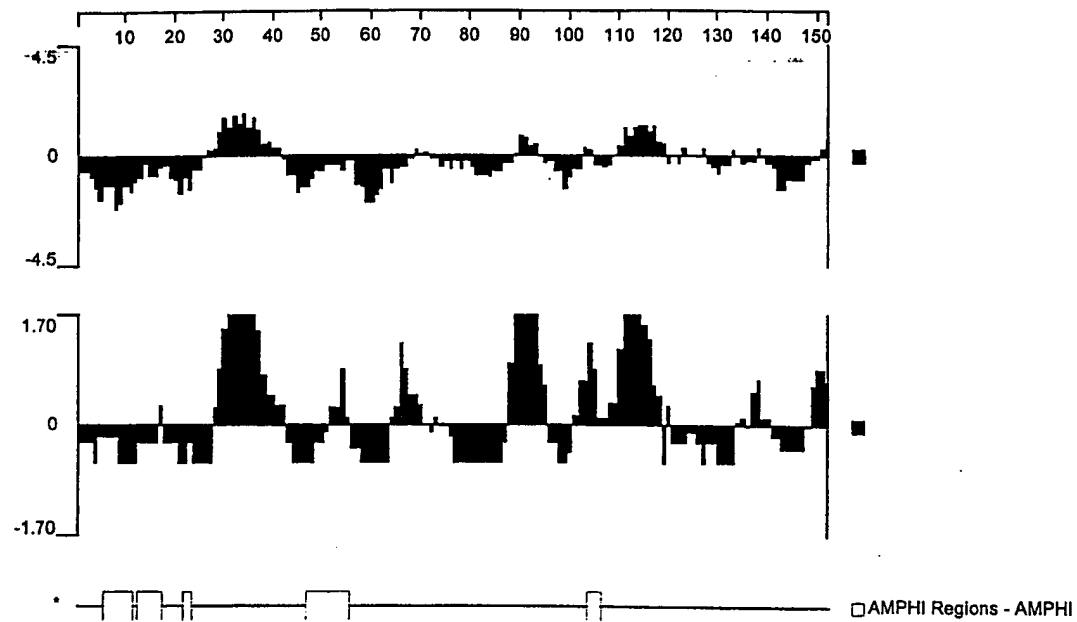
279Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 11

11/30

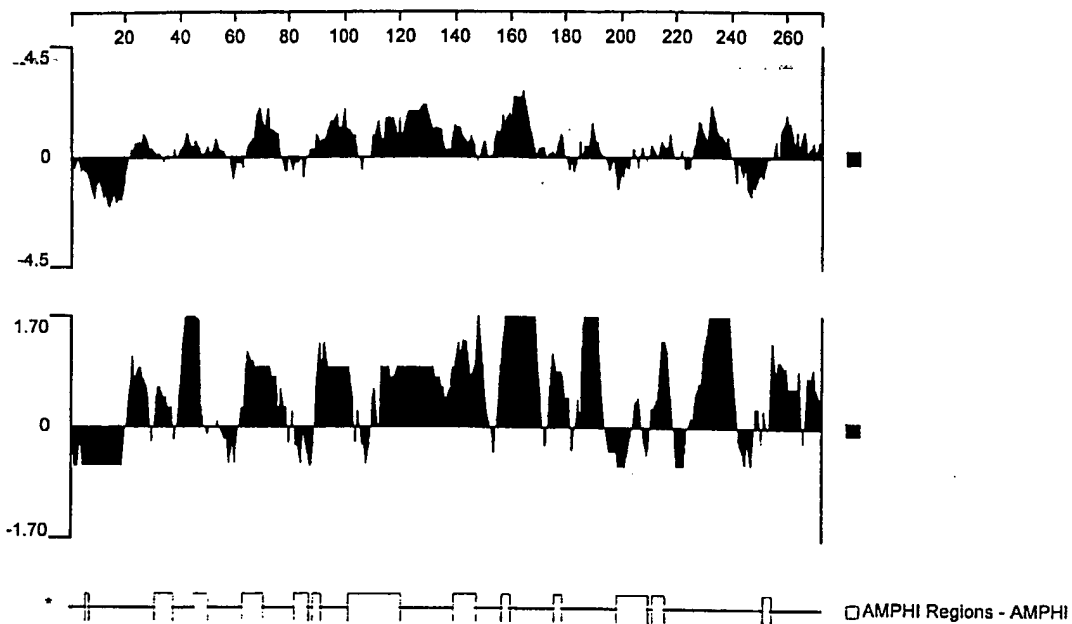
576-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 12

12/30

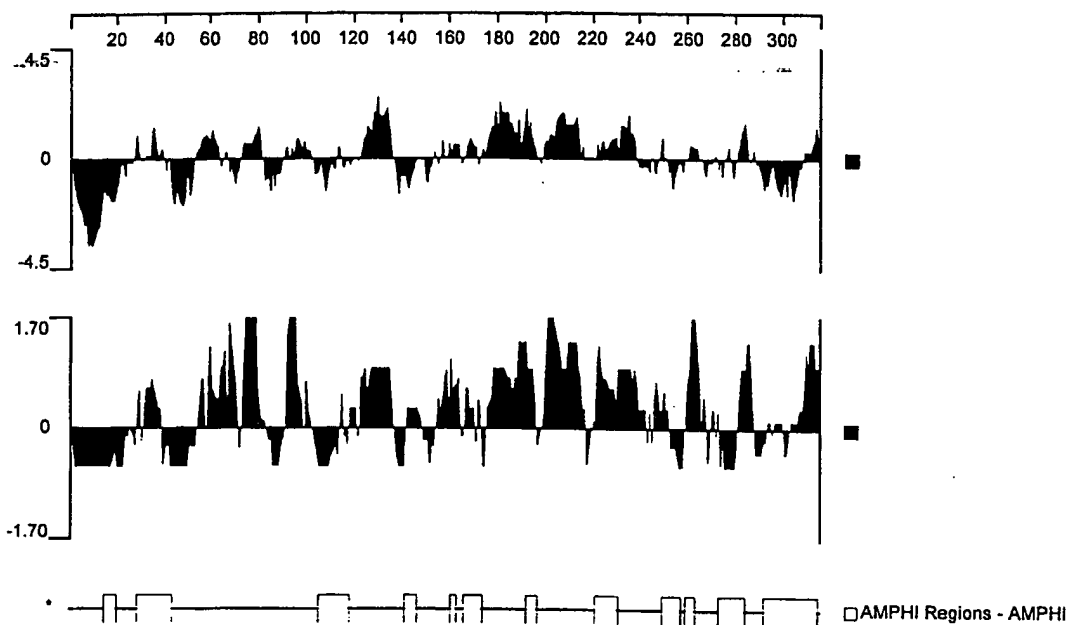
519-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 13

13/30

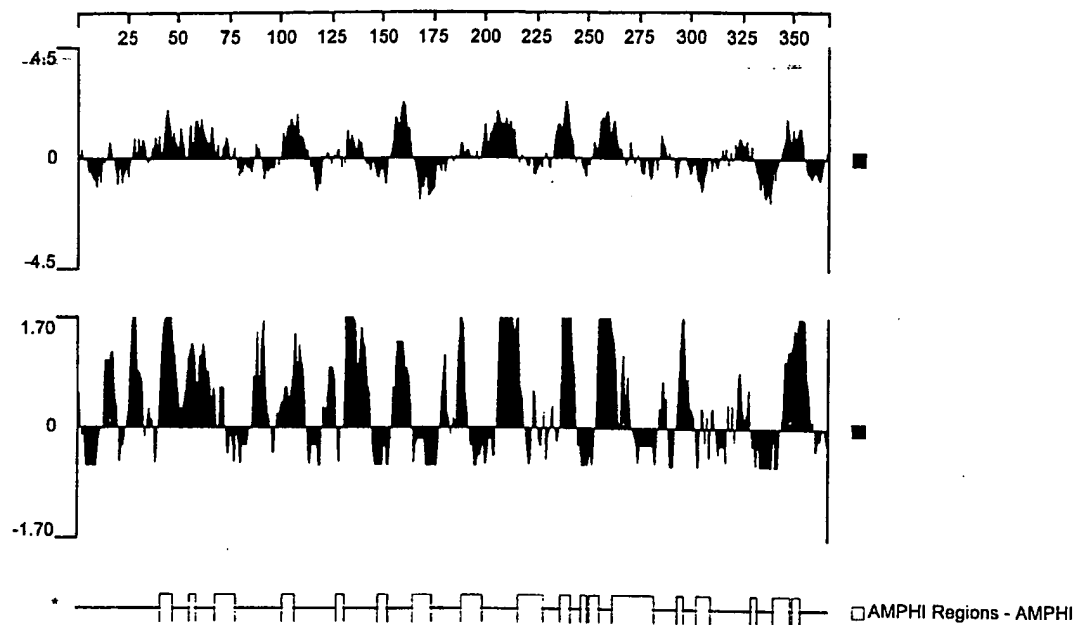
121-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 14

14/30

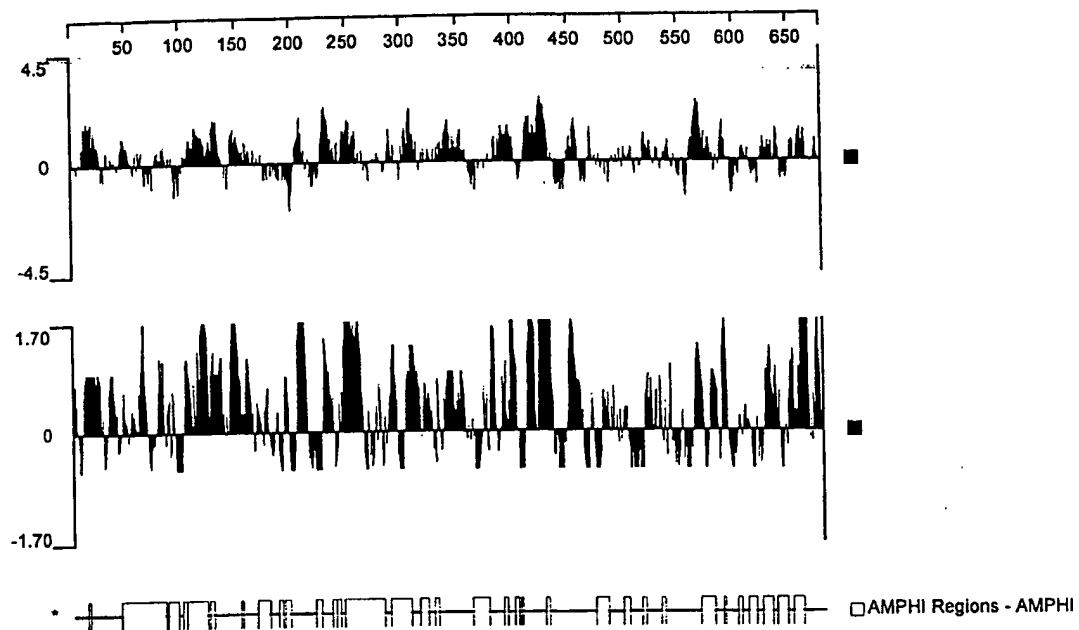
128-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 15

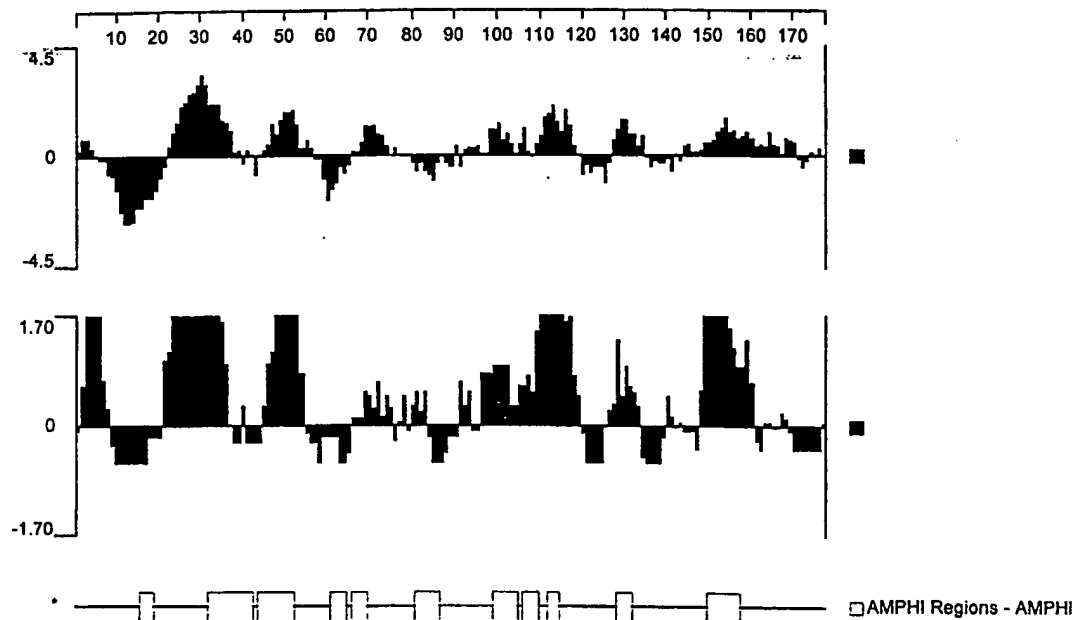
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 16



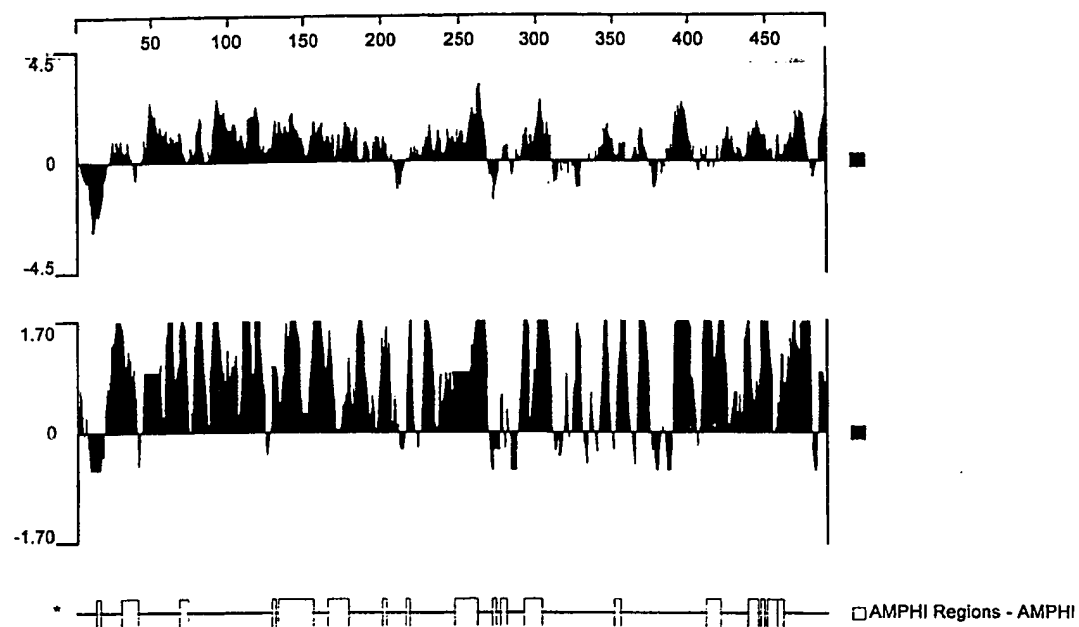
287Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 17

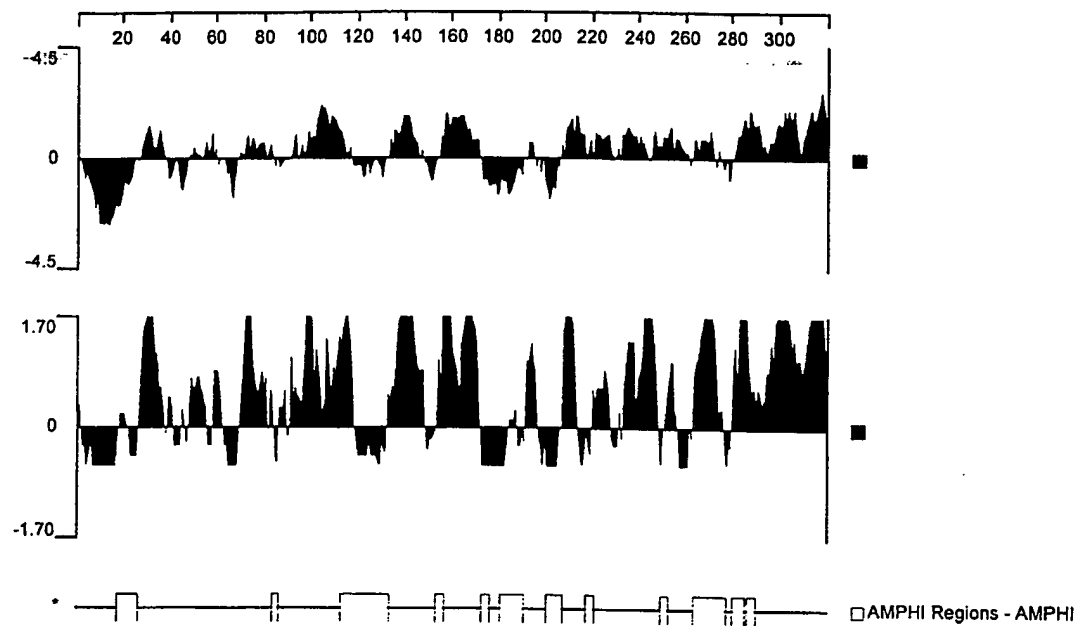
406Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 18

**Fig. 19A**



zo05_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo08_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
z2491	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo11_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo20_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo01_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo09_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo12_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo22_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo23_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo24_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo25_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo26_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo96_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo02_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo04_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo06_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo07_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo10_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo14_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo16_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo17_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo18_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo19_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo21_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo27_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo28_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo29_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo13_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo03_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo15_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
fa1090	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo32_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo33_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Fig. 19C

**Fig. 20A**



```

287_14 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVVE .....KETEA
287_2 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVVE .....KETEA
287_21 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVVE .....KETEA
z2491 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVVE .....KETEA
287_9 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVVE .....KETEA
fa1090 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVVE .....KETEA
      1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPAAPVVVE .....KETEA

287_14 50 KEDAPQAGGQGGGAPSAQGGQDMAAVSEENTGNGGAATDKPKNEDEGAQNMDPQNAADT
287_2 50 KEDAPQAGGQGGGAPSAQGGQDMAAVSEENTGNGGAATDKPKNEDEGAQNMDPQNAADT
287_21 50 KEDAPQAGGQGGGAPSAQGGQDMAAVSEENTGNGGAATDKPKNEDEGAQNMDPQNAADT
z2491 50 KEDAPQAGGQGGGAPSAQGGQDMAAVSEENTGNGGAATDKPKNEDEGAQNMDPQNAADT
287_9 61 VSGAPQADT...ODATAGKGGQDMAAVSAENTGNGGAATDKPKNEDEGAQNMDPQNAADT
fa1090 61 AGGAPQADT...ODATAGKGGQDMAAVSAENTGNGGAATDKPKNEDEGAQNMDPQNAADT

287_14 110 DSLTPNHTPASNMPAGNMEQAPDAGESLQPANQPDMAANTADGMQGGDDPSAGGENAGNTA
287_2 110 DSLTPNHTPASNMPAGNMEQAPDAGESLQPANQPDMAANTADGMQGGDDPSAGGENAGNTA
287_21 110 DSLTPNHTPASNMPAGNMEQAPDAGESLQPANQPDMAANTADGMQGGDDPSAGGENAGNTA
z2491 110 DSLTPNHTPASNMPAGNMEQAPDAGESLQPANQPDMAANTADGMQGGDDPSAGGENAGNTA
287_9 119 DSLTPNHTPASNMPAGNMEQAPDAGESLQPANQPDMAANTADGMQGGDDPSAGGENAGNTA
fa1090 117 .....

287_14 170 AQGTNOALNNOTAGSQNPASSTNPSATNSGGEFGRTNKNSVVIDGPSQNTLTHCKGDS
287_2 170 AQGTNOALNNOTAGSQNPASSTNPSATNSGGEFGRTNKNSVVIDGPSQNTLTHCKGDS
287_21 170 AQGTNOALNNOTAGSQNPASSTNPSATNSGGEFGRTNKNSVVIDGPSQNTLTHCKGDS
z2491 170 AQGTNOALNNOTAGSQNPASSTNPSATNSGGEFGRTNKNSVVIDGPSQNTLTHCKGDS
287_9 178 DOLANOALNNOTAGSQNPASSTNPSATNSGGEFGRTNKNSVVIDGPSQNTLTHCKGDS
fa1090 117 .ESANTGNNQAPAGSDSAPASNPAPANGGSDGFGRTNKNSVVIDGPSQNTLTHCKGDS

287_14 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNKRFVGLVADSVQMKGINOYII
287_2 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNKRFVGLVADSVQMKGINOYII
287_21 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNKRFVGLVADSVQMKGINOYII
z2491 230 CSGNNFLDEEVQLKSEFEKLSDAKISNYKKDGKNDGKNKRFVGLVADSVQMKGINOYII
287_9 238 CORDFLDEEAPPKSEFEKLSDAKISNYKKDGKNDGKNKRFVGLVADSVQMKGINOYII
fa1090 176 CNGNDLDEEAPPKSEFEKLSDAKISNYKKDGKNDGKNKRFVGLVADSVQMKGINOYII

287_14 290 FYKQKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
287_2 290 FYKQKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
287_21 286 FYKQKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
z2491 286 FYKQKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
287_9 293 IYKQKSA...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
fa1090 232 FYTDKPTT.....RSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG

287_14 348 NYRYLTYGAELPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPTGRFAA
287_2 348 NYRYLTYGAELPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPTGRFAA
287_21 344 NYRYLTYGAELPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPTGRFAA
z2491 344 NYRYLTYGAELPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPTGRFAA
287_9 353 NYRYLTYGAELPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPTGRFAA
fa1090 285 NYRYLTYGAELPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPTGRFAA

287_14 408 KVDFGSKSVDGIIDSGDLHMGTOQKFKAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
287_2 408 KVDFGSKSVDGIIDSGDLHMGTOQKFKAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
287_21 404 KVDFGSKSVDGIIDSGDLHMGTOQKFKAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
z2491 404 KVDFGSKSVDGIIDSGDLHMGTOQKFKAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
287_9 413 KVDFGSKSVDGIIDSGDLHMGTOQKFKAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
fa1090 345 KVDFGSKSVDGIIDSGDLHMGTOQKFKAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA

```

FIG. 21A



287_14	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_2	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_21	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
z2491	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_9	473	GKYSYRPTDAEKGGFGVFAGKKEQD*
fa1090	405	GKYSYRPTDAEKGGFGVFAGKKEQD*

FIG. 21B

z2491_519	121	RMELDKTFFEEDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv26_519	121	RMELDKTFFEEDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv22_519aaa	121	RMELDKTFFEEDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
fa1090_519	121	RMELDKTFFEEDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv32_519	121	RMELDKTFFEEDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv11_519	121	RMELDKTFFEEDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv28_519	121	RMELDKTFFEEDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv96_519	121	RMELDKTFFEEDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv02_519	121	RMELDKTFFEEDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv03_519	121	RMELDKTFFEEDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv04_519	121	RMELDKTFFEEDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv05_519	121	RMELDKTFFEEDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv01_519	121	RMELDKTFFEEDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv07_519	121	RMELDKTFFEEDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv12_519	121	RMELDKTFFEEDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv18_519	121	RMELDKTFFEEDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv19_519	121	RMELDKTFFEEDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv21_519aaa	121	RMELDKTFFEEDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv27_519	121	RMELDKTFFEEDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv20_519aaa	121	RMELDKTFFEEDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv06_519aaa	121	RMELDKTFFEEDEINSTVVA	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
zv29_519aaa	121	RMELDKTFFEEDEINSTVVS	ALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERK

FIG. 22A

```

z2491_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv26_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv22_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
fa1090_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv32_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv11_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv28_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv96_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv02_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv03_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv04_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv05_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv01_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv07_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv12_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv18_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv19_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv21_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv27_519 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv20_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv06_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv29_519ass 181 KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR

```

```

z2491_519 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv26_519 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv22_519ass 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
fa1090_519 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv32_519 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv11_519 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv28_519 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv96_519 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv02_519 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv03_519 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv04_519 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv05_519 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv01_519 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv07_519 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv12_519 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv18_519 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv19_519 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv21_519ass 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv27_519 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv20_519ass 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv06_519ass 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSM
zv29_519ass 241 LVAEANAFAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL

```

```

z2491_519 301 ISAGMKIIDSSKTAK*
zv26_519 301 ISAGMKIIDSSKTAK*
zv22_519ass 301 ISAGMKIIDSSKTAK*
fa1090_519 301 ISAGMKIIDSSKTAK*
zv32_519 301 ISAGMKIIDSSKTAK*
zv11_519 301 ISAGMKIIDSSKTAK*
zv28_519 301 ISAGMKIIDSSKTAK*
zv96_519 301 ISAGMKIIDSSKTAK*
zv02_519 301 ISAGMKIIDSSKTAK*
zv03_519 301 ISAGMKIIDSSKTAK*
zv04_519 301 ISAGMKIIDSSKTAK*
zv05_519 301 ISAGMKIIDSSKTAK*
zv01_519 301 ISAGMKIIDSSKTAK*
zv07_519 301 ISAGMKIIDSSKTAK*
zv12_519 301 ISAGMKIIDSSKTAK*
zv18_519 301 ISAGMKIIDSSKTAK*
zv19_519 301 ISAGMKIIDSSKTAK*
zv21_519ass 301 ISAGMKIIDSSKTAK*
zv27_519 301 ISAGMKIIDSSKTAK*
zv20_519ass 301 ISAGMKIIDSSKTAK*
zv06_519ass 301 ISAGMKIIDSSKTAK*
zv29_519ass 301 ISAGMKIIDSSKTAK*

```

Fig. 22B

**Fig. 23A**

**Fig. 23B**

**Fig. 23C**

fa1090	361	DDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm33asbc	361	DDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm32asbc	361	DDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm23asbc	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm27bc	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm09	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm10	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm24	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm25	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm14	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm04	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm11asbc	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm08n	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm96	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm01	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm02	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm03	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm07	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm12	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm18	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm19	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm20	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm21	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm06	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm17	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm13	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm05	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
z2491	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm22	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm26	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm28	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm29asbc	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm16	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm15	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm31asbc	361	VDRHYITLGAPLEFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
fa1090	421	QKTTGYVWQLLPNGMKPEYRP*
zm33asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm32asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm23asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm27bc	421	QKTTGYVWQLLPNGMKPEYRP*
zm09	421	QKTTGYVWQLLPNGMKPEYRP*
zm10	421	QKTTGYVWQLLPNGMKPEYRP*
zm24	421	QKTTGYVWQLLPNGMKPEYRP*
zm25	421	QKTTGYVWQLLPNGMKPEYRP*
zm14	421	QKTTGYVWQLLPNGMKPEYRP*
zm04	421	QKTTGYVWQLLPNGMKPEYRP*
zm11asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm08n	421	QKTTGYVWQLLPNGMKPEYRP*
zm96	421	QKTTGYVWQLLPNGMKPEYRP*
zm01	421	QKTTGYVWQLLPNGMKPEYRP*
zm02	421	QKTTGYVWQLLPNGMKPEYRP*
zm03	421	QKTTGYVWQLLPNGMKPEYRP*
zm07	421	QKTTGYVWQLLPNGMKPEYRP*
zm12	421	QKTTGYVWQLLPNGMKPEYRP*
zm18	421	QKTTGYVWQLLPNGMKPEYRP*
zm19	421	QKTTGYVWQLLPNGMKPEYRP*
zm20	421	QKTTGYVWQLLPNGMKPEYRP*
zm21	421	QKTTGYVWQLLPNGMKPEYRP*
zm06	421	QKTTGYVWQLLPNGMKPEYRP*
zm17	421	QKTTGYVWQLLPNGMKPEYRP*
zm13	421	QKTTGYVWQLLPNGMKPEYRP*
zm05	421	QKTTGYVWQLLPNGMKPEYRP*
z2491	421	QKTTGYVWQLLPNGMKPEYRP*
zm22	421	QKTTGYVWQLLPNGMKPEYRP*
zm26	421	QKTTGYVWQLLPNGMKPEYRP*
zm28	421	QKTTGYVWQLLPNGMKPEYRP*
zm29asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm16	421	QKTTGYVWQLLPNGMKPEYRP*
zm15	421	QKTTGYVWQLLPNGMKPEYRP*
zm31asbc	421	QKTTGYVWQLLPNGMKPEYRP*

Fig. 23D